

Qy 2 SSNLS 7
|||||
Db 5 SSNLS 10

RESULT 38
ABM55576 standard; protein; 83 AA.

ABM55576;

20-OCT-2003 (first entry)

Propionibacterium acnes predicted ORF-encoded polypeptide #20252.

Acne vulgaris; antibiorrhoeic; dermatological; antibacterial;

immunostimulant; immune response; vaccine.

Propionibacterium acnes.

WO2003033515-A1.

24-APR-2003.

11-OCT-2002; 2002WO-US032727.

15-OCT-2001; 2001US-00978825.

(CORI-) CORIXA CORP.

Mitcham JL, Skeiky YAW, Persing DH, Bhatia A, Maisonneuve JL,

Zhang Y, Wang S, Jen S, Lodes MJ, Benson DR, Jones R, Carter D,

Barth B, Vallave-Douglas J;

WPI; 2003-381789/36.

N-PSDB; ACP64526.

New Propionibacterium acnes polypeptides and polynucleotides encoding the polypeptide, useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein.

Example 1; SEQ ID NO 20252; 1481bp; English.

The invention relates to an isolated polynucleotide (ACF64435-ACF64733)

encoding a Propionibacterium acnes protein. The invention also relates to polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to immunogenic fragments of P. acnes polypeptides. The invention

additionally encompasses expression vectors and host cells comprising a polynucleotide of the invention; antibodies against polypeptides of the invention; fusion proteins comprising a polypeptide of the invention; a method for stimulating an immune response specific for a P. acnes

polypeptide and an isolated T cell population comprising T cells prepared via this method; a vaccine composition (comprising P. acnes polypeptides, polynucleotides, antibodies, fusion proteins, T cell populations, or

antigen-presenting cells that express the polypeptide); a method and kit for detecting or determining the presence or absence of P. acnes in a patient; and a method for inhibiting the development of P. acnes in a

patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion proteins, T cell populations or antigen-presenting cells that express the

polypeptides are useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes

protein. The polynucleotides can also be used as probes or primers for nucleic acid hybridisation. The vaccine composition is useful for the

stimulation of an immune response against P. acnes, or for treating acne, and the kit is useful for performing a diagnostic assay. The present

sequence represents a polypeptide predicted to be encoded by an ORF (open reading frame) contained within the P. acnes polynucleotides of the

invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly

from WPIO at http://wipo.int/pub/published_pct_sequences

Sequence 83 AA;

Query Match 81.1%; Score 30; DB 6; Length 83;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SSNLS 7
|||||
Db 5 SSNLS 10

RESULT 39

ABU27913 standard; protein; 167 AA.

ABU27913;

19-JUN-2003 (first entry)

Protein encoded by Prokaryotic essential gene #13440.

Antisense; prokaryotic essential gene; cell proliferation; drug design.

Enterobacter cloacae.

WO200277183-A2.

03-OCT-2002.

21-MAR-2002; 2002WO-US009107.

21-MAR-2001; 2001US-00815242.

06-SEP-2001; 2001US-00948993.

25-OCT-2001; 2001US-0342923P.

08-FEB-2002; 2002US-00072851.

06-MAR-2002; 2002US-0362699P.

(ELIT-) ELITRA PHARM INC.

Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zykkind JW;

Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

WPI; 2003-029926/02.

N-PSDB; ACA31783.

New antisense nucleic acids, useful for identifying proteins or screening

for homologous nucleic acids required for cellular proliferation to

isolate candidate molecules for rational drug discovery programs.

Claim 25; SEQ ID NO 55837; 1766bp; English.

The invention relates to an isolated nucleic acid comprising any one of

the 623 antisense sequences given in the specification where expression

of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid

encoding a polypeptide whose expression is inhibited by the antisense

nucleic acid; (2) a host cell containing the vector; (3) an isolated

polypeptide or its fragment whose expression is inhibited by the

antisense nucleic acid; (4) an antibody capable of specifically binding

the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular

proliferation or the activity of a gene in an operon required for

proliferation; (7) identifying a compound that influences the activity of

the gene product or that has an activity against a biological pathway

required for proliferation, or that inhibits cellular proliferation; (8)

identifying a gene required for cellular proliferation or the biological

pathway in which a proliferation-required gene or its gene product lies

or a gene on which the test compound that inhibits proliferation of an

organism acts; (9) manufacturing an antibiotic; (10) profiling a

compound's activity; (11) a culture comprising strains in which the gene

product is overexpressed or underexpressed; (12) determining the extent

to which each of the strains is present in a culture or collection of

strains; or (13) identifying the target of a compound that inhibits the

proliferation of an organism. The antisense nucleic acids are useful for

identifying proteins or screening for homologous nucleic acids required

for cellular proliferation to isolate candidate molecules for rational

CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pcc_sequences
XX
SQ Sequence 167 AA;

Query Match 81.1%; Score 30; DB 6; Length 167;
Best Local Similarity 83.3%; Pred. No. 4e+02; Mismatches 0; Gaps 0;
Matches 5; Conservative 1; Indels 0; Gaps 0;

QY 1 YSSNLH 6
|:||||
Db 19 YASNLH 24

RESULT 40
AAG49871
ID AAG49871 standard; protein; 182 AA.
XX
AC AAG49871;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 63135.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
PD
XX 06-SEP-2000.
PF
XX 25-FEB-2000; 2000EP-00301439.
XX
PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 23-APR-1999; 99US-0130891P.
PR 28-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 06-MAY-1999; 99US-0132487P.
PR 07-MAY-1999; 99US-0132863P.
PR 11-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134370P.
PR 18-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135629P.

PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139492P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139500P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144086P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144312P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144684P.
PR 21-JUL-1999; 99US-0144614P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145244P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145813P.
PR 27-JUL-1999; 99US-0145818P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.

PR 03-AUG-1999; 99US-0147038P.
 PR 04-AUG-1999; 99US-0147204P.
 PR 04-AUG-1999; 99US-0147302P.
 PR 05-AUG-1999; 99US-0147192P.
 PR 05-AUG-1999; 99US-0147260P.
 PR 06-AUG-1999; 99US-0147203P.
 PR 06-AUG-1999; 99US-0147416P.
 PR 09-AUG-1999; 99US-0147493P.
 PR 10-AUG-1999; 99US-0147935P.
 PR 11-AUG-1999; 99US-0148319P.
 PR 12-AUG-1999; 99US-0148341P.
 PR 13-AUG-1999; 99US-0148565P.
 PR 13-AUG-1999; 99US-0148684P.
 PR 16-AUG-1999; 99US-0149368P.
 PR 17-AUG-1999; 99US-0149175P.
 PR 18-AUG-1999; 99US-0149426P.
 PR 20-AUG-1999; 99US-0149722P.
 PR 20-AUG-1999; 99US-0149723P.
 PR 20-AUG-1999; 99US-0149929P.
 PR 23-AUG-1999; 99US-0149902P.
 PR 23-AUG-1999; 99US-0149930P.
 PR 25-AUG-1999; 99US-0150566P.
 PR 26-AUG-1999; 99US-0150884P.
 PR 27-AUG-1999; 99US-0151065P.
 PR 27-AUG-1999; 99US-0151066P.
 PR 27-AUG-1999; 99US-0151080P.
 PR 30-AUG-1999; 99US-0151303P.
 PR 31-AUG-1999; 99US-0151438P.
 PR 01-SEP-1999; 99US-0151930P.
 PR 07-SEP-1999; 99US-0152363P.
 PR 10-SEP-1999; 99US-0153070P.
 PR 13-SEP-1999; 99US-0153758P.
 PR 15-SEP-1999; 99US-0154018P.
 PR 16-SEP-1999; 99US-0154039P.
 PR 20-SEP-1999; 99US-0154779P.
 PR 22-SEP-1999; 99US-0155139P.
 PR 23-SEP-1999; 99US-0155486P.
 PR 24-SEP-1999; 99US-0155659P.
 PR 28-SEP-1999; 99US-0156458P.
 PR 29-SEP-1999; 99US-0156596P.
 PR 04-OCT-1999; 99US-0157117P.
 PR 05-OCT-1999; 99US-0157753P.
 PR 06-OCT-1999; 99US-0157865P.
 PR 07-OCT-1999; 99US-0158029P.
 PR 08-OCT-1999; 99US-0158232P.
 PR 12-OCT-1999; 99US-0158369P.
 PR 13-OCT-1999; 99US-0159293P.
 PR 13-OCT-1999; 99US-0159294P.
 PR 13-OCT-1999; 99US-0159295P.
 PR 14-OCT-1999; 99US-0159329P.
 PR 14-OCT-1999; 99US-0159330P.
 PR 14-OCT-1999; 99US-0159331P.
 PR 14-OCT-1999; 99US-0159637P.
 PR 14-OCT-1999; 99US-0159638P.
 PR 18-OCT-1999; 99US-0159584P.
 PR 21-OCT-1999; 99US-0160741P.
 PR 21-OCT-1999; 99US-0160767P.
 PR 21-OCT-1999; 99US-0160768P.
 PR 21-OCT-1999; 99US-0160770P.
 PR 21-OCT-1999; 99US-0160814P.
 PR 21-OCT-1999; 99US-0160815P.
 PR 22-OCT-1999; 99US-0160980P.
 PR 22-OCT-1999; 99US-0160981P.
 PR 22-OCT-1999; 99US-0160989P.
 PR 25-OCT-1999; 99US-0161404P.
 PR 25-OCT-1999; 99US-0161405P.
 PR 25-OCT-1999; 99US-0161406P.
 PR 26-OCT-1999; 99US-0161359P.
 PR 26-OCT-1999; 99US-0161360P.
 PR 26-OCT-1999; 99US-0161361P.
 PR 28-OCT-1999; 99US-016120P.
 PR 28-OCT-1999; 99US-0161992P.

PR 28-OCT-1999; 99US-0161993P.
 PR 29-OCT-1999; 99US-0162142P.

Query Match 81.1%; Score 30; DB 3; Length 182;
 Best Local Similarity 71.4%; Pred. No. 4.4e+02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSSNLS 7
 :|||
 Db 100 FSTNLS 106

Search completed: December 17, 2004, 18:29:05
 Job time : 23.2753 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using SW model

Run on: December 17, 2004, 18:13:27 ; Search time 4.24719 Seconds
(without alignments)
109.302 Million cell updates/sec

Title: US-10-089-500-7

Perfect score: 37

Sequence: 1 YSSNLS 7

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents, AA:*
1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/ECTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37	100.0	128	4	US-09-225-322B-10
2	37	100.0	128	4	US-09-225-322B-19
3	37	100.0	128	4	US-09-764-304-10
4	37	100.0	128	4	US-09-764-304-19
5	34	91.9	273	2	US-08-403-853-18
6	33	89.2	474	4	US-09-823-823-24
7	32	86.5	36	4	US-09-570-921-100
8	32	86.5	489	1	US-08-434-702-4
9	31	83.8	347	4	US-09-495-406-13
10	31	83.8	347	4	US-09-816-028A-17
11	31	83.8	347	4	US-10-303-162-17
12	30	81.1	172	4	US-09-248-796A-23868
13	30	81.1	172	4	US-09-270-767-41649
14	30	81.1	238	4	US-09-270-767-45029
15	30	81.1	410	4	US-09-252-991A-28155
16	30	81.1	458	4	US-09-538-092-1356
17	30	81.1	609	4	US-09-198-452A-579
18	30	81.1	741	4	US-09-328-352-5898
19	30	81.1	788	3	US-08-630-915A-30
20	30	81.1	788	4	US-09-879-957-30
21	29	78.4	107	2	US-08-652-558-2
22	29	78.4	107	2	US-08-652-558-35
23	29	78.4	107	4	US-09-254-189-1
24	29	78.4	219	4	US-09-270-767-45934
25	29	78.4	329	4	US-09-252-991A-21191
26	29	78.4	496	4	US-09-710-279-1386
27	29	78.4	497	3	US-09-134-001C-4411

28	29	78.4	677	2	US-08-522-269B-3	Sequence 3, Appl1
29	29	78.4	677	3	US-09-294-923-3	Sequence 3, Appl1
30	29	78.4	747	3	US-09-291-922-2	Sequence 2, Appl1
31	28	75.7	7	1	US-08-137-117D-118	Sequence 18, App
32	28	75.7	7	2	US-08-480-434-78	Sequence 78, Appl
33	28	75.7	7	2	US-08-436-717-118	Sequence 118, App
34	28	75.7	7	2	US-08-053-451B-78	Sequence 78, Appl
35	28	75.7	7	3	US-08-649-100-13	Sequence 13, Appl
36	28	75.7	7	4	US-08-649-100-29	Sequence 29, Appl
37	28	75.7	7	4	US-09-563-222C-39	Sequence 39, Appl
38	28	75.7	32	3	US-08-525-539A-14	Sequence 14, Appl
39	28	75.7	98	4	US-09-134-000C-5271	Sequence 5271, Ap
40	28	75.7	99	4	US-09-248-796A-19786	Sequence 19786, A
41	28	75.7	102	3	US-09-199-149-10	Sequence 10, Appl
42	28	75.7	102	3	US-09-199-149-29	Sequence 29, Appl
43	28	75.7	105	3	US-09-199-149-31	Sequence 31, Appl
44	28	75.7	107	1	US-08-458-516-8	Sequence 8, Appl1
45	28	75.7	107	1	US-08-458-516-9	Sequence 9, Appl1

ALIGNMENTS

```

RESULT 1
US-09-225-322B-10
; Sequence 10, Application US/09225322B
; Patent No. 6437098
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUMANA, YOSHIOHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-103
; CURRENT APPLICATION NUMBER: US/09/225,322B
; CURRENT FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 10
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CDNA KM-641
US-09-225-322B-10

Query Match          100.0%  Score 37;  DB 4;  Length 128;
Best Local Similarity 100.0%  Pred. No. 5.9;
Matches 7;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

QY      1 YSSNLS 7
Db       70 YSSNLS 76

RESULT 2
US-09-225-322B-19
; Sequence 19, Application US/09225322B
; Patent No. 6437098
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO

```

APPLICANT: HASEGAWA, MAMORU
APPLICANT: MIYAJI, HIROMASA
APPLICANT: KUMAWA, YOSHITAKA
TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
FILE REFERENCE: 249-101
CURRENT APPLICATION NUMBER: US/09/225,322B
CURRENT FILING DATE: 1999-01-05
PRIOR APPLICATION NUMBER: US 08/454,680
PRIOR FILING DATE: 1995-05-31
PRIOR APPLICATION NUMBER: US 08/408,133
PRIOR FILING DATE: 1995-03-21
PRIOR APPLICATION NUMBER: US 08/292,178
PRIOR FILING DATE: 1994-08-17
PRIOR APPLICATION NUMBER: US07/947,674
PRIOR FILING DATE: 1992-09-17
PRIOR APPLICATION NUMBER: JP 3-238375
PRIOR FILING DATE: 1991-09-18
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 19
LENGTH: 128
TYPE: PRF
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:light chain
US-09-225-322B-19

Query Match 100.0%; Score 37; DB 4; Length 128;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSSNLS 7
Db 70 YSSNLS 76

RESULT 3
US-09-764-304-10
Sequence 10, Application US/09764304
Patent No. 6495666
GENERAL INFORMATION:
APPLICANT: SHITTARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: HASEGAWA, MAMORU
APPLICANT: MIYAJI, HIROMASA
APPLICANT: KUMAWA, YOSHITAKA
TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
FILE REFERENCE: 249-101
CURRENT APPLICATION NUMBER: US/09/764,304
CURRENT FILING DATE: 2001-01-19
PRIOR APPLICATION NUMBER: 09/225,322
PRIOR FILING DATE: 1999-01-05
PRIOR APPLICATION NUMBER: US 08/454,680
PRIOR FILING DATE: 1995-05-31
PRIOR APPLICATION NUMBER: US 08/408,133
PRIOR FILING DATE: 1995-03-21
PRIOR APPLICATION NUMBER: US 08/292,178
PRIOR FILING DATE: 1994-08-17
PRIOR APPLICATION NUMBER: US07/947,674
PRIOR FILING DATE: 1992-09-17
PRIOR APPLICATION NUMBER: JP 3-238375
PRIOR FILING DATE: 1991-09-18
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 10
LENGTH: 128
TYPE: PRF
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: CDNA KM-641
US-09-764-304-10

Query Match 100.0%; Score 37; DB 4; Length 128;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSSNLS 7
Db 70 YSSNLS 76

RESULT 4
US-09-764-304-19
Sequence 19, Application US/09764304
Patent No. 6495666
GENERAL INFORMATION:
APPLICANT: SHITTARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: HASEGAWA, MAMORU
APPLICANT: MIYAJI, HIROMASA
APPLICANT: KUMAWA, YOSHITAKA
TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
FILE REFERENCE: 249-101
CURRENT APPLICATION NUMBER: US/09/764,304
CURRENT FILING DATE: 2001-01-19
PRIOR APPLICATION NUMBER: 09/225,322
PRIOR FILING DATE: 1999-01-05
PRIOR APPLICATION NUMBER: US 08/454,680
PRIOR FILING DATE: 1995-05-31
PRIOR APPLICATION NUMBER: US 08/408,133
PRIOR FILING DATE: 1995-03-21
PRIOR APPLICATION NUMBER: US 08/292,178
PRIOR FILING DATE: 1994-08-17
PRIOR APPLICATION NUMBER: US07/947,674
PRIOR FILING DATE: 1992-09-17
PRIOR APPLICATION NUMBER: JP 3-238375
PRIOR FILING DATE: 1991-09-18
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 19
LENGTH: 128
TYPE: PRF
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: light chain
OTHER INFORMATION: variable region
US-09-764-304-19

Query Match 100.0%; Score 37; DB 4; Length 128;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSSNLS 7
Db 70 YSSNLS 76

RESULT 5
US-08-403-853-18
Sequence 18, Application US/08403853
Patent No. 5844094
GENERAL INFORMATION:
APPLICANT: HUDSON, Peter J.
APPLICANT: LAH, Maria
APPLICANT: KORRT, Alex A.
APPLICANT: IRVING, Robert A.
APPLICANT: ATWELL, John L.
APPLICANT: MALBY, Rodyn L.
APPLICANT: POWER, Barbara E.
APPLICANT: COLMAN, Peter M.
TITLE OF INVENTION: TARGET BINDING POLYPEPTIDE
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500

CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/403,853
FILING DATE: 30-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/AU93/00491
FILING DATE: 24-SEP-1993
APPLICATION NUMBER: AU PL 4973
FILING DATE: 25-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16786/189/CHAC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-403-853-18

Query Match 91.9%; Score 34; DB 2; Length 273;
Best Local Similarity 85.7%; Pred. No. 47;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLS 7
Db 208 YTSNLS 214

RESULT 6
US-09-823-823-24
Sequence 24, Application US/09823823
Patent No. 6635904
GENERAL INFORMATION:
APPLICANT: Yamamoto, Satoshi
APPLICANT: Kasai, Hiroaki
APPLICANT: Nakamura, Shoko
APPLICANT: Suzuki, Makoto
APPLICANT: Hamada, Tohtu
TITLE OF INVENTION: METHOD FOR IDENTIFICATION AND DETECTION OF MICROORGANISMS USING G
FILE REFERENCE: 12817-004001
CURRENT APPLICATION NUMBER: US/09/823,823
CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: US 09/208,688
PRIOR FILING DATE: 1998-12-10
PRIOR APPLICATION NUMBER: JP 97/343316
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 80
SOFTWARE: PatentIn version 2.0
SEQ ID NO 24
LENGTH: 474
TYPE: PRT
ORGANISM: Cytophaga lytica
US-09-823-823-24

Query Match 89.2%; Score 33; DB 4; Length 474;
Best Local Similarity 85.7%; Pred. No. 1.3e+02;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 YSSNLS 7
Db 164 YSNLS 170

RESULT 7
US-09-570-921-100
Sequence 100, Application US/09570921
Patent No. 6455265
GENERAL INFORMATION:
APPLICANT: SERRES, PIERRE-FRANCOIS
TITLE OF INVENTION: METHOD FOR OBTAINING VACCINES FOR PREVENTING THE
FILE REFERENCE: 106213
CURRENT APPLICATION NUMBER: US/09/570,921
CURRENT FILING DATE: 2000-05-15
PRIOR APPLICATION NUMBER: PCT/FR98/02447
PRIOR FILING DATE: 1998-11-17
PRIOR APPLICATION NUMBER: FR/97/14387
PRIOR FILING DATE: 1997-11-17
NUMBER OF SEQ ID NOS: 144
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 100
LENGTH: 36
TYPE: PRT
ORGANISM: Human
US-09-570-921-100

Query Match 86.5%; Score 32; DB 4; Length 36;
Best Local Similarity 71.4%; Pred. No. 14;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLS 7
Db 16 YTSNLS 22

RESULT 8
US-08-434-702-4
Sequence 4, Application US/08434702
Patent No. 5554743
GENERAL INFORMATION:
APPLICANT: Bennett, Alan B.
APPLICANT: Fischer, Robert L.
APPLICANT: Lashbrook, Coralie
TITLE OF INVENTION: Endo-1,4-beta-Glucanase Genes and Their
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew
STREET: One Market Plaza, Stewart Street Tower
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/434,702
FILING DATE: 04-MAY-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/271,883
FILING DATE: 07-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/687,466
FILING DATE: 18-APR-1991

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/511,417
; FILING DATE: 20-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 02307E-30430US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-5043
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 489 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-434-702-4

Query Match      86.5%; Score 32; DB 1; Length 489;
Best Local Similarity 85.7%; Pred. No. 2e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 YSSNLS 7
Db      216 YSSLS 222

RESULT 9
US-09-495-406-13
; Sequence 13, Application US/09495406
; Patent No. 6503744
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Michel
; APPLICANT: Wakarchuk, Warren W.
; TITLE OF INVENTION: National Research Council of Canada
; TITLE OF INVENTION: Gangliosides and Ganglioside Mimics
; FILE REFERENCE: 019633-000110US
; CURRENT APPLICATION NUMBER: US/09/495,406
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: US 60/118,213
; PRIOR FILING DATE: 1999-02-01
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 13
; LENGTH: 347
; TYPE: PRT
; ORGANISM: Campylobacter jejuni
US-09-495-406-13

Query Match      83.8%; Score 31; DB 4; Length 347;
Best Local Similarity 71.4%; Pred. No. 2.2e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 YSSNLS 7
Db      268 FSSNHS 274

RESULT 10
US-09-816-028A-17
; Sequence 17, Application US/09816028A
; Patent No. 6699705
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Michel
; APPLICANT: Wakarchuk, Warren W.
; TITLE OF INVENTION: National Research Council of Canada
; TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
; FILE REFERENCE: 019633-000110US
; CURRENT APPLICATION NUMBER: US/09/816,028A
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/118,213
; PRIOR FILING DATE: 1999-02-01
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 13
; LENGTH: 347
; TYPE: PRT
; ORGANISM: Campylobacter jejuni
US-09-816-028A-17
```

```

; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: US 09/495,406
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 17
; LENGTH: 347
; TYPE: PRT
; ORGANISM: Campylobacter jejuni
; FEATURE:
; OTHER INFORMATION: beta-1,4 N-acetylglactosaminyl (GalNAc)
; OTHER INFORMATION: transferase from C. jejuni strain OH4384 (ORF 5a)
; OTHER INFORMATION: of lipooligosaccharide (LOS) biosynthesis locus)
US-09-816-028A-17

Query Match      83.8%; Score 31; DB 4; Length 347;
Best Local Similarity 71.4%; Pred. No. 2.2e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 YSSNLS 7
Db      268 FSSNHS 274

RESULT 11
US-10-303-162-17
; Sequence 17, Application US/10303162
; Patent No. 6723545
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Michel
; APPLICANT: Wakarchuk, Warren W.
; APPLICANT: National Research Council of Canada
; TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
; TITLE OF INVENTION: Gangliosides and Ganglioside Mimics
; FILE REFERENCE: 019633-000110US
; CURRENT APPLICATION NUMBER: US/10/303,162
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US/09/816,028
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/118,213
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: US 09/495,406
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 17
; LENGTH: 347
; TYPE: PRT
; ORGANISM: Campylobacter jejuni
; FEATURE:
; OTHER INFORMATION: beta-1,4 N-acetylglactosaminyl (GalNAc)
; OTHER INFORMATION: transferase from C. jejuni strain OH4384 (ORF 5a)
; OTHER INFORMATION: of lipooligosaccharide (LOS) biosynthesis locus)
US-10-303-162-17

Query Match      83.8%; Score 31; DB 4; Length 347;
Best Local Similarity 71.4%; Pred. No. 2.2e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 YSSNLS 7
Db      268 FSSNHS 274

RESULT 12
US-09-248-796A-22868
; Sequence 22868, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
```

;; CURRENT APPLICATION NUMBER: US/09/248,796A
;; CURRENT FILING DATE: 1999-02-12
;; PRIOR APPLICATION NUMBER: US 60/074,725
;; PRIOR FILING DATE: 1998-02-13
;; PRIOR APPLICATION NUMBER: US 60/096,409
;; PRIOR FILING DATE: 1998-08-13
;; NUMBER OF SEQ ID NOS: 28208
;; SEQ ID NO 22868
;; LENGTH: 67
;; TYPE: PRT
;; ORGANISM: *Candida albicans*
US-09-248-796A-22868

Query Match 81.1%; Score 30; DB 4; Length 67;
Best Local Similarity 83.3%; Pred. No. 65;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSSNLH 6
Db 44 YSSNLH 49

RESULT 13

US-09-270-767-41649
; Sequence 41649, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 41649
; LENGTH: 172
; TYPE: PRT
; ORGANISM: *Drosophila melanogaster*
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-41649

Query Match 81.1%; Score 30; DB 4; Length 172;
Best Local Similarity 83.3%; Pred. No. 1,7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSSNLH 6
Db 157 YSSNLH 162

RESULT 14

US-09-270-767-45029
; Sequence 45029, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45029
; LENGTH: 238
; TYPE: PRT
; ORGANISM: *Drosophila melanogaster*
US-09-270-767-45029

Query Match 81.1%; Score 30; DB 4; Length 238;
Best Local Similarity 85.7%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YSSNLH 7
Db 232 YSSNLH 238

RESULT 15
US-09-252-991A-28155
; Sequence 28155, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,768
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 28155
; LENGTH: 410
; TYPE: PRT
; ORGANISM: *Pseudomonas aeruginosa*
US-09-252-991A-28155

Query Match 81.1%; Score 30; DB 4; Length 410;
Best Local Similarity 83.3%; Pred. No. 4.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSSNLH 6
Db 260 YSSNLH 265

RESULT 16
US-09-538-092-1356
; Sequence 1356, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Glot, Loic
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CurafastSeqFormatter Version 0.9
; SEQ ID NO 1356
; LENGTH: 458
; TYPE: PRT
; ORGANISM: *Homo sapiens*
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number Q16600
US-09-538-092-1356

Query Match 81.1%; Score 30; DB 4; Length 458;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SSNLH 7
Db 443 SSNLH 448

RESULT 17

US-09-198-452A-579
; Sequence 579, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 579
; LENGTH: 609
; TYPE: PRF
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; NAME/KEY: SITE
; LOCATION: 1...609
; OTHER INFORMATION: Xaa=unknown or other
US-09-198-452A-579

Query Match
Best Local Similarity 81.1%; Score 30; DB 4; Length 609;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSNLS 7
Db 126 SSNLS 131

RESULT 18
US-09-328-352-5898
; Sequence 5898, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5898
; LENGTH: 741
; TYPE: PRF
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5898

Query Match
Best Local Similarity 81.1%; Score 30; DB 4; Length 741;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLS 6
Db 512 YSSNLS 517

RESULT 19
US-08-630-915A-30
; Sequence 30, Application US/08630915A
; Patent No. 6309820
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: HOFFMAN, No. 6309820h
; APPLICANT: KAY, Brian K.
; APPLICANT: FOWLES, Dana M.
; APPLICANT: MCCONNELL, Stephen J.
; TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
; TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
; NUMBER OF SEQUENCES: 227
; CORRESPONDENCE ADDRESS:

ADDRESSER: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,915A
FILING DATE: 03-APR-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Mirock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-174
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 788 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-630-915A-30

Query Match
Best Local Similarity 81.1%; Score 30; DB 3; Length 788;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLS 7
Db 388 YSSNLS 394

RESULT 20
US-09-879-957-30
; Sequence 30, Application US/09879957
; Patent No. 6709821
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: HOFFMAN, No. 6709821h
; APPLICANT: KAY, Brian K.
; APPLICANT: FOWLES, Dana M.
; APPLICANT: MCCONNELL, Stephen J.
; TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
; TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
; NUMBER OF SEQUENCES: 227
; CORRESPONDENCE ADDRESS:
ADDRESSER: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/879,957
FILING DATE: 13-Jun-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/630,915

FILING DATE: 03-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Miarock, S. Leslie
REGISTRATION NUMBER: 18-872
REFERENCE/DOCKET NUMBER: 1101-174
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 788 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-09-879-957-30

Query Match 81.1%; Score 30; DB 4; Length 788;
Best Local Similarity 71.4%; Pred. No. 7.9e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YSSSLHS 7
Db 388 YSSNPHA 394

RESULT 21
US-08-652-558-2
Sequence 2, Application US/08652558
Patent No. 586155
GENERAL INFORMATION:
APPLICANT: LIN, AUGUSTINE YEE-THARN
TITLE OF INVENTION: HUMANIZED ANTIBODIES AND USES
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: BANNER & WITCOFF
STREET: 75 STATE STREET, 23RD FLOOR
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,558
FILING DATE: JUNE 6, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IB94/00387
FILING DATE: NOVEMBER 21, 1994
ATTORNEY/AGENT INFORMATION:
NAME: YANKWICH, LEON R.
REGISTRATION NUMBER: 30,237
REFERENCE/DOCKET NUMBER: 95,497-L
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-345-9100
TELEFAX: 617-345-9111
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-652-558-2

Query Match 78.4%; Score 29; DB 2; Length 107;
Best Local Similarity 71.4%; Pred. No. 1.6e+02;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 1 YSSSLHS 7
Db 50 YTSLSHS 56

RESULT 22
US-08-652-558-35
Sequence 35, Application US/08652558
Patent No. 586155
GENERAL INFORMATION:
APPLICANT: LIN, AUGUSTINE YEE-THARN
TITLE OF INVENTION: HUMANIZED ANTIBODIES AND USES
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: BANNER & WITCOFF
STREET: 75 STATE STREET, 23RD FLOOR
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,558
FILING DATE: JUNE 6, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IB94/00387
FILING DATE: NOVEMBER 21, 1994
ATTORNEY/AGENT INFORMATION:
NAME: YANKWICH, LEON R.
REGISTRATION NUMBER: 30,237
REFERENCE/DOCKET NUMBER: 95,497-L
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-345-9100
TELEFAX: 617-345-9111
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-652-558-35

Query Match 78.4%; Score 29; DB 2; Length 107;
Best Local Similarity 71.4%; Pred. No. 1.6e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSSSLHS 7
Db 50 YTSLSHS 56

RESULT 23
US-09-254-189-1
Sequence 1, Application US/09254189
Patent No. 6150792
GENERAL INFORMATION:
APPLICANT: Lundquist, Tomas
TITLE OF INVENTION: Sequence Listing
FILE REFERENCE: 3526/00000
CURRENT APPLICATION NUMBER: US/09/254,189
EARLIER FILING DATE: 1999-03-02
PRIOR APPLICATION NUMBER: 00/000,000
NUMBER OF SEQ ID NOS: 6

```
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:humanized
; OTHER INFORMATION: monoclonal antibody
US-09-254-189-1

Query Match
Best Local Similarity 78.4%; Score 29; DB 3; Length 107;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLHS 7
|:|:|
Db 50 YTSLSLHS 56

RESULT 24
US-09-270-767-45934
; Sequence 45934, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 45934
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-45934

Query Match
Best Local Similarity 78.4%; Score 29; DB 4; Length 219;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLHS 7
|:|:|
Db 146 YATNIHS 152

RESULT 25
US-09-252-991A-21191
; Sequence 21191, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 21191
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-21191

Query Match
Best Local Similarity 78.4%; Score 29; DB 4; Length 329;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 YSSNLHS 7
|:|:|
Db 188 YSRNLHT 194

RESULT 26
US-09-710-279-1386
; Sequence 1386, Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/09/710,279
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1386
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-710-279-1386

Query Match
Best Local Similarity 78.4%; Score 29; DB 4; Length 496;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLH 6
|:|:|
Db 274 YDSNLH 279

RESULT 27
US-09-134-001C-4411
; Sequence 4411, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 4411
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4411

Query Match
Best Local Similarity 78.4%; Score 29; DB 3; Length 497;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLH 6
|:|:|
Db 275 YDSNLH 280

RESULT 28
US-08-522-269B-3
; Sequence 3, Application US/08522269B
; Patent No. 5919690
```


GENERAL INFORMATION:
APPLICANT: Knapp, Inge Helmer
APPLICANT: Hjort, Carsten M.
APPLICANT: Halkier, Torben
APPLICANT: Kofoed, Lene Venke
TITLE OF INVENTION: An Alpha-Galactosidase Enzyme
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 59196900 No. 59196900dsk of No. 59196900h America, Inc.
STREET: 405 Lexington Avenue, Suite 6400
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/522,269B
FILING DATE: 12-SEP-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gregg, Valecia A.
REGISTRATION NUMBER: 37,125
REFERENCE/DOCKET NUMBER: 3935.204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 867 0123
TELEFAX: 212 867 0298
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 677 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-522-269B-3

Query Match 78.4%; Score 29; DB 2; Length 677;
Best Local Similarity 71.4%; Pred. No. 1e+03;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 YSSNLS 7
DB 212 YSSHLN 218

RESULT 29
US-09-294-923-3
Sequence 3, Application US/09294923
Patent No. 6197566
GENERAL INFORMATION:
APPLICANT: Knapp, Inge Helmer
APPLICANT: Hjort, Carsten M.
APPLICANT: Halkier, Torben
APPLICANT: Kofoed, Lene Venke
TITLE OF INVENTION: An Alpha-Galactosidase Enzyme
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 61975660 No. 6197566dsk of No. 6197566ch America, Inc.
STREET: 405 Lexington Avenue, Suite 6400
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/294,923

FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/522,269
FILING DATE: 12-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Gregg, Valecia A.
REGISTRATION NUMBER: 37,125
REFERENCE/DOCKET NUMBER: 3935.204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 867 0123
TELEFAX: 212 867 0298
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 677 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-294-923-3

Query Match 78.4%; Score 29; DB 3; Length 677;
Best Local Similarity 71.4%; Pred. No. 1e+03;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 YSSNLS 7
DB 212 YSSHLN 218

RESULT 30
US-09-291-922-2
Sequence 2, Application US/09291922
Patent No. 6183776
GENERAL INFORMATION:
APPLICANT: Allen, Steve
APPLICANT: Hiltz, Bill
APPLICANT: Kinney, Tony
APPLICANT: Tingey, Scott
TITLE OF INVENTION: Plant Sugar Transport Proteins
FILE REFERENCE: BB-1163
CURRENT APPLICATION NUMBER: US/09/291,922
EARLIER FILING DATE: 1999-04-14
EARLIER APPLICATION NUMBER: 60/083,044
EARLIER FILING DATE: April 24, 1998
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Microsoft Office 97
SEQ ID NO 2
LENGTH: 747
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
NAME/KEY: UNSURE
LOCATION: (129)
FEATURE:
NAME/KEY: UNSURE
LOCATION: (133) ..(134)
FEATURE:
NAME/KEY: UNSURE
LOCATION: (144)
FEATURE:
NAME/KEY: UNSURE
LOCATION: (178)
FEATURE:
NAME/KEY: UNSURE
LOCATION: (207)
FEATURE:
NAME/KEY: UNSURE
LOCATION: (218)
FEATURE:
NAME/KEY: UNSURE
LOCATION: (220)
FEATURE:

NAME/KEY: UNSURE
LOCATION: (236)
US-09-291-922-2

Query Match 78.4%; Score 29; DB 3; Length 747;
Best Local Similarity 71.4%; Pred. No. 1.2e+03;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YSNNLHS 7
Db 368 YEDNLS 374

RESULT 31
US-08-137-117D-118
; Sequence 118, Application US/08137117D
; Patent No. 5795965
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masaayuki
; APPLICANT: SATO, Koh
; APPLICANT: BENDIG, Mary
; APPLICANT: JONES, Steven
; APPLICANT: SAIIDANHA, Jose
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
; NUMBER OF SEQUENCES: 158
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/137,117D
; FILING DATE: 20-DEC-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/JP92/00544
; FILING DATE: 24-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 4-32084
; FILING DATE: 19-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 3-95476
; FILING DATE: 25-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 53466/126/AOK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ. ID NO: 118:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-137-117D-118

Query Match 75.7%; Score 28; DB 1; Length 7;
Best Local Similarity 71.4%; Pred. No. 3.8e+05;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 YSNNLHS 7
Db 1 YSNNLHS 7

Db 1 YTSRLHS 7

RESULT 32
US-08-480-434-78
; Sequence 78, Application US/08480434
; Patent No. 5811248
; GENERAL INFORMATION:
; APPLICANT: Charles C. Dillow, et al.
; TITLE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC ANTIGENS,
; TITLE OF INVENTION: ANTIBODIES THERETO, AND USES THEREOF
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,434
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Albert P. Halliwin
; REGISTRATION NUMBER: 25,227
; REFERENCE/DOCKET NUMBER: 7606-053
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 854-3660
; TELEFAX: (415) 854-3694
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ. ID NO: 78:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: N
; ANTI-SENSE: N
US-08-480-434-78

Query Match 75.7%; Score 28; DB 2; Length 7;
Best Local Similarity 71.4%; Pred. No. 3.8e+05;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YSNNLHS 7
Db 1 YTSRLHS 7

RESULT 33
US-08-436-717-118
; Sequence 118, Application US/08436717
; Patent No. 5817790
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masaayuki
; APPLICANT: SATO, Koh
; APPLICANT: BENDIG, Mary
; APPLICANT: JONES, Steven
; APPLICANT: SAIIDANHA, Jose
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
; NUMBER OF SEQUENCES: 158
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington

STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,717
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117
FILING DATE: 20-DEC-1993
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 4-32084
FILING DATE: 19-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 3-95476
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/126/AOK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 118:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-436-717-118

Query Match
Best Local Similarity 75.7%; Score 28; DB 2; Length 7;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YSSNLS 7
Db 1 YTSRLHS 7

RESULT 34
US-08-053-451B-78
Sequence 78, Application US/08053451B
Patent No. 595584
GENERAL INFORMATION:
APPLICANT: Chen, Francis W.
APPLICANT: D'Clow, Charles C.
APPLICANT: Calenoff, Emanuel
TITLE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC
TITLE OF INVENTION: ANTIGENS, ANTIBODIES THEREOF, AND USES THEREOF
NUMBER OF SEQUENCES: 176
CORRESPONDENCE ADDRESS:
ADDRESSEE: Penile & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/053,451B

FILING DATE: 26-APR-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 7606-033-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-3660
TELEFAX: 415-854-3694
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 78:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA
HYPOTHETICAL: N
ANTI-SENSE: N
US-08-053-451B-78

Query Match
Best Local Similarity 75.7%; Score 28; DB 2; Length 7;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YSSNLS 7
Db 1 YASRLHS 7

RESULT 35
US-08-649-100-13
Sequence 13, Application US/08649100
Patent No. 6114507
GENERAL INFORMATION:
APPLICANT: SHIRAKAWA, KAMON
APPLICANT: MATSUE, TOMOKAZU
APPLICANT: NAGATA, SHIGEKAZU
APPLICANT: CO, MAN SUNG
APPLICANT: VASQUEZ, MAXIMILIANO
TITLE OF INVENTION: ANTI-FAS LIGAND ANTIBODY AND ASSAY
TITLE OF INVENTION: METHOD USING THE ANTI-FAS LIGAND ANTIBODY
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: PO BOX 747
CITY: FALLS CHURCH
STATE: VA
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/649,100
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR, GERALD M
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1110-160
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide

US-08-649-100-13

Query Match 75.7%; Score 28; DB 3; Length 7;
Best Local Similarity 71.4%; Pred. No. 3.8e+05;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSNNLS 7
|:|
DB 1 YTSRLHS 7

RESULT 36
US-08-649-100-29
; Sequence 29, Application US/08649100
; Patent No. 6114507

; GENERAL INFORMATION:
; APPLICANT: SHIRAKAWA, KAMON
; APPLICANT: MATSUUE, TOMOKAZU
; APPLICANT: NAGATA, SHIGEKAZU
; APPLICANT: CO, MAN SUNG
; APPLICANT: VASQUEZ, MAXIMILIANO
; TITLE OF INVENTION: ANTI-FAS LIGAND ANTIBODY AND ASSAY
; TITLE OF INVENTION: METHOD USING THE ANTI-FAS LIGAND ANTIBODY
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
; STREET: PO BOX 747
; CITY: FALLS CHURCH
; STATE: VA
; COUNTRY: USA
; ZIP: 22040-0747

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/649,100
; FILING DATE:
; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:
; NAME: MURPHY JR, GERALD M
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 1110-160
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)
US-08-649-100-29

Query Match 75.7%; Score 28; DB 3; Length 7;
Best Local Similarity 71.4%; Pred. No. 3.8e+05;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSNNLS 7
|:|
DB 1 YTSRLHS 7

RESULT 37
US-09-563-222C-39
; Sequence 39, Application US/09563222C
; Patent No. 6696620

; GENERAL INFORMATION:
; APPLICANT: EPICYTE PHARMACEUTICALS, INC.
; APPLICANT: HIATT, ANDREW C.
; APPLICANT: HEIN, MITCH B.

; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS
; FILE REFERENCE: 068904-0501
; CURRENT APPLICATION NUMBER: US/09/563,222C
; CURRENT FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: PCT/US01/14349
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/563,222
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 39
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-563-222C-39

Query Match 75.7%; Score 28; DB 4; Length 7;
Best Local Similarity 71.4%; Pred. No. 3.8e+05;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSNNLS 7
|:|
DB 1 YASRLHS 7

RESULT 38
US-08-525-539A-14
; Sequence 14, Application US/08525539A
; Patent No. 6309636

; GENERAL INFORMATION:
; APPLICANT: DO COUTO, FERNANDO J.R.
; APPLICANT: CERIANI, ROBERTO L.
; APPLICANT: PETERSON, JERRY A.
; TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE
; TITLE OF INVENTION: MC3 ANTI-BA46 ANTIBODY, METHODS OF USE THEREOF, AND
; TITLE OF INVENTION: METHODS OF HUMANIZING ANTIBODY PEPTIDES
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/525,539A
; FILING DATE: 14-SEP-1995
; CLASSIFICATION: 424

; ATTORNEY/AGENT INFORMATION:
; NAME: DYLAN, TYLER
; REGISTRATION NUMBER: 37,612
; REFERENCE/DOCKET NUMBER: 27633-20001.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141

; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-525-539A-14

Query Match 75.7%; Score 28; DB 3; Length 32;
Best Local Similarity 71.4%; Pred. No. 73;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 YSSNLS 7
|:|:|
Db 1 YTSRLHS 7

RESULT 39
US-09-134-000C-5271

; Sequence 5271, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5271
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-5271

Query Match 75.7%; Score 28; DB 4; Length 98;
Best Local Similarity 57.1%; Pred. No. 2.3e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 YSSNLS 7
|:|:|
Db 54 YANNLHA 60

RESULT 40
US-09-248-796A-19786

; Sequence 19786, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 19786
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-19786

Query Match 75.7%; Score 28; DB 4; Length 99;
Best Local Similarity 83.3%; Pred. No. 2.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YSSNLS 6
|:|:|
Db 23 YSSSLH 28

Search completed: December 17, 2004, 18:32:09
Job time : 4.24719 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 17, 2004, 18:20:33 ; Search time 13.5281 Seconds
(without alignments)
185.159 Million cell updates/sec

Title: US-10-089-500-7

Perfect score: 37

Sequence: 1 YSSNLHS 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1589859 seqs, 357834939 residues

Total number of hits satisfying chosen parameters: 1589859

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA.*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37	100.0	128	9	US-09-764-304-10
2	37	100.0	128	9	US-09-764-304-10
3	37	100.0	128	14	US-10-265-713-10
4	37	100.0	128	14	US-10-265-713-10
5	37	100.0	128	14	US-10-166-626-10
6	37	100.0	128	14	US-10-166-626-10
7	34	91.9	107	17	US-10-741-657A-16
8	34	91.9	2207	16	US-10-437-963-189767
9	33	89.2	91	15	US-10-424-599-201107
10	33	89.2	303	15	US-10-424-599-208863
11	33	89.2	306	15	US-10-425-114-49623
12	33	89.2	474	9	US-09-823-829-24
13	33	89.2	474	9	US-09-823-823-24

14	33	89.2	503	16	US-10-437-963-197006	Sequence 197006,
15	32	86.5	47	17	US-10-425-115-227775	Sequence 227775,
16	32	86.5	59	15	US-10-424-599-190057	Sequence 190057,
17	32	86.5	500	10	US-09-970-367-2	Sequence 2, Appl1
18	31	83.8	61	17	US-10-425-115-316851	Sequence 316851,
19	31	83.8	277	15	US-10-282-122A-53384	Sequence 53384, A
20	31	83.8	347	9	US-09-816-028A-17	Sequence 17, Appl
21	31	83.8	347	14	US-10-303-161-17	Sequence 17, Appl
22	31	83.8	347	14	US-10-303-118-17	Sequence 17, Appl
23	31	83.8	347	14	US-10-303-128-17	Sequence 17, Appl
24	31	83.8	347	14	US-10-303-134-17	Sequence 17, Appl
25	31	83.8	347	14	US-10-303-162-17	Sequence 17, Appl
26	31	83.8	347	14	US-10-820-536-17	Sequence 17, Appl
27	31	83.8	347	17	US-10-845-408-17	Sequence 17, Appl
28	31	83.8	347	17	US-10-845-412-17	Sequence 17, Appl
29	31	83.8	347	17	US-10-846-219-17	Sequence 17, Appl
30	31	83.8	347	17	US-10-821-573-17	Sequence 17, Appl
31	31	83.8	347	17	US-10-821-604-17	Sequence 17, Appl
32	31	83.8	347	17	US-10-847-963-17	Sequence 17, Appl
33	31	83.8	385	17	US-10-425-115-320203	Sequence 320203,
34	31	83.8	385	17	US-10-739-930-7620	Sequence 7620, Ap
35	31	83.8	392	15	US-10-425-114-49028	Sequence 49028, A
36	31	83.8	407	15	US-10-425-114-64369	Sequence 64369, A
37	31	83.8	442	15	US-10-425-599-285570	Sequence 285570,
38	31	83.8	501	17	US-10-425-115-192258	Sequence 231545,
39	31	83.8	529	15	US-10-425-115-242547	Sequence 242547,
40	30	81.1	62	17	US-10-425-115-223534	Sequence 223534,
41	30	81.1	74	15	US-10-424-599-264246	Sequence 264246,
42	30	81.1	79	17	US-10-425-115-193189	Sequence 193189,
43	30	81.1	81	17	US-10-425-115-189365	Sequence 189365,
44	30	81.1	97	17	US-10-425-115-189365	Sequence 189365,
45	30	81.1	104	15	US-10-424-599-165308	Sequence 165308,

ALIGNMENTS

RESULT 1
US-09-764-304-10
Sequence 10, US20020026036A1
Patent No. US20020026036A1
GENERAL INFORMATION:
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: HASEGAWA, MAMORU
APPLICANT: MIYAJI, HIROMASA
APPLICANT: KUMANA, YOSHIHISA
TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
FILE REFERENCE: 249-101
CURRENT APPLICATION NUMBER: US/09/764,304
EARLIER APPLICATION NUMBER: 09/225,322
EARLIER FILING DATE: 2001-01-19
EARLIER APPLICATION NUMBER: US 08/454,680
EARLIER FILING DATE: 1999-01-05
EARLIER APPLICATION NUMBER: US 08/408,133
EARLIER FILING DATE: 1995-05-31
EARLIER APPLICATION NUMBER: US 08/292,178
EARLIER FILING DATE: 1995-03-21
EARLIER APPLICATION NUMBER: 08/292,178
EARLIER FILING DATE: 1994-08-17
EARLIER APPLICATION NUMBER: US07/947,674
EARLIER FILING DATE: 1992-09-17
EARLIER APPLICATION NUMBER: JP-3-238375
EARLIER FILING DATE: 1991-09-18
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 10
LENGTH: 128
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: CDNA KM-641
US-09-764-304-10

Query Match 100.0%; Score 37; DB 9; Length 128;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLS 7
Db 70 YSSNLS 76

RESULT 2
US-09-764-304-19
; Sequence 19, Application US/09764304
; Patent No. US20020026036A1
; GENERAL INFORMATION:
; APPLICANT: SHITTARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUMANA, YOSHITISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/09/764,304
; EARLIER APPLICATION NUMBER: 09/225,322
; EARLIER FILING DATE: 1999-01-05
; EARLIER APPLICATION NUMBER: US 08/454,680
; EARLIER FILING DATE: 1995-05-31
; EARLIER APPLICATION NUMBER: US 08/408,133
; EARLIER FILING DATE: 1995-03-21
; EARLIER APPLICATION NUMBER: US 08/292,178
; EARLIER FILING DATE: 1994-08-17
; EARLIER APPLICATION NUMBER: US07/947,674
; EARLIER FILING DATE: 1992-09-17
; EARLIER APPLICATION NUMBER: JP 3-238375
; EARLIER FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: light chain
; OTHER INFORMATION: variable region
US-09-764-304-19

Query Match 100.0%; Score 37; DB 9; Length 128;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLS 7
Db 70 YSSNLS 76

RESULT 3
US-10-265-713-10
; Sequence 10, Application US/10265713
; Publication No. US2003009564A1
; GENERAL INFORMATION:
; APPLICANT: SHITTARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUMANA, YOSHITISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/10/265,713
; CURRENT FILING DATE: 2002-10-08
; PRIOR APPLICATION NUMBER: US/09/225,322
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31

; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cDNA KM-641
US-10-265-713-10

Query Match 100.0%; Score 37; DB 14; Length 128;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLS 7
Db 70 YSSNLS 76

RESULT 4
US-10-265-713-19
; Sequence 19, Application US/10265713
; Publication No. US2003009564A1
; GENERAL INFORMATION:
; APPLICANT: SHITTARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUMANA, YOSHITISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/10/265,713
; CURRENT FILING DATE: 2002-10-08
; PRIOR APPLICATION NUMBER: US/09/225,322
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: light chain
; OTHER INFORMATION: variable region
US-10-265-713-19

Query Match 100.0%; Score 37; DB 14; Length 128;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLS 7
Db 70 YSSNLS 76

RESULT 5
US-10-166-626-10
; Sequence 10, Application US/10166626
; Publication No. US20030166876A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUMAWA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/10/166,626
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US/09/225,322B
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CDNA KM-641
US-10-166-626-10

Query Match 100.0%; Score 37; DB 14; Length 128;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLS 7
|:|||||
DB 70 YSSNLS 76

RESULT 6
US-10-166-626-19
; Sequence 19, Application US/10166626
; Publication No. US20030166876A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUMAWA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/10/166,626
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US/09/225,322B
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 19
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: light chain
US-10-166-626-19

Query Match 100.0%; Score 37; DB 14; Length 128;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLS 7
|:|||||
DB 70 YSSNLS 76

RESULT 7
US-10-741-657A-16
; Sequence 16, Application US/10741657A
; Publication No. US20040197325A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs
; TITLE OF INVENTION: ANTIBODIES AGAINST GPR64 AND USES THEREOF
; FILE REFERENCE: 05882.0177.NPUS01
; CURRENT APPLICATION NUMBER: US/10/741,657A
; CURRENT FILING DATE: 2003-12-19
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mus sp.
US-10-741-657A-16

Query Match 91.9%; Score 34; DB 17; Length 107;
Best Local Similarity 85.7%; Pred. No. 65;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLS 7
|:|||||
DB 50 YSSNLS 56

RESULT 8
US-10-437-963-189767
; Sequence 189767, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovacic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 189767
; LENGTH: 2207
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(2207)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:

OTHER INFORMATION: Clone ID: PAT_MRT3847_23625C.1.pep
US-10-424-599-201107

Query Match 91.9%; Score 34; DB 16; Length 2207;
Best Local Similarity 85.7%; Pred. No. 1.3e+03;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSNNLHS 7
:|||||
Db 850 YSNNLHS 856

RESULT 9
US-10-424-599-201107
Sequence 201107, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
FILE REFERENCE: 38-21(53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 201107
LENGTH: 91
TYPE: PRT
ORGANISM: Glycine max
FEATURE:

OTHER INFORMATION: Clone ID: PAT_MRT3847_23625C.1.pep
US-10-424-599-201107

Query Match 89.2%; Score 33; DB 15; Length 91;
Best Local Similarity 85.7%; Pred. No. 86;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSNNLHS 7
:|||||
Db 8 FSSNNLHS 14

RESULT 10
US-10-424-599-200863
Sequence 200863, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
FILE REFERENCE: 38-21(53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 200863
LENGTH: 303
TYPE: PRT
ORGANISM: Glycine max
FEATURE:

OTHER INFORMATION: Clone ID: PAT_MRT3847_30631C.1.pep
US-10-424-599-200863

Query Match 89.2%; Score 33; DB 15; Length 303;
Best Local Similarity 85.7%; Pred. No. 2.8e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSNNLHS 7
:|||||

Db 9 FSSNNLHS 15

RESULT 11
US-10-425-114-49629
Sequence 49629, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:

APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E.
APPLICANT: Tabaska, Jack E.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
FILE REFERENCE: 38-21(53313) B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 49629
LENGTH: 306
TYPE: PRT
ORGANISM: Glycine max
FEATURE:

OTHER INFORMATION: Clone ID: 700739771_FLI.pep
US-10-425-114-49629

Query Match 89.2%; Score 33; DB 15; Length 306;
Best Local Similarity 85.7%; Pred. No. 2.9e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSNNLHS 7
:|||||
Db 12 FSSNNLHS 18

RESULT 12
US-09-823-829-24
Sequence 24, Application US/09823829
Patent No. US20020146697A1
GENERAL INFORMATION:

APPLICANT: Yamamoto, Satoshi
APPLICANT: Nakamura, Shoko
APPLICANT: Suzuki, Makoto
APPLICANT: Kasai, Hiroaki
APPLICANT: Hamada, Tohru
TITLE OF INVENTION: METHOD FOR IDENTIFICATION AND DETECTION OF MICROORGANISMS
FILE REFERENCE: 12817-004001
CURRENT APPLICATION NUMBER: US/09/823,829
CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: US 09/208,688
PRIOR FILING DATE: 1998-12-10
PRIOR APPLICATION NUMBER: JP 97/343316
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 82
SOFTWARE: PatentIn version 2.0
SEQ ID NO 24
LENGTH: 474
TYPE: PRT
ORGANISM: Cytophaga lytica
US-09-823-829-24

Query Match 89.2%; Score 33; DB 9; Length 474;
Best Local Similarity 85.7%; Pred. No. 4.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSNNLHS 7
:|||||
Db 164 YSNNLHS 170

RESULT 13
US-09-823-823-24
; Sequence 24, Application US/09823823
; Patent No. US20020171092A1
; GENERAL INFORMATION:
; APPLICANT: Yamamoto, Satoshi
; APPLICANT: Kasai, Hiroaki
; APPLICANT: Nakamura, Shoko
; APPLICANT: Suzuki, Makoto
; APPLICANT: Hamada, Toku
; TITLE OF INVENTION: METHOD FOR IDENTIFICATION AND DETECTION OF MICROORGANISMS USING
; FILE REFERENCE: 12817-004001
; CURRENT APPLICATION NUMBER: US/09/823,823
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/208,688
; PRIOR FILING DATE: 1998-12-10
; PRIOR APPLICATION NUMBER: JP 97/343316
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: Patent version 2.0
; SEQ ID NO 24
; LENGTH: 474
; TYPE: PRT
; ORGANISM: Cytophaga lycica
US-09-823-823-24

Query Match 89.2%; Score 33; DB 9; Length 474;
Best Local Similarity 85.7%; Pred. No. 4.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLS 7
DB 164 YSENLS 170

RESULT 14
US-10-437-963-197006
; Sequence 197006, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 197006
; LENGTH: 503
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_92805C.1.pap
US-10-437-963-197006

Query Match 89.2%; Score 33; DB 16; Length 503;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLS 6
DB 84 YSSNLS 89

RESULT 15

US-10-425-115-227775
; Sequence 227775, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 227775
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_139326C.1.pap
US-10-425-115-227775

Query Match 86.5%; Score 32; DB 17; Length 47;
Best Local Similarity 85.7%; Pred. No. 63;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLS 7
DB 12 HSSNLS 18

RESULT 16
US-10-424-599-190057
; Sequence 190057, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 190057
; LENGTH: 59
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_142640C.1.pap
US-10-424-599-190057

Query Match 86.5%; Score 32; DB 15; Length 59;
Best Local Similarity 85.7%; Pred. No. 86;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLS 7
DB 9 YSSNLS 15

RESULT 17
US-09-970-367-2
; Sequence 2, Application US/09970367
; Publication No. US20030106092A1
; GENERAL INFORMATION:
; APPLICANT: Davis, Eric L.
; APPLICANT: Goellner, Melissa
; TITLE OF INVENTION: ENDUGLUCANASE GENE PROMOTER UPREGULATED BY NEMATODES
; FILE REFERENCE: 5051.587
; CURRENT APPLICATION NUMBER: US/09/970,367

;; CURRENT FILING DATE: 2001-10-02
;; NUMBER OF SEQ ID NOS: 21
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 2
;; LENGTH: 500
;; TYPE: PRT
;; ORGANISM: Nicotiana tabacum
US-09-970-367-2

Query Match 86.5%; Score 32; DB 10; Length 500;
Best Local Similarity 85.7%; Pred. No. 7.2e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLS 7
Db 228 YSSSLHS 234

RESULT 18
US-10-425-115-316851
; Sequence 316851, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovacic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 316851
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_5203C.1.pcp
US-10-425-115-316851

Query Match 83.8%; Score 31; DB 17; Length 61;
Best Local Similarity 85.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLS 7
Db 52 YSINLS 58

RESULT 19
US-10-282-122A-53384
; Sequence 53384, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zybskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21

;; PRIOR APPLICATION NUMBER: 60/206,848
;; PRIOR FILING DATE: 2000-05-23
;; PRIOR APPLICATION NUMBER: 60/207,727
;; PRIOR FILING DATE: 2000-05-26
;; PRIOR APPLICATION NUMBER: 60/230,335
;; PRIOR FILING DATE: 2000-09-06
;; PRIOR APPLICATION NUMBER: 60/230,347
;; PRIOR FILING DATE: 2000-09-09
;; PRIOR APPLICATION NUMBER: 60/242,578
;; PRIOR FILING DATE: 2000-10-23
;; PRIOR APPLICATION NUMBER: 60/253,625
;; PRIOR FILING DATE: 2000-11-27
;; PRIOR APPLICATION NUMBER: 60/257,931
;; PRIOR FILING DATE: 2000-12-22
;; PRIOR APPLICATION NUMBER: 60/267,636
;; PRIOR FILING DATE: 2001-02-09
;; PRIOR APPLICATION NUMBER: 60/269,308
;; PRIOR FILING DATE: 2001-02-16
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 78614
;; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 53384
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Clostridium difficile
US-10-282-122A-53384

Query Match 83.8%; Score 31; DB 15; Length 277;
Best Local Similarity 83.3%; Pred. No. 6.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLS 6
Db 94 YSSNLS 99

RESULT 20
US-09-816-028A-17
; Sequence 17, Application US/09816028A
; Patent No. US20020042369A1
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Michel
; APPLICANT: Wakarchuk, Warren W.
; APPLICANT: National Research Council of Canada
; TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
; TITLE OF INVENTION: Campylobacter and Ganglioside Mimics
; FILE REFERENCE: 019633-000111US
; CURRENT APPLICATION NUMBER: US/09/816,028A
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/118,213
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: US 09/495,406
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 347
; TYPE: PRT
; ORGANISM: Campylobacter jejuni
; FEATURE:
; OTHER INFORMATION: beta-1,4 N-acetylglactosaminyl (GalNAc)
; OTHER INFORMATION: transferase from C. jejuni strain OH4384 (ORF 5a
; OTHER INFORMATION: of lipooligosaccharide (LOS) biosynthesis locus)
US-09-816-028A-17

Query Match 83.8%; Score 31; DB 9; Length 347;
Best Local Similarity 71.4%; Pred. No. 7.8e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLS 7
Db 268 FSSNLS 274

RESULT 21
US-10-303-161-17
; Sequence 17, Application US/10303161
; Publication No. US20030148459A1
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Michel
; APPLICANT: Wakarchuk, Warren W.
; APPLICANT: National Research Council of Canada
; TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
; FILE REFERENCE: 019633-000111US
; CURRENT APPLICATION NUMBER: US/10/303,161
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US/09/816,028
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/118,213
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: US 09/495,406
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 347
; TYPE: PRT
; ORGANISM: Campylobacter jejuni
; FEATURE:
; OTHER INFORMATION: beta-1,4 N-acetylglactosaminyl (GalNAc)
; OTHER INFORMATION: transferase from C. jejuni strain OH4384 (ORF 5a
; OTHER INFORMATION: of lipooligosaccharide (LOS) biosynthesis locus)
US-10-303-161-17

Query Match 83.8%; Score 31; DB 14; Length 347;
Best Local Similarity 71.4%; Pred. No. 7.8e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 YSSNLS 7
Db 268 PSSNHS 274

RESULT 22
US-10-303-118-17
; Sequence 17, Application US/10303118
; Publication No. US20030157655A1
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Michel
; APPLICANT: Wakarchuk, Warren W.
; APPLICANT: National Research Council of Canada
; TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
; FILE REFERENCE: 019633-000111US
; CURRENT APPLICATION NUMBER: US/10/303,118
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US/09/816,028
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/118,213
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: US 09/495,406
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 347
; TYPE: PRT
; ORGANISM: Campylobacter jejuni
; FEATURE:
; OTHER INFORMATION: beta-1,4 N-acetylglactosaminyl (GalNAc)
; OTHER INFORMATION: transferase from C. jejuni strain OH4384 (ORF 5a
; OTHER INFORMATION: of lipooligosaccharide (LOS) biosynthesis locus)
US-10-303-118-17

Query Match 83.8%; Score 31; DB 14; Length 347;

Best Local Similarity 71.4%; Pred. No. 7.8e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 YSSNLS 7
Db 268 PSSNHS 274

RESULT 23
US-10-303-128-17
; Sequence 17, Application US/10303128
; Publication No. US20030157656A1
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Michel
; APPLICANT: Wakarchuk, Warren W.
; APPLICANT: National Research Council of Canada
; TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
; FILE REFERENCE: 019633-000111US
; CURRENT APPLICATION NUMBER: US/10/303,128
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US/09/816,028
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/118,213
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: US 09/495,406
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 347
; TYPE: PRT
; ORGANISM: Campylobacter jejuni
; FEATURE:
; OTHER INFORMATION: beta-1,4 N-acetylglactosaminyl (GalNAc)
; OTHER INFORMATION: transferase from C. jejuni strain OH4384 (ORF 5a
; OTHER INFORMATION: of lipooligosaccharide (LOS) biosynthesis locus)
US-10-303-128-17

Query Match 83.8%; Score 31; DB 14; Length 347;
Best Local Similarity 71.4%; Pred. No. 7.8e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 YSSNLS 7
Db 268 PSSNHS 274

RESULT 24
US-10-303-134-17
; Sequence 17, Application US/10303134
; Publication No. US20030157657A1
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Michel
; APPLICANT: Wakarchuk, Warren W.
; APPLICANT: National Research Council of Canada
; TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
; FILE REFERENCE: 019633-000111US
; CURRENT APPLICATION NUMBER: US/10/303,134
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US/09/816,028
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/118,213
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: US 09/495,406
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 347
; TYPE: PRT
; ORGANISM: Campylobacter jejuni

FEATURE:
OTHER INFORMATION: beta-1,4 N-acetylglactosaminyl (GalNAc) (ORF 5a)
OTHER INFORMATION: transferase from C. jejuni strain OH4384 (ORF 5a)
OTHER INFORMATION: of lipooligosaccharide (LOS) biosynthesis locus)
US-10-303-134-17

Query Match
Best Local Similarity 83.8%; Score 31; DB 14; Length 347;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLS 7
:||||:
Db 268 FSSNHS 274

RESULT 25
US-10-303-162-17
Sequence 17, Application US/10303162
Publication No. US20030157658A1
GENERAL INFORMATION:
APPLICANT: Gilbert, Michel
APPLICANT: Wakarchuk, Warren W.
APPLICANT: National Research Council of Canada
TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
FILE REFERENCE: 019633-000111US
CURRENT APPLICATION NUMBER: US/10/303,162
PRIOR FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US/09/816,028
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: US 60/118,213
PRIOR FILING DATE: 1999-02-01
PRIOR APPLICATION NUMBER: US 09/495,406
PRIOR FILING DATE: 2000-01-31
NUMBER OF SEQ ID NOS: 49
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 17
LENGTH: 347
TYPE: PRT
ORGANISM: Campylobacter jejuni
FEATURE:
OTHER INFORMATION: beta-1,4 N-acetylglactosaminyl (GalNAc)
OTHER INFORMATION: transferase from C. jejuni strain OH4384 (ORF 5a)
OTHER INFORMATION: of lipooligosaccharide (LOS) biosynthesis locus)
US-10-303-162-17

Query Match
Best Local Similarity 83.8%; Score 31; DB 14; Length 347;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLS 7
:||||:
Db 268 FSSNHS 274

RESULT 26
US-10-820-536-17
Sequence 17, Application US/10820536
Publication No. US20040203103A1
GENERAL INFORMATION:
APPLICANT: Gilbert, Michel
APPLICANT: Wakarchuk, Warren W.
APPLICANT: National Research Council of Canada
TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
FILE REFERENCE: 019633-000111US
CURRENT APPLICATION NUMBER: US/10/820,536
PRIOR FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: 10/303,128
PRIOR FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US/09/816,028
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: US 60/118,213

PRIOR FILING DATE: 1999-02-01
PRIOR APPLICATION NUMBER: US 09/495,406
PRIOR FILING DATE: 2000-01-31
NUMBER OF SEQ ID NOS: 49
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 17
LENGTH: 347
TYPE: PRT
ORGANISM: Campylobacter jejuni
FEATURE:
OTHER INFORMATION: beta-1,4 N-acetylglactosaminyl (GalNAc)
OTHER INFORMATION: transferase from C. jejuni strain OH4384 (ORF 5a)
OTHER INFORMATION: of lipooligosaccharide (LOS) biosynthesis locus)
US-10-820-536-17

Query Match
Best Local Similarity 83.8%; Score 31; DB 17; Length 347;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLS 7
:||||:
Db 268 FSSNHS 274

RESULT 27
US-10-845-408-17
Sequence 17, Application US/10845408
Publication No. US20040203112A1
GENERAL INFORMATION:
APPLICANT: Gilbert, Michel
APPLICANT: Wakarchuk, Warren W.
APPLICANT: National Research Council of Canada
TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
FILE REFERENCE: 019633-000111US
CURRENT APPLICATION NUMBER: US/10/845,408
PRIOR FILING DATE: 2004-05-12
PRIOR APPLICATION NUMBER: US/09/816,028
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: US 60/118,213
PRIOR FILING DATE: 1999-02-01
PRIOR APPLICATION NUMBER: US 09/495,406
PRIOR FILING DATE: 2000-01-31
NUMBER OF SEQ ID NOS: 49
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 17
LENGTH: 347
TYPE: PRT
ORGANISM: Campylobacter jejuni
FEATURE:
OTHER INFORMATION: beta-1,4 N-acetylglactosaminyl (GalNAc)
OTHER INFORMATION: transferase from C. jejuni strain OH4384 (ORF 5a)
OTHER INFORMATION: of lipooligosaccharide (LOS) biosynthesis locus)
US-10-845-408-17

Query Match
Best Local Similarity 83.8%; Score 31; DB 17; Length 347;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLS 7
:||||:
Db 268 FSSNHS 274

RESULT 28
US-10-845-412-17
Sequence 17, Application US/10845412
Publication No. US20040203113A1
GENERAL INFORMATION:
APPLICANT: Gilbert, Michel
APPLICANT: Wakarchuk, Warren W.
APPLICANT: National Research Council of Canada
TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of

TITLE OF INVENTION: Gangliosides and Ganglioside Mimics
FILE REFERENCE: 019633-000111US
CURRENT APPLICATION NUMBER: US/10/845,412
CURRENT FILING DATE: 2004-05-12
PRIOR APPLICATION NUMBER: US/10/303,128
PRIOR FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US/09/816,028
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: US 60/118,213
PRIOR FILING DATE: 1999-02-01
PRIOR APPLICATION NUMBER: US 09/495,406
PRIOR FILING DATE: 2000-01-31
NUMBER OF SEQ ID NOS: 49
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 17
LENGTH: 347
TYPE: PRF
ORGANISM: Campylobacter jejuni
FEATURE:
OTHER INFORMATION: beta-1,4 N-acetylglactosaminyl (GalNAc)
OTHER INFORMATION: transferase from C. jejuni strain OH4384 (ORF 5a)
OTHER INFORMATION: of lipooligosaccharide (LOS) biosynthesis locus)
US-10-845-412-17

Query Match 83.8%; Score 31; DB 17; Length 347;
Best Local Similarity 71.4%; Pred. No. 7.8e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLS 7
:|||||
Db 268 FSSNLS 274

RESULT 29
US-10-846-219-17
Sequence 17, Application US/10846219
Publication No. US20040219638A1
GENERAL INFORMATION:
APPLICANT: Gilbert, Michel
APPLICANT: Makarchuk, Warren W.
APPLICANT: National Research Council of Canada
TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
FILE REFERENCE: 019633-000111US
CURRENT APPLICATION NUMBER: US/10/846,219
CURRENT FILING DATE: 2004-05-14
PRIOR APPLICATION NUMBER: US/09/816,028
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: US 60/118,213
PRIOR FILING DATE: 1999-02-01
PRIOR APPLICATION NUMBER: US 09/495,406
PRIOR FILING DATE: 2000-01-31
NUMBER OF SEQ ID NOS: 49
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 17
LENGTH: 347
TYPE: PRF
ORGANISM: Campylobacter jejuni
FEATURE:
OTHER INFORMATION: beta-1,4 N-acetylglactosaminyl (GalNAc)
OTHER INFORMATION: transferase from C. jejuni strain OH4384 (ORF 5a)
OTHER INFORMATION: of lipooligosaccharide (LOS) biosynthesis locus)
US-10-846-219-17

Query Match 83.8%; Score 31; DB 17; Length 347;
Best Local Similarity 71.4%; Pred. No. 7.8e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLS 7
:|||||
Db 268 FSSNLS 274

RESULT 30
US-10-821-573-17
Sequence 17, Application US/10821573
Publication No. US20040229313A1
GENERAL INFORMATION:
APPLICANT: Gilbert, Michel
APPLICANT: Makarchuk, Warren W.
APPLICANT: National Research Council of Canada
TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
FILE REFERENCE: 019633-000111US
CURRENT APPLICATION NUMBER: US/10/821,573
CURRENT FILING DATE: 2004-04-08
PRIOR APPLICATION NUMBER: 10/303,128
PRIOR FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US/09/816,028
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: US 60/118,213
PRIOR FILING DATE: 1999-02-01
PRIOR APPLICATION NUMBER: US 09/495,406
PRIOR FILING DATE: 2000-01-31
NUMBER OF SEQ ID NOS: 49
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 17
LENGTH: 347
TYPE: PRF
ORGANISM: Campylobacter jejuni
FEATURE:
OTHER INFORMATION: beta-1,4 N-acetylglactosaminyl (GalNAc)
OTHER INFORMATION: transferase from C. jejuni strain OH4384 (ORF 5a)
OTHER INFORMATION: of lipooligosaccharide (LOS) biosynthesis locus)
US-10-821-573-17

Query Match 83.8%; Score 31; DB 17; Length 347;
Best Local Similarity 71.4%; Pred. No. 7.8e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLS 7
:|||||
Db 268 FSSNLS 274

RESULT 31
US-10-821-604-17
Sequence 17, Application US/10821604
Publication No. US20040229263A1
GENERAL INFORMATION:
APPLICANT: Gilbert, Michel
APPLICANT: Makarchuk, Warren W.
APPLICANT: National Research Council of Canada
TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
FILE REFERENCE: 019633-000111US
CURRENT APPLICATION NUMBER: US/10/821,604
CURRENT FILING DATE: 2004-04-08
PRIOR APPLICATION NUMBER: 10/303,128
PRIOR FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US/09/816,028
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: US 60/118,213
PRIOR FILING DATE: 1999-02-01
PRIOR APPLICATION NUMBER: US 09/495,406
PRIOR FILING DATE: 2000-01-31
NUMBER OF SEQ ID NOS: 49
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 17
LENGTH: 347
TYPE: PRF
ORGANISM: Campylobacter jejuni
FEATURE:
OTHER INFORMATION: beta-1,4 N-acetylglactosaminyl (GalNAc)
OTHER INFORMATION: transferase from C. jejuni strain OH4384 (ORF 5a)
OTHER INFORMATION: of lipooligosaccharide (LOS) biosynthesis locus)
US-10-821-604-17

Query Match 83.8%; Score 31; DB 17; Length 347;
Best Local Similarity 71.4%; Pred. No. 7.8e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

US-10-821-604-17

Query Match 83.8%; Score 31; DB 17; Length 347;
Best Local Similarity 71.4%; Pred. No. 7.8e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLHS 7
:|||||
DB 268 FSSNIHS 274

RESULT 32

US-10-847-983-17
; Sequence 17, Application US/10847983
; Publication No. US20040229272A1
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Michel
; APPLICANT: Makarchuk, Warren W.
; TITLE OF INVENTION: National Research Council of Canada
; TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
; FILE REFERENCE: 019633-000111US
; CURRENT APPLICATION NUMBER: US/10/847,983
; CURRENT FILING DATE: 2004-05-17
; PRIOR APPLICATION NUMBER: US/09/816,028
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/118,213
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: US 09/495,406
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 347
; TYPE: PRT
; ORGANISM: Campylobacter jejuni
; FEATURE:
; OTHER INFORMATION: beta-1,4 N-acetylglactosaminyl (galNAc)
; OTHER INFORMATION: transferase from C. jejuni strain OH4384 (ORF 5a
; OTHER INFORMATION: of lipooligosaccharide (LOS) biosynthesis locus)
US-10-847-983-17

Query Match 83.8%; Score 31; DB 17; Length 347;
Best Local Similarity 71.4%; Pred. No. 7.8e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLHS 7
:|||||
DB 268 FSSNIHS 274

RESULT 33

US-10-425-115-320203
; Sequence 320203, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 320203
; LENGTH: 385
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_55091C.1.pep
US-10-425-115-320203

Query Match 83.8%; Score 31; DB 17; Length 385;
Best Local Similarity 85.7%; Pred. No. 8.6e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLHS 7
:|||||
DB 165 YSSNOHS 171

RESULT 34

US-10-739-930-7620
; Sequence 7620, Application US/10739930
; Publication No. US20040216190A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53377)B
; CURRENT APPLICATION NUMBER: US/10/739,930
; CURRENT FILING DATE: 2003-12-18
; NUMBER OF SEQ ID NOS: 11088
; SEQ ID NO 7620
; LENGTH: 385
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: ZEAMA-23APR03-C21375_2.p
US-10-739-930-7620

Query Match 83.8%; Score 31; DB 17; Length 385;
Best Local Similarity 85.7%; Pred. No. 8.6e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLHS 7
:|||||
DB 165 YSSNOHS 171

RESULT 35

US-10-425-114-49028
; Sequence 49028, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 49028
; LENGTH: 392
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700726516_FLI.pep
US-10-425-114-49028

Query Match 83.8%; Score 31; DB 15; Length 392;
Best Local Similarity 85.7%; Pred. No. 8.8e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLHS 7
:|||||
DB 195 YSSGLHS 201

RESULT 36
US-10-425-114-64369
; Sequence 64369, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 64369
; LENGTH: 407
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3689-224-H11_F11.pep
US-10-425-114-64369

Query Match
Best Local Similarity 83.8%; Score 31; DB 15; Length 407;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 YSSNLS 7
Db 187 YSSNLS 193

RESULT 37
US-10-424-599-285570
; Sequence 285570, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 285570
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_9989C.1.pep
US-10-424-599-285570

Query Match
Best Local Similarity 83.8%; Score 31; DB 15; Length 442;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 YSSNLS 7
Db 25 YSSNLS 31

RESULT 38
US-10-425-115-192258
; Sequence 192258, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 192258
; LENGTH: 501
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_106925C.1.pep
US-10-425-115-192258

Query Match
Best Local Similarity 83.8%; Score 31; DB 17; Length 501;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 YSSNLS 7
Db 477 YSSNLS 483

RESULT 39
US-10-424-599-231545
; Sequence 231545, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 231545
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_51106C.1.pep
US-10-424-599-231545

Query Match
Best Local Similarity 83.8%; Score 31; DB 15; Length 529;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 YSSNLS 7
Db 332 YSSNLS 338

RESULT 40
US-10-425-115-242547
; Sequence 242547, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 242547

; LENGTH: 62
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_152789C.1.pep
US-10-425-115-242547

Query Match 81.1%; Score 30; DB 17; Length 62;
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLH 6
Db 40 YSTNLH 45

Search completed: December 17, 2004, 18:38:01
Job time : 14.5281 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using SW model

Run on: December 17, 2004, 18:11:22 ; Search time 2.75281 seconds
(without alignments)
244.665 Million cell updates/sec

Title: US-10-089-500-7

Perfect score: 37

Sequence: 1 YSSNLS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:
2: p1r2:
3: p1r3:
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	33	89.2	219	2 T30122	hypothetical prote
2	33	89.2	368	2 G86895	hypothetical prote
3	32	86.5	324	2 S61447	cellulase (EC 3.2.
4	32	86.5	489	2 T06350	cellulase (EC 3.2.
5	31	83.8	107	2 A48677	Ig kappa chain V-J
6	31	83.8	380	2 A81198	conserved hypochet
7	31	83.8	380	2 A81833	conserved hypochet
8	30	81.1	243	2 AF0777	probable transcrip
9	30	81.1	290	2 A12054	hypothetical prote
10	30	81.1	313	2 T48439	probable RNA-bindi
11	30	81.1	412	2 S72617	alcohol dehydrogen
12	30	81.1	424	2 C86247	hypothetical prote
13	30	81.1	427	2 T23954	hypothetical prote
14	30	81.1	458	2 P97296	UDP-N-acetylmuram
15	30	81.1	459	2 AF2847	two component sens
16	30	81.1	459	2 E97624	osmolarity sensor
17	30	81.1	472	2 AD2532	hypothetical prote
18	30	81.1	816	2 T17257	hypothetical prote
19	30	81.1	844	2 B81336	probable fibrillar
20	30	81.1	1042	1 G86895	beta-galactosidase
21	30	81.1	1042	2 E85968	evolved beta-D-gal
22	30	81.1	1042	2 F91123	evolved beta-D-gal
23	30	81.1	1723	2 H86557	polymorphic membra
24	30	81.1	1723	2 E72067	polymorphic membra
25	30	81.1	1732	2 C81601	polymorphic membra
26	29	78.4	108	1 KVM573	Ig kappa chain V r
27	29	78.4	111	2 G38740	Ig kappa chain V r
28	29	78.4	111	2 A38740	Ig kappa chain V r
29	29	78.4	111	2 E38740	Ig kappa chain V r

30	29	78.4	111	2 C38740	Ig kappa chain V r
31	29	78.4	227	2 T11242	ribosomal protein
32	29	78.4	243	2 G89567	protein T08A9.2 [1
33	29	78.4	334	1 TVMSJA	transcription fact
34	29	78.4	334	2 S12742	transcription fact
35	29	78.4	347	2 T25192	hypothetical prote
36	29	78.4	391	2 T38822	hypothetical prote
37	29	78.4	451	2 B69675	glucose-6-phosphat
38	29	78.4	465	2 G96655	unknown protein, 2
39	29	78.4	516	2 T33061	hypothetical prote
40	29	78.4	550	2 P90407	molybdopterin bios
41	29	78.4	572	2 T51525	hypothetical prote
42	29	78.4	732	2 A12158	hypothetical prote
43	29	78.4	746	2 S74219	alpha-galactosidas
44	29	78.4	787	2 T00798	hypothetical prote
45	29	78.4	867	2 T14777	hypothetical prote

ALIGNMENTS

RESULT 1
T30122
hypothetical protein F22H10.6 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: T30122
R/Jangston, Y.; Hawking, J.
submitted to the EMBL Data Library, September 1996
A/Description: The sequence of C. elegans cosmid F22H10.
A/Reference number: Z20740
A/Accession: T30122
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1219 <LAN>
A/Cross-references: UNIPROT:Q94192; EMBL:U70845; PIDD:AA09103.1; GSPDB:GN00028; CESP:F2;
A/Experimental source: strain Bristol N2; clone F22H10
C/Genetics:
A/Genes: CESP:F22H10.6
A/Map position: X
A/Introns: 47/1; 67/1; 107/3; 135/3

Query Match
Best Local Similarity 89.2%; Score 33; DB 2; Length 219;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLS 7
Db 22 FSSNLS 28
:|||||

RESULT 2
G86895
hypothetical protein yweB [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C/Species: Lactococcus lactis subsp. lactis
C/Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
C/Accession: G86895
R/Bolotin, A.; Wincker, P.; Manger, S.; Jallion, O.; Malarne, K.; Weissenbach, J.; Ehrlich
Genome Res. 11, 731-753, 2001
A/Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssi
A/Reference number: A86625; NCBI:21235186; PMID:11337471
A/Accession: G86895
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-368 <STO>
A/Cross-references: UNIPROT:Q9CD01; GB:AE005176; PIDD:G12725228; PIDD:AAK06265.1; GSPDB:G
A/Experimental source: strain IL1403
C/Genetics:
A/Genes: yweB

Query Match
Best Local Similarity 89.2%; Score 33; DB 2; Length 368;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLSHS 7
 : |||||
 Db 121 FSSNLSHS 127

RESULT 3

S61447
 cellulase (EC 3.2.1.4) CX3 - pepper (fragment)
 C/Accession: A48677
 C/Species: Capsicum annuum (pepper)
 C/Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
 C/Accession: S61447
 R/Farrar, L.; Trinocci, L.; Moretto, P.; Polverino de Laureto, P.; Rascio, N.; Casad
 Plant Mol. Biol. 29, 735-747, 1995
 A/Title: Differential ethylene-inducible expression of cellulase in pepper plants.
 A/Reference number: S61445; MUID:96128016; PMID:8541500
 A/Accession: S61447
 A/Status: nucleic acid sequence not shown
 A/Molecule type: mRNA
 A/Residues: 1-324 <PER>
 A/Cross-references: UNIPROT:Q43751; EMBL:X83711
 C/Superfamily: Arabidopsis membrane-anchored cellulase KOR
 C/Keywords: glycosidase; hydrolase

Query Match 86.5%; Score 32; DB 2; Length 324;
 Best Local Similarity 85.7%; Pred. No. 27;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLSHS 7
 : |||||
 Db 144 YSSSLSHS 150

RESULT 4

T06350
 cellulase (EC 3.2.1.4) Cel2 precursor - tomato
 N/Alternate names: endo-1,4-beta-glucanase
 C/Species: Lycopersicon esculentum (tomato)
 C/Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004
 R/Asashiro, C.C.; Gonzalez-Bosch, C.; Bennett, A.B.
 Plant Cell 6, 1485-1493, 1994
 A/Title: Two divergent endo-beta-1,4-glucanase genes exhibit overlapping expression in
 A/Reference number: Z15614; MUID:95086382; PMID:7994180
 A/Accession: T06350
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-489 <LAS>
 A/Cross-references: UNIPROT:Q42872; EMBL:U13055; NID:9531904; PIDN:AAA69909.1; PID:95319
 A/Experimental source: strain Castlemart; tissue-type pericarp
 C/Genetics:
 A/Gene: Cel2
 C/Function:
 A/Description: hydrolysis of 1,4-beta-D-glucosidic linkages in beta-D-glucans such as ce
 A/Pathway: cellulose degradation
 C/Superfamily: Arabidopsis membrane-anchored cellulase KOR
 C/Keywords: glycosidase; hydrolase; polysaccharide degradation
 F/1-23/Domain: signal sequence #status predicted <SIG>
 F/24-489/Product: cellulase 2 #status predicted <MAT>

Query Match 86.5%; Score 32; DB 2; Length 489;
 Best Local Similarity 85.7%; Pred. No. 42;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLSHS 7
 : |||||
 Db 216 YSSSLSHS 222

RESULT 5

A48677
 Ig kappa chain V-J region (48) - mouse (fragment)
 C/Species: Mus musculus (house mouse)

C/Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 21-Jan-2000
 C/Accession: A48677
 R/Farrar, L.; Trinocci, L.; Moretto, P.; Polverino de Laureto, P.; Rascio, N.; Casad
 Proc. Natl. Acad. Sci. U.S.A. 90, 9508-9512, 1993
 A/Title: Molecular characterization of monoclonal CRI-A-positive anti-arsenate antibodies
 A/Reference number: A48677; MUID:94022404; PMID:8415731
 A/Accession: A48677
 A/Status: preliminary; not compared with conceptual translation
 A/Molecule type: mRNA
 A/Residues: 1-107 <TAS>
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: immunoglobulin
 F/16-90/Domain: immunoglobulin homology <IMM>

Query Match 83.8%; Score 31; DB 2; Length 107;
 Best Local Similarity 85.7%; Pred. No. 13;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLSHS 7
 : |||||
 Db 50 YSSRLHS 56

RESULT 6

A81198
 conserved hypothetical protein NMB0455 [imported] - Neisseria meningitidis (strain MC58
 C/Species: Neisseria meningitidis
 C/Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
 C/Accession: A81198
 R/Retlein, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.
 Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
 et al.; H.; Qin, H.; Vamathavan, J.; Gill, J.; Scarlato, V.; Maignan, V.; Pizzi, M.
 Science 287, 1809-1815, 2000
 A/Authors: Grandi, G.; Sun, L.; Smith, H.O.; Frazer, C.M.; Moxon, E.R.; Rappelli, R.; Ver
 A/Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
 A/Reference number: A81000; MUID:20175755; PMID:10710307
 A/Accession: A81198
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-380 <TET>
 A/Cross-references: UNIPROT:Q9K0V4; GB:AE002401; GB:AE002098; NID:97225669; PIDN:AAF40892
 A/Experimental source: serogroup B, strain MC58
 C/Genetics:
 A/Gene: NMB0455
 C/Superfamily: Bacillus conserved hypothetical protein ypsc

Query Match 83.8%; Score 31; DB 2; Length 380;
 Best Local Similarity 71.4%; Pred. No. 53;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLSHS 7
 : |||||
 Db 48 YANLSHS 54

RESULT 7

A81833
 conserved hypothetical protein NMA2030 [imported] - Neisseria meningitidis (strain Z2491
 C/Species: Neisseria meningitidis
 C/Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
 C/Accession: A81833
 R/Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
 J.; Holroyd, S.; Jagsels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
 Nature 404, 502-506, 2000
 A/Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
 A/Reference number: A81775; MUID:20222556; PMID:10761919
 A/Accession: A81833
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-380 <PAR>
 A/Cross-references: UNIPROT:Q9R0W4; GB:AL162757; GB:AL157959; NID:97380371; PIDN:CAB85245
 A/Experimental source: serogroup A, strain Z2491
 C/Genetics:

A:Gene: NMA2030
C:Superfamily: Bacillus conserved hypothetical protein ypsc

Query Match 83.8%; Score 31; DB 2; Length 380;
Best Local Similarity 71.4%; Pred. No. 53;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLS 7
DB 48 YANLHS 54

RESULT 8

AF077777
probable transcription regulator STY2390 [imported] - Salmonella enterica subsp. enteric

C:Species: Salmonella enterica subsp. enterica serovar Typhi
A:Note: this species has also been called Salmonella typhi

C>Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C/Accession: AF07777

R:Parthill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, P.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001

A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: AF07777

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-243 <PAR>

A:Cross-references: GB:AL513382; PIDN:CAD02540.1; PID:G16503401; GSPDB:GN00176
C:Genetics:

A:Gene: STY2390
C:Superfamily: probable transcription regulator yscE

Query Match 81.1%; Score 30; DB 2; Length 243;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSNLS 7
DB 94 SSNLS 99

RESULT 9
AI2054
hypothetical protein all1991 [imported] - Nostoc sp. (strain PCC 7120)

C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C>Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C/Accession: AI2054

R:Kaneko, T.; Nakamura, Y.; Molk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriuchika, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena PCC 7120
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AI2054

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-290 <KUR>

A:Cross-references: UNIPROT:Q8YV17; GB:BA000019; PIDN:BA073690.1; PID:G17131081; GSPDB:G17131081
A:Experimental source: strain PCC 7120
C:Genetics:

A:Gene: all1991

Query Match 81.1%; Score 30; DB 2; Length 290;
Best Local Similarity 83.3%; Pred. No. 65;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLS 6
DB 190 YSNLH 195

RESULT 10
T48439
probable RNA-binding protein - Arabidopsis thaliana

N:Alternate names: protein T32M21.30
C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C/Accession: T48439

R:Bevan, M.; Terry, N.; Ardiles, W.; Buyschaert, C.; Dasseville, R.; De Clerck, R.; De Waele, H.W.; Rudd, S.; Lemcke, K.; Mayer, K.F.X.
submitted to the Protein Sequence Database, March 2000

A:Reference number: Z24487
A:Accession: T48439

A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-313 <BEV>

A:Cross-references: UNIPROT:Q9L282; EMBL:AL162875
A:Experimental source: cultivar Columbia; BAC clone T32M21

C:Genetics:

A:Map position: 5
A:Interons: 29/1; 108/3; 144/2; 209/1; 229/3; 261/3; 282/2
A:Note: T32M21.30

Query Match 81.1%; Score 30; DB 2; Length 313;
Best Local Similarity 71.4%; Pred. No. 70;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLS 7
DB 197 YSNVHS 203

RESULT 11

S72617
alcohol dehydrogenase homolog B11-4 [imported] - Neurospora crassa

N:Alternate names: protein B24M22.250
C:Species: Neurospora crassa

C>Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C/Accession: S72617; T51229

R:Brucher, J.J.P.; Eberle, J.; Kohler, W.; Kruff, V.; Radford, A.; Russo, V.E.A.
Mol. Gen. Genet. 252, 223-229, 1996

A:Title: b11-4, a gene that is rapidly induced by blue light, encodes a novel mitochondri A:Reference number: S72617; MUID:96439828; PMID:8842141
A:Accession: S72617

A:Molecule type: mRNA
A:Residues: 1-412 <BRU>

A:Cross-references: UNIPROT:Q92247; EMBL:X89499; NID:G1620434; PIDN:CAA61670.1; PID:G1620434
A:Experimental source: mycelium, strain Stc

A:Genetics: BRU1
R:Schulte, U.; Aign, V.; Hohenstein, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura, submitted to the Protein Sequence Database, July 2000

A:Reference number: Z25286
A:Accession: T51229

A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-412 <SCH>
A:Cross-references: EMBL:AL390354; PIDN:CA09393.1; GSPDB:GN00116; NCSP:B24M22.250
A:Experimental source: strain OR74A

A:Genetics: SCH1
C:Genetics: <BRU>

A:Gene: b11-4
A:Map position: 11

C:Genetics: <SCH>
A:Gene: B24M22.250

A:Map position: 6
A:Interons: 67/3; 320/2

C:Function:

A:Description: may play a role as an (NAD⁺)-dependent alcohol dehydrogenase in mitochondri A:Note: induced by blue light
C:Keywords: mitochondrion

Query Match 81.1%; Score 30; DB 2; Length 412;
Best Local Similarity 100.0%; Pred. No. 95;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 SSNNHS 7
|||||
Db 240 SSNNHS 245

RESULT 12
C86247
hypothetical protein [imported] - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C/Accession: C86247
R/Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maltli, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A/Authors: Salzberg, S.L.; Schwartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A/Reference number: A86141; MUID:21016719; PMID:1130712
A/Accession: C86247
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-424 <STO>
A/Cross-references: UNIPROT:Q9SEX7; GB:AE005172; NID:95734725; PIDN:AAD49990.1; GSPDB:GN C/Genetics:
A/Map position: 1

Query Match 81.1%; Score 30; DB 2; Length 424;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 SSNNHS 7
|||||
Db 277 SSNNHS 282

RESULT 13
T23954
hypothetical protein R06B9.1 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: T23954
R/Baynes, C. the EMBL Data Library, December 1996
submitted to the EMBL Data Library, December 1996
A/Reference number: Z19823
A/Accession: T23954
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1427 <WIL>
A/Cross-references: UNIPROT:O17981; EMBL:Z83237; PIDN:CA805786.1; GSPDB:GN00020; CESP:RD A/Experimental source: Clone R06B9
C/Genetics:
A/Gene: CESP:R06B9.1
A/Map position: 2
A/Introns: 62/2; 97/3; 156/1; 380/1
C/Superfamily: Caenorhabditis elegans hypothetical protein R06B9.1

Query Match 81.1%; Score 30; DB 2; Length 427;
Best Local Similarity 83.3%; Pred. No. 98;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 YSSNNH 6
|||||
Db 77 YSSNNH 82

RESULT 14
P97296

UDP-N-acetylmutamate-alanine ligase [imported] - Clostridium acetobutylicum
C/Species: Clostridium acetobutylicum
C/Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C/Accession: P97296
R/Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
U. Bacteriol. 183, 4823-4838, 2001
A/Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clostridium acetobutylicum
A/Reference number: A96900; MUID:21359325; PMID:21359325
A/Accession: P97296
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-458 <KUR>
A/Cross-references: UNIPROT:Q97889; GB:AE001437; PIDN:AAK81161.1; PID:915026298; GSPDB:GN A/Experimental source: Clostridium acetobutylicum ATCC824
C/Genetics:
A/Gene: CAC3225
C/Superfamily: UDP-N-acetylmutamate-alanine ligase

Query Match 81.1%; Score 30; DB 2; Length 458;
Best Local Similarity 100.0%; Pred. No. 11e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 SSNNHS 7
|||||
Db 417 SSNNHS 422

RESULT 15
AF2847
two component sensor kinase envZ [imported] - Agrobacterium tumefaciens (strain C58, Dupx C/Species: Agrobacterium tumefaciens
C/Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C/Accession: AF2847
R/Wood, D.W.; Sebubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.; erage, G.; Giller, W.; Grant, C.; Guenther, D.; Kutayavln, T.; Levy, R.; Li, M.; McClellan, Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A/Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, E ster, B.W.
A/Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A/Reference number: AB2577; MUID:21608550; PMID:11743193
A/Accession: AF2847
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-459 <KUR>
A/Cross-references: UNIPROT:Q8UDC0; GB:AE008688; PIDN:AAL43196.1; PID:917740676; GSPDB:GN A/Experimental source: strain C58 (dupont)
C/Genetics:
A/Gene: envZ
A/Map position: circular chromosome

Query Match 81.1%; Score 30; DB 2; Length 459;
Best Local Similarity 83.3%; Pred. No. 11e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 YSSNNH 6
|||||
Db 371 YSSNNH 376

RESULT 16
E97624
osmolarity sensor protein envZ (envZ) rp426 [imported] - Agrobacterium tumefaciens (strain C/Species: Agrobacterium tumefaciens
C/Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C/Accession: E97624
R/Goodner, B.; Hinkle, G.; Gatlung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
A/Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumefaciens
A/Reference number: A97359; MUID:21608551; PMID:11743194
A/Accession: E97624

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-459 <KUR>
A:Cross-references: UNIPROT:Q8UDC0; GB:AE007869; PIDN:AAK87950.1; PID:G15157354; GSPDB:C
C:Genetics: AGR_C4011
A:Gene: AGR_C4011
A:Map position: circular chromosome

Query Match
Best Local Similarity 81.1%; Score 30; DB 2; Length 459;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLMH 6
DB 371 YASNLMH 376

RESULT 17

AD2532
hypothetical protein alr7543 [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120b
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C>Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C:Accession: AD2532
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kurlitz, T.; Sasamoto, S.; Watanabe, A.; Iriyuchi, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A:Reference number: AB1807; MWID:21595285; PMID:11759640
A:Accession: AD2532
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-472 <KUR>
A:Cross-references: UNIPROT:Q8ZSG7; GB:AP003602; PIDN:BAW77186.1; PID:G17134628; GSPDB:C
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: alr7543
A:Genome: plasmid

Query Match
Best Local Similarity 81.1%; Score 30; DB 2; Length 472;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLMH 6
DB 170 YSTNLMH 175

RESULT 18

T17257
hypothetical protein DKFZP586P1422.1 - human
C:Species: Homo sapiens (man)
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T17257
R:Koehler, K.; Beyer, A.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
Submitted to the Protein Sequence Database, September 1999
A:Reference number: Z18722
A:Accession: T17257
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-816 <KOE>
A:Cross-references: UNIPROT:Q9UFT2; EMBL:AL117472
A:Experimental source: adult uterus; clone DKFZP586P1422
C:Genetics:
A:Note: DKFZP586P1422.1

Query Match
Best Local Similarity 81.1%; Score 30; DB 2; Length 816;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLMH 7
DB 492 YSSNLMH 498

RESULT 19

B83136
probable fimbrial biogenesis usher protein PA084 [imported] - Pseudomonas aeruginosa (str
C:Species: Pseudomonas aeruginosa
C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C:Accession: B83136
R:Stover, C.K.; Pham, X.Q.; EWING, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lapidis, K.; Lim,
., Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A:Reference number: A82950; MWID:20437337; PMID:10984043
A:Accession: B83136
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-844 <STO>
A:Cross-references: UNIPROT:Q9HWU4; GB:AE004824; GB:AE004091; NID:G9950277; PIDN:AMG07473
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA084
C:superfamily: outer membrane usher protein fimb

Query Match
Best Local Similarity 81.1%; Score 30; DB 2; Length 844;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLMH 6
DB 169 YSSNLMH 174

RESULT 20

GBECB
beta-galactosidase (EC 3.2.1.23) alpha chain - Escherichia coli (strain K-12)
N:Alternate names: beta-D-galactoside galactohydrolase; lactase; phospho-beta-D-galactos
C:Species: Escherichia coli
C>Date: 30-Sep-1987 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C:Accession: A65096; A25751; S09206
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MWID:97426617; PMID:9278503
A:Accession: A65096
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-1042 <BLAT>
A:Cross-references: UNIPROT:P06864; UNIPROT:Q47170; GB:AE000389; GB:U00096; NID:G1789451;
A:Experimental source: strain K-12, substrain MG1655
R:Stokes, H.W.; Betts, P.W.; Hall, B.G.
Mol. Biol. Evol. 2, 469-477, 1985
A:Title: Sequence of the ebgA gene of Escherichia coli: comparison with the lacZ gene.
A:Reference number: A93056; MWID:88216133; PMID:3939707
A:Accession: A25751
A:Molecule type: DNA
A:Residues: 80-476, 'R', 478-651, 'S', 653-660, 'P', 662-674, 'CRSWTPAKRS', 685-724, 'KCAVS', 730-'
A:Cross-references: GB:X03228; GB:M13700; GB:M13796; NID:G41311; PIDN:CAA26978.1; PID:G41
J. Biol. Chem. 258, 10204-10207, 1983
A:Title: The active site regions of lacZ and ebg beta-galactosidases are homologous.
A:Reference number: A92390; MWID:83290932; PMID:6111710
A:Contents: annotation; active site regions
R:Hall, B.G.; Betts, P.W.; Wootton, J.C.
Genetics 123, 635-648, 1989
A:Title: DNA sequence analysis of artificially evolved ebg enzyme and ebg repressor genes
A:Reference number: S09206; MWID:90128218; PMID:2515108
A:Accession: S09206
A:Molecule type: DNA
A:Residues: 13-476, 'R', 478-651, 'S', 653-660, 'P', 662-674, 'M', 780-1037, 'T', 1039-1042 <HAL>
A:Cross-references: EMBL:X52031; NID:G41307; PIDN:CAA36274.1; PID:G41309
C:Comment: The wild-type enzyme is an ineffective lactase. Two classes of point mutations

```
C/Genetics:
A:Gene: ebga
A:Map position: 68 min
C:Complex: homohexamer
C:Superfamily: beta-galactosidase
C:Keyword: glycosidase; hexamer; hydrolase; magnesium
F:/113,415,461/Binding site: magnesium (Glu, His, Glu) #status predicted
F:/461,502,524/Active site: Glu, Tyr, Glu #status predicted

Query Match
Best Local Similarity 81.1%; Score 30; DB 1; Length 1042;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLS 7
DB 1032 FSTNLS 1038

RESULT 21
E85968
evolved beta-D-galactosidase alpha subunit [imported] - Escherichia coli (strain O157:H7)
C/Species: Escherichia coli
C/Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C/Accession: E85968
R:/Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
Miller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimlantia, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A:/Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:/Reference number: A85480; MUID:21074935; PMID:11206551
A:/Accession: E85968
A:/Status: preliminary
A:/Molecule type: DNA
A:/Residues: 1-1042 <STO>
A:/Cross-references: UNIPROT:Q8XAM9; GB:AE005174; NID:912517660; PIDN:AAG58209.1; GSPDB:G
C:/Genetics:
A:Gene: ebga
C:/Superfamily: beta-galactosidase

Query Match
Best Local Similarity 81.1%; Score 30; DB 2; Length 1042;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLS 7
DB 1032 FSTNLS 1038

RESULT 22
F91123
evolved beta-D-galactosidase alpha subunit [imported] - Escherichia coli (strain O157:H7)
C/Species: Escherichia coli
C/Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C/Accession: F91123
R:/Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kohata, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:/Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc
A:/Reference number: A99629; MUID:21156231; PMID:11258796
A:/Accession: F91123
A:/Status: preliminary
A:/Molecule type: DNA
A:/Residues: 1-1042 <HAV>
A:/Cross-references: UNIPROT:Q8XAM9; GB:BA000007; PIDN:BA837381.1; PID:G13363431; GSPDB:G
C:/Genetics:
A:Gene: EC63958
C:/Superfamily: beta-galactosidase

Query Match
Best Local Similarity 81.1%; Score 30; DB 2; Length 1042;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 YSSNLS 7
DB 1032 FSTNLS 1038

RESULT 23
H86557
polymorphic membrane protein B Family [imported] - Chlamydia pneumoniae (strain J138)
C/Species: Chlamydia pneumoniae, Chlamydia pneumoniae
C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C/Accession: H86557
R:/Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Ist
Nucleic Acids Res. 28, 2311-2314, 2000
A:/Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A:/Reference number: A86491; MUID:20330349; PMID:10871362
A:/Accession: H86557
A:/Status: preliminary
A:/Molecule type: DNA
A:/Residues: 1-1723 <STO>
A:/Cross-references: UNIPROT:Q9Z812; GB:BA000008; NID:G8978911; PIDN:BA98746.1; GSPDB:GN
A:/Experimental source: strain J138
C:/Genetics:
A:Gene: pmp_20

Query Match
Best Local Similarity 81.1%; Score 30; DB 2; Length 1723;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSNLS 7
DB 105 SSNLS 110

RESULT 24
E72067
polymorphic membrane protein B family - Chlamydia pneumoniae (strain CWL029)
C/Species: Chlamydia pneumoniae, Chlamydia pneumoniae
C/Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C/Accession: E72067
R:/Kaiman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.;
Nature Genet. 21, 385-389, 1999
A:/Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.
A:/Reference number: A72000; MUID:99206606; PMID:10192388
A:/Accession: E72067
A:/Status: preliminary
A:/Molecule type: DNA
A:/Residues: 1-1723 <ARN>
A:/Cross-references: UNIPROT:Q9Z812; GB:AE001638; GB:AE001363; NID:94376819; PIDN:AAD1868(
A:/Experimental source: strain CWL029
C:/Genetics:
A:Gene: pmp_20

Query Match
Best Local Similarity 81.1%; Score 30; DB 2; Length 1723;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSNLS 7
DB 105 SSNLS 110

RESULT 25
C81601
polymorphic membrane protein B/C family CP0212 [imported] - Chlamydia pneumoniae (str
C/Species: Chlamydia pneumoniae, Chlamydia pneumoniae
C/Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 11-May-2000
C/Accession: C81601
R:/Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heideberg, J.F.; White, O.; Hickey, I
C.; Dodson, R.; Gwin, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000
A:/Title: Genome sequences of Chlamydia trachomatis McPn and Chlamydia pneumoniae AR39.
A:/Reference number: A81500; MUID:20150255; PMID:10684935
A:/Accession: C81601
```


A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1732 <REA>
A:Cross-references: GB:AE002182; GB:AE002161; NID:G7189140; PID:AAF38082.1; PID:G718914
A:Experimental source: strain AR39, HL cells
C:Genetics:
A:Gene: CP0212

Query Match
Best Local Similarity 100.0%; Score 30; DB 2; Length 1732;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YSSNLS 7
Db 114 SSNLS 119

RESULT 26

KWMS73
Ig kappa chain V region (MOPC 173) - mouse (tentative sequence)

C:Species: Mus musculus (house mouse)
C>Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 09-Jul-2004

C:Accession: A01926

R:Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
Eur. J. Biochem. 59, 525-537, 1975

A:Title: Determination of the primary structure of a mouse IgG2a immunoglobulin. Amino-
A:Reference number: A01926; MUID:76091934; PMID:812696

A:Accession: A01926

A:Molecule type: protein

A:Residues: 1-108 <SCH>
A:Cross-references: UNIPROT:P01643

C:Comment: This chain was isolated from a myeloma protein.
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa)

chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 16
C:Keywords: heterotetramer

F:16-90/Domain: immunoglobulin homology <IMM>
F:23-88/Disulfide bonds: #status predicted

Query Match
Best Local Similarity 78.4%; Score 29; DB 1; Length 108;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSSNLS 7
Db 50 YTSLS 56

RESULT 27

G38740
Ig kappa chain V region (Py69) - mouse

C:Species: Mus musculus (house mouse)
C>Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 09-Jul-2004

C:Accession: G38740

R:Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
J. Biol. Chem. 266, 6607-6613, 1991

A:Title: Heavy and light chain variable region sequences and antibody properties of anti-
A:Reference number: A38740; MUID:91177923; PMID:1706720

A:Accession: G38740

A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A:Molecule type: mRNA

A:Residues: 1-111 <RUF>
A:Cross-references: UNIPROT:Q91WS9

C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

F:19-93/Domain: immunoglobulin homology <IMM>

Query Match
Best Local Similarity 78.4%; Score 29; DB 2; Length 111;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSSNLS 7
Db 114 SSNLS 119

Db 53 YTSLS 59

RESULT 28

A38740
Ig kappa chain V region (Py20) - mouse

C:Species: Mus musculus (house mouse)
C>Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 09-Jul-2004

C:Accession: A38740

R:Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
J. Biol. Chem. 266, 6607-6613, 1991

A:Title: Heavy and light chain variable region sequences and antibody properties of anti-
A:Reference number: A38740; MUID:91177923; PMID:1706720

A:Accession: A38740

A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A:Molecule type: mRNA

A:Residues: 1-111 <RUF>
A:Cross-references: UNIPROT:Q91WS9

C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

F:19-93/Domain: immunoglobulin homology <IMM>

Query Match
Best Local Similarity 78.4%; Score 29; DB 2; Length 111;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSSNLS 7
Db 53 YTSLS 59

RESULT 29

E38740
Ig kappa chain V region (Py54) - mouse

C:Species: Mus musculus (house mouse)
C>Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 09-Jul-2004

C:Accession: E38740

R:Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
J. Biol. Chem. 266, 6607-6613, 1991

A:Title: Heavy and light chain variable region sequences and antibody properties of anti-
A:Reference number: A38740; MUID:91177923; PMID:1706720

A:Accession: E38740

A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A:Molecule type: mRNA

A:Residues: 1-111 <RUF>
A:Cross-references: UNIPROT:Q91WS9

C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

F:19-93/Domain: immunoglobulin homology <IMM>

Query Match
Best Local Similarity 78.4%; Score 29; DB 2; Length 111;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSSNLS 7
Db 53 YTSLS 59

RESULT 30

G38740
Ig kappa chain V region (Py2) - mouse

C:Species: Mus musculus (house mouse)
C>Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 09-Jul-2004

C:Accession: G38740

R:Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
J. Biol. Chem. 266, 6607-6613, 1991

A:Title: Heavy and light chain variable region sequences and antibody properties of anti-
A:Reference number: A38740; MUID:91177923; PMID:1706720

A:Accession: G38740

A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A:Molecule type: mRNA

A:Residues: 1-111 <RUF>

A:Cross-references: UNIPROT:Q91WS9
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotrimer; immunoglobulin
 F:19-93/Domain: immunoglobulin homology <IMM>

Query Match 78.4%; Score 29; DB 2; Length 111;
 Best Local Similarity 71.4%; Pred. No. 38;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLS 7
 ||:||||
 Db 53 YSSLS 59

RESULT 31
 T11242
 ribosomal protein S3, mitochondrial - red alga (Porphyra purpurea) mitochondrion
 C:Species: mitochondrion Porphyra purpurea
 C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
 C/Accession: T11242
 R:Burger, G.; Saint-Louis, D.; Gray, M.W.; Lang, B.F.
 A:Title: Induction of the EMBL Data Library, December 1998
 A:Description: Complete sequence of the mitochondrial DNA of the red alga, Porphyra purf
 A:Reference number: Z17255
 A:Accession: T11242
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-227 <BUR>

A:Cross-references: UNIPROT:O99993; EMBL:AF114794; NID:g4106927; PID:g4106954; PIDN:AAD0
 C:Genetics:
 A:Gene: rps3
 A:Genome: mitochondrion
 C:Function:
 A:Pathway: protein biosynthesis
 C:Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match 78.4%; Score 29; DB 2; Length 227;
 Best Local Similarity 71.4%; Pred. No. 82;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLS 7
 ||:||||
 Db 205 YSSSLHT 211

RESULT 32
 G89567
 protein T08A9.2 [imported] - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Nov-2001
 C/Accession: G89567
 R:anonymous, The C. elegans Sequencing Consortium.
 A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
 Science 282, 2012-2018, 1998
 A:Reference number: A75000; PMID:9069613; PMID:9851916
 A:Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C_elg
 A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
 A:Accession: G89567
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-241 <STO>
 A:Cross-references: GB:chr.X; PIDN:AAA81419.1; PID:g1065500; GSPDB:GN00028; CESP:T08A9.2
 A:Note: similar to C. elegans protein C40H1.5
 C:Genetics:
 A:Gene: T08A9.2
 A:Map position: X

Query Match 78.4%; Score 29; DB 2; Length 243;
 Best Local Similarity 83.3%; Pred. No. 88;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLS 6
 |||||

Db 150 YSSNPF 155

RESULT 33
 TWMSJA

transcription factor AP-1 - mouse
 N:Alternate names: fos-associated 39K protein; protein PEA1; transcription factor, TGACTC
 C:Species: Mus musculus (house mouse)
 C>Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 09-Jul-2004
 C/Accession: A31345; S04683; S04537

R: Ryder, K.; Nathans, D.
 Proc. Natl. Acad. Sci. U.S.A. 85, 8464-8467, 1988
 A:Title: Induction of proto-oncogene c-jun by serum growth factors.
 A:Reference number: A31345; PMID:89042204; PMID:3186736

A:Accession: A31345
 A:Molecule type: mRNA
 A:Residues: 1-334 <RYD>
 A:Cross-references: UNIPROT:P05627; GB:J04115; NID:g192577; PIDN:AAA37419.1; PID:g309169
 R:Lamp, W.W.; Mamajek, P.; Sabosone-Corsi, P.; Verma, I.M.
 Nature 334, 629-631, 1988
 A:Title: Induction of proto-oncogene JUN/AP-1 by serum and TPA.
 A:Reference number: S04683; PMID:88302467; PMID:2457172

A:Accession: S04683
 A:Molecule type: mRNA
 A:Residues: 1-334 <LAM>

A:Cross-references: EMBL:X12740; NID:g52762; PIDN:CAA31336.1; PID:g52763
 R: Rybeck, R.P.; Hirai, S.I.; Yaniv, M.; Bravo, R.
 Nature 334, 535-537, 1988

A:Title: Transcriptional activation of c-jun during the G(0)/G(1) transition in mouse fib
 A:Reference number: S04537; PMID:88302446; PMID:3136397

A:Molecule type: mRNA
 A:Residues: 1-182, 'C', 184-334 <RYS>

A:Cross-references: EMBL:X12761; NID:g52758; PIDN:CAA31352.1; PID:g52759

C:Genetics:

A:Gene: jun-A
 C:Superfamily: jun transforming protein; fos/jun DNA-binding domain homology
 C:Keywords: DNA binding; leucine zipper; phosphoprotein; proto-oncogene; transcription fa
 F:550-590/Domain: fos/jun DNA-binding domain homology <FJD>
 F:283-311/Region: leucine zipper motif

Query Match 78.4%; Score 29; DB 1; Length 334;
 Best Local Similarity 71.4%; Pred. No. 1.2e+02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLS 7
 ||:||||
 Db 159 YSASLS 165

RESULT 34
 S12742
 transcription factor AP-1 - rat
 N:Alternate names: transforming protein (jun)
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
 C/Accession: S12742; S20028; A37381
 R:Kitabayashi, I.; Saka, F.; Gachelin, G.; Yokoyama, K.
 Nucleic Acids Res. 18, 3400, 1990
 A:Title: Nucleotide sequence of rat c-jun protooncogene.
 A:Reference number: S12742; PMID:90287724; PMID:2113275
 A:Accession: S12742
 A:Molecule type: DNA
 A:Residues: 1-334 <KIT>
 A:Cross-references: UNIPROT:P17325; EMBL:X17215; NID:g57079; PIDN:CAA35084.1; PID:g57080
 R:Kitabayashi, I.; Kawakami, Z.; Chiu, R.; Ozawa, K.; Matsuo, T.; Toyoshima, S.; Umesor
 EMBO J. 11, 167-175, 1992
 A:Title: Transcriptional regulation of the c-jun gene by retinoic acid and E1A during dif
 A:Reference number: S20028; PMID:92155155; PMID:1310930
 A:Accession: S20028
 A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-334 <KIT>

A/Cross-references: EMBL:X17215; NID:g57079; PIDN:CAA35084.1; PID:g57080
R:Sakai, M.; Okuda, A.; Hatayama, I.; Sato, K.; Nishi, S.; Muramatsu, M.
Cancer Res. 49, 5633-5637, 1999
A/Title: Structure and expression of the rat c-jun messenger RNA: tissue distribution at
A/Reference number: A37381; MUID:90002916; PMID:2507134
A/Accession: A37381
A/Molecule type: mRNA
A/Residues: 1-334 <SAS>
A/Cross-references: GB:X17163; NID:g57819; PIDN:CAA35041.1; PID:g57820
C/Genetics:
A/Genes: jun
C/Function:
A/Description: transcription factor
C/Superfamily: jun transforming protein; fos/jun DNA-binding domain homology
C/Keywords: DNA binding; leucine zipper; nucleus; phosphoprotein; transcription factor;
F:250-290/Domain: fos/jun DNA-binding domain homology <F0D>
F:283-311/Region: leucine zipper motif

Query Match 78.4%; Score 29; DB 2; Length 334;
Best Local Similarity 71.4%; Pred. No. 1.2e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLS 7
DB 159 YSASLHS 165

RESULT 35

hypothetical protein T23G11.2 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
R:Gardner, A.
submitted to the EMBL Data Library, October 1996
A/Reference number: Z19993
A/Accession: T23192
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-347 <ML>
A/Cross-references: UNIPROT:Q45811; EMBL:Z81130; PIDN:CAE03416.1; GSPDB:GN00019; CESP:T2
A/Experimental source: clone T23G11
C/Genetics:
A/Genes: CESP:T23G11.2
A/Map position: 1
A/Introns: 74/2; 128/3; 250/2

Query Match 78.4%; Score 29; DB 2; Length 347;
Best Local Similarity 83.3%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLS 6
DB 151 YSKNLS 156

RESULT 36

hypothetical protein SPAC4F10.18 - fission yeast (Schizosaccharomyces pombe)
T38822
C/Species: Schizosaccharomyces pombe
C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
R:Connor, R.; Churcher, C.M.; Barrett, B.G.; Rajadream, M.A.; Wood, V.
submitted to the EMBL Data Library, September 1997
A/Reference number: Z21813
A/Accession: T38822
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-331 <CON>
A/Cross-references: UNIPROT:O36030; EMBL:Z298980; PIDN:CAB11721.1; GSPDB:GN00066; SPDB:SH
A/Experimental source: strain 97zh-; cosmid c4F10
C/Genetics:
A/Genes: SPDB:SPAC4F10.18

A/Map position: 1
A/Introns: 9/2; 35/1
C/Superfamily: Schizosaccharomyces pombe hypothetical protein SPAC4F10.18

Query Match 78.4%; Score 29; DB 2; Length 391;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLS 6
DB 81 YSENLS 86

RESULT 37

glucose-6-phosphate isomerase pgl - Bacillus subtilis
B69675
C/Species: Bacillus subtilis
C/Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
R:Kunert, P.; Ogasawara, N.; Moser, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertec
C.; Bron, S.; Brouillet, S.; Bruch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A/Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallerc
lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Hoisappel, S.; Hosono, S.; Hullo, M.F.
Koester, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois
A/Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Mauda, S.; Meusel
Y, M.; Ogasawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadate, Y.; Sato, T.; Scanlon
A/Authors: Schleich, S.; Schroeder, R.; Scollone, F.; Sekiguchi, U.; Sekowska, A.; Seror
akuch, M.; Tanakoshi, A.; Tanaka, T.; Tepsara, P.; Tognoli, A.; Tosato, V.; Uchiyama
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A/Authors: Yoshikawa, H.F.; Zamesteln, E.; Yoshikawa, H.; Darchin, A.
A/Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A/Reference number: A63580; MUID:98044033; PMID:9384377
A/Accession: B69675
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-451 <KUN>
A/Cross-references: UNIPROT:P80860; GB:Z99120; GB:AL009126; NID:g2635613; PIDN:CAB15124.3
A/Experimental source: strain 168
C/Genetics:
A/Genes: pgl
C/Superfamily: glucose-6-phosphate isomerase

Query Match 78.4%; Score 29; DB 2; Length 451;
Best Local Similarity 71.4%; Pred. No. 1.7e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLS 7
DB 307 YSTDLS 313

RESULT 38

unknown protein 29405-27288 [imported] - Arabidopsis thaliana
G96655
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
R/Accession: G96655
C/Accession: G96655
R/Theologas, A.; Ecker, J.R.; Palm, C.D.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
anen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luoro, J.S.; Malt, R.; Martini,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A/Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A/Reference number: AB6141; MUID:21016719; PMID:11130712
A/Accession: G96655
A/Status: preliminary

A:Molecule type: DNA
A:Residues: 1-465 <STO>
A:Cross-references: UNIPROT:Q9CAN8; GB:AE005173; NID:G659844; PIDN:AAF18699.1; GSPDB:GN
C:Genetics:
A:Gene: F16M19.14
A:Map position: 1

Query Match 78.4%; Score 29; DB 2; Length 465;
Best Local Similarity 83.3%; Pred. No. 1.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 YSSNLH 6
Db 63 FSSNLH 68

RESULT 39
T33061
hypothetical protein F56C3.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: T33061
R:Stonking, T.
submitted to the EMBL Data Library, May 1998
A:Description: The sequence of C. elegans cosmid F56C3.
A:Reference number: Z21276
A:Accession: T33061
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-516 <STO>
A:Cross-references: UNIPROT:O61758; EMBL:AF067214; PIDN:AACT7005.1; GSPDB:GND00028; CESP:
A:Experimental source: strain Bristol N2; clone F56C3
C:Genetics:
A:Gene: CESP:F56C3.2
A:Map position: X
A:Introns: 69/2; 144/3; 230/2; 446/3
C:Superfamily: Caenorhabditis elegans hypothetical protein F47H4.4

Query Match 78.4%; Score 29; DB 2; Length 516;
Best Local Similarity 83.3%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLH 6
Db 257 YQSNLH 262

RESULT 40
F90407
molybdopterin biosynthesis protein (moa-2) [imported] - Sulfolobus solfataricus
C:Species: Sulfolobus solfataricus
C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 16-Aug-2004
C:Accession: F90407
R:She, O.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, F.
arrett, R.A.; Regan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to Genbank, April 2001
A:Description: Sulfolobus solfataricus complete genome.
A:Reference number: A99139
A:Accession: F90407
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-550 <KUR>
A:Cross-references: UNIPROT:Q97W71; GB:AE006641; NID:G13815669; PIDN:AAK42517.1; GSPDB:G
C:Genetics:
A:Gene: moa-2
C:Superfamily: Molybdenum cofactor molybdenum incorporation protein MoaA with molybdate-

Query Match 78.4%; Score 29; DB 2; Length 550;
Best Local Similarity 83.3%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLH 6

Db 208 YSSNLH 213

Search completed: December 17, 2004, 18:30:16
Job time : 3.75281 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Comphen Ltd.

OM protein - protein search, using sw model

Run on: December 17, 2004, 18:29:23 ; Search time 20.9213 Seconds
(without alignments)
192.513 Million cell updates/sec

Title: US-10-089-500-7
Perfect score: 37
Sequence: 1 YSSNLS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37	100.0	4780	2	Q8IE54
2	34	91.9	404	2	Q7RI06
3	34	91.9	468	1	SKIP MOUSE
4	34	91.9	468	1	Ash66112 mus muscu
5	34	91.9	642	2	Q9RC03
6	34	91.9	744	2	Q62788
7	33	89.2	219	2	Q94192
8	33	89.2	368	2	Q9CD01
9	33	89.2	391	2	Q8RR04
10	33	89.2	470	2	Q845X4
11	33	89.2	474	2	Q9AJ10
12	33	89.2	474	2	Q9ERT8
13	33	89.2	474	2	Q9ERT9
14	33	89.2	474	2	Q9F1Y8
15	33	89.2	474	2	Q9F1Y9
16	33	89.2	474	2	Q9F1Z0
17	33	89.2	474	2	Q9FAV1
18	33	89.2	474	2	Q9FAV9
19	33	89.2	474	2	Q9FAW0
20	33	89.2	474	2	Q9FAW1
21	33	89.2	474	2	Q9FAW2
22	33	89.2	480	2	Q9FAW4
23	33	89.2	817	2	Q7PK57
24	32	86.5	169	2	Q9S350
25	32	86.5	172	2	Q70Y33
26	32	86.5	172	2	CAD44274
27	32	86.5	325	2	Q43751
28	32	86.5	331	2	Q22124
29	32	86.5	478	2	Q8ES05
30	32	86.5	480	2	Q6BDD4
31	32	86.5	481	2	Q9PFE4

32	32	86.5	485	2	Q96547	Q96547 capsicum an
33	32	86.5	489	2	Q42872	Q42872 lycopersico
34	32	86.5	500	2	Q93W20	Q93W20 nicotiana t
35	32	86.5	536	2	Q83Z58	Q83Z58 mesoplasma
36	32	86.5	598	2	Q708M6	Q708M6 anopheles g
37	32	86.5	615	2	Q9RP84	Q9RP84 acholepasm
38	31	83.8	335	2	Q8RPN2	Q8RPN2 fusobacteri
39	31	83.8	347	2	Q9J9Q6	Q9J9Q6 campylobact
40	31	83.8	347	2	Q9LAK4	Q9LAK4 campylobact
41	31	83.8	347	2	Q9F0N1	Q9F0N1 campylobact
42	31	83.8	347	2	Q938X8	Q938X8 campylobact
43	31	83.8	347	2	AAB82873	AAB82873 campyloba
44	31	83.8	380	2	Q9RM00	Q9RM00 neisseria m
45	31	83.8	380	2	Q9K0V4	Q9K0V4 neisseria m

ALIGNMENTS

```

RESULT 1
ID Q8IE54 PRELIMINARY; PRT; 4780 AA.
AC Q8IE54;
DT 01-MAR-2003 (T-EMBLrel. 23, Created)
DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
DE 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Hypothetical protein PF13_0148.
GN Name=PF13_0148;
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=96329;
RN [1]
RP SEQUENCE FROM N.A.
RA Harris B., Lennard N., Clark L., Line A., Barron A., Corton C.,
RA Berriman M., Pain A., Hall N., Atkin R., Chillingworth C., Doggett J.,
RA Ormond D., Sanders M., Hayes R., Hall S., Quail M., Barrett B.,
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL844509; CAD52412.1; -
DR InterPro; IPR008266; Tyr_kinase AS.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; UNKNOWN_1.
KM Hypothetical protein.
SQ SEQUENCE 4780 AA; 575455 MW; 568F461F83657D44 CRC64;

Query Match 100.0%; Score 37; DB 2; Length 4780;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLS 7
Db 1325 YSSNLS 1331

RESULT 2
ID Q7RI06 PRELIMINARY; PRT; 404 AA.
AC Q7RI06;
DT 01-MAR-2004 (T-EMBLrel. 26, Created)
DT 01-MAR-2004 (T-EMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Asparagine-rich protein.
GN Name=PY03561;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=173XNL;
RC PubMed=12368865;
RA Carlton J.M., Anguioni S.V., Suh B.B., Kooij T.W., Pereira M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallow S.V., van Aken S.E., Riedmiller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoabli A., Cummings L.M.,

```

RA Florens L., Yates F.R. III, Raine J.D., Sindén R.E., Harris M.A.,
 RA Cunningham D.A., Preiser P.R., Bergman L.W., Valdivia A.B.,
 RA van Lin L.H., Jance C.J., Waters A.P., Smith H.O., White O.R.,
 RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
 RA Carucci D.J.,
 RT "Genome sequence and comparative analysis of the model rodent malaria
 parasite Plasmodium yoelii yoelii".
 RL Nature 419:512-519(2002).
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data
 DR EMBL:AA01001031; EMBL5290.1; -;
 SQ SEQUENCE 404 AA; 47311 MW; 79D9BACAF487ADC CRC64;
 QY Query Match 91.9%; Score 34; DB 2; Length 404;
 Best Local Similarity 85.7%; Pred. No. 77;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Db 302 YSNNLHS 308
 QY 1 YSNNLHS 7
 Db 302 YSNNLHS 308
 RESULT 3
 SKIP MOUSE STANDARD; PRT; 468 AA.
 ID SKIP MOUSE
 AC 08C5L6; 009040;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 29-MAR-2004 (Rel. 43, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Skeletal muscle and kidney enriched inositol phosphatase
 DE (EC 3.1.3.56).
 GN Name=Skip; Synonyms=Pps;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97325785; PubMed=9182797;
 RA Hamilton B.A., Smith D.J., Mueller K.L., Kerrebrock A.W.,
 RA Bronson R.T., van Berkel V., Daly M.J., Kruglyak L., Reeve M.P.,
 RA Nemauser U.L., Hawkins T.L., Rubin E.M., Lander E.S.,
 RT "The vibrator mutation causes neurodegeneration via reduced expression
 RT of PTP alpha: positional complementation cloning and extragenic
 RT suppression."
 RL Neuron 18:711-722(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=11S, and 1S;
 RA Ehringer M.A., Thompson J., Conroy O., Xu Y., Yang F., Caniffi J.,
 RA Beeson M., Gordon L., Bennett B., Johnson T.E., Sikela J.M.,
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=057BL/6J; TISSUE=Medulla oblongata, and Ovary;
 RX MEDLINE=22354683; PubMed=1246851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaido I., Otsu N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojodori T.,
 RA Balderelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schirml L.M., Kampin A., Matsuda H., Batalov S., Beisels K.W.,
 RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbett L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Kongsaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Pereira G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Sempile C.A., Setou M., Shimada K.,

RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wyner L., Wynshaw-Boris A., Yanagisawa M., Yang L.,
 RA Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hironaka-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai U., Mizawa K., Arikawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs."
 RL Nature 420:563-573(2002).
 CC -1- FUNCTION: Inositol 5-phosphatase which acts on inositol 1,4,5-
 CC triphosphate, inositol 1,3,4,5-tetrakisphosphate,
 CC phosphatidylinositol 4,5-bisphosphate and phosphatidylinositol
 CC 3,4,5-trisphosphate. Has 6-fold higher affinity for
 CC phosphatidylinositol 4,5-bisphosphate than for inositol 1,4,5-
 CC triphosphate. May negatively regulate assembly of the actin
 CC cytoskeleton (By similarity).
 CC -1- CATALYTIC ACTIVITY: D-myo-inositol 1,4,5-trisphosphate + H(2)O =
 CC myo-inositol 1,4-bisphosphate + phosphate.
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum. Following stimulation
 CC with EGF, translocates to membrane ruffles (By similarity).
 CC -1- SIMILARITY: Belongs to the inositol-1,4,5-trisphosphate 5-
 CC phosphatase type II family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: U96724; AAC53265.1; -;
 DR EMBL: U96726; AAC60757.1; -;
 DR EMBL: AF483522; AAL90796.1; -;
 DR EMBL: AF483523; AAL90797.1; -;
 DR EMBL: AK054436; BAC35778.1; -;
 DR EMBL: AK078104; BAC37126.1; -;
 DR HSSP: O43001; 1192.
 DR WGD; MG1:1194899; Ppe.
 DR GO; GO:0005829; C:cytosol; ISS.
 DR GO; GO:0043005; C:neuronal cell projection; ISS.
 DR GO; GO:0016312; F:inositol bisphosphate phosphatase activity; ISS.
 DR GO; GO:0046030; F:inositol trisphosphate phosphatase activity; ISS.
 DR GO; GO:0042577; F:lipid phosphatase activity; ISS.
 DR GO; GO:0030036; P:actin cytoskeleton organization and biogenesis; ISS.
 DR InterPro; IPR005135; Exo_endo_phos.
 DR InterPro; IPR000300; IPpe.
 DR Pfam; PF03372; Exo_endo_phos; 1.
 DR SMART; SM00129; IPpe; 1.
 DR Endoplasmic reticulum, Hydrolase.
 FT DOMAIN 34 337 Catalytic (Potential).
 FT DOMAIN 340 468 Required for ruffle localization.
 FT CONFLICT 329 329 D -> E (in Ref. 3; BAC37126).
 SQ SEQUENCE 468 AA; 54158 MW; F2E1CA370B97A8A1 CRC64;
 QY Query Match 91.9%; Score 34; DB 1; Length 468;
 Best Local Similarity 85.7%; Pred. No. 91;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Db 434 YSNNLHS 440
 QY 1 YSNNLHS 7
 Db 434 YSNNLHS 440
 RESULT 4
 AAH66112 PRELIMINARY; PRT; 468 AA.
 ID AAH66112
 AC AAH66112;
 DT 14-APR-2004 (TrEMBLrel. 27, Created)

DT 14-APR-2004 (TREMBLrel. 27, last sequence update)
 DT 14-APR-2004 (TREMBLrel. 27, last annotation update)
 DE Pps protein.
 GN Pps.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Goughwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywicki M.T., Skalske U., Smalls D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Maira M.A.,
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX Strauberg R.,
 RA Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 RL EMBL; BC066112; AAH66112.1;
 DR EMBL; BC066112; AAH66112.1;
 SQ SEQUENCE 468 AA; 54158 MW; F2E1CA370B97A0A1 CRC64;
 QY 1 YSSNLS 7
 DB 434 YSSNLS 440
 Query Match 91.9%; Score 34; DB 2; Length 468;
 Best Local Similarity 85.7%; Pred. No. 91;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RA Warren T., Wietzorrek A., Woodward J.R., Barrell J.G., Parkhill J.,
 RA Hopwood D.A.,
 RT "Complete genome sequence of the model actinomycete Streptomyces
 RT coelicolor A3(2)." ;
 RL Nature 417:141-147(2002).
 DR EMBL; AL939130; CAC01579.1; -.
 DR HSSP; P82974; 1J3G.
 DR GO; GO:008745; F:N-acetyl[muramoyl]-L-alanine amidase activity; IEA.
 DR GO; GO:0009253; P:peptidoglycan catabolism; IEA.
 DR InterPro; IPR002502; Amidase_2.
 DR Pfam; PF01510; Amidase_2; 1.
 DR SMART; SM00644; Aml_2; 1.
 KW Complete proteome.
 SQ SEQUENCE 642 AA; 67149 MW; 4659E442C31A033 CRC64;
 QY 1 YSSNLS 7
 DB 323 YSSNLS 329
 Query Match 91.9%; Score 34; DB 2; Length 642;
 Best Local Similarity 85.7%; Pred. No. 1.3e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 6
 Q62788 PRELIMINARY; PRT; 744 AA.
 AC 062788;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, last annotation update)
 DE Cys2/His2 zinc finger protein.
 GN Name=CXK2;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_TaxId=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96033674; PubMed=7595478;
 RA Post U., Thiesen H.J., Colello R.J., Schwab M.E.,
 RT "A new Cys2/His2 zinc finger gene, CXK2, is expressed in
 RT differentiated rat oligodendrocytes and encodes a protein with a
 RT functional repressor domain." ;
 RL J. Neurochem. 65:1955-1966(1995).
 DR EMBL; U27186; AAB60512.1; -.
 DR HSSP; P25490; 1ZNM.
 DR GO; GO:005634; C:nucleus; IEA.
 DR GO; GO:0003676; F:nucleic acid binding; IEA.
 DR GO; GO:0008270; F:zinc ion binding; IEA.
 DR GO; GO:006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR001909; KRAB.
 DR InterPro; IPR007087; Znf_C2H2.
 DR Pfam; PF01352; KRAB; 1.
 DR Pfam; PF00096; zf-C2H2; 19.
 DR Prodom; PD000003; Znf_C2H2; 17.
 DR SMART; SM00349; KRAB; 1.
 DR SMART; SM00355; Znf_C2H2; 19.
 DR PROSITE; PS50805; KRAB; 1.
 DR PROSITE; PS50028; ZINC_FINGER_C2H2_1; 17.
 DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 17.
 SQ SEQUENCE 744 AA; 85421 MW; 02EDA246E4EA0F5 CRC64;
 QY 1 YSSNLS 7
 DB 501 YSSNLS 507
 Query Match 91.9%; Score 34; DB 2; Length 744;
 Best Local Similarity 85.7%; Pred. No. 1.5e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 7

```
O94192
ID O94192 PRELIMINARY; PRT; 219 AA.
AC O94192;
DT 01-FEB-1997 (TEMBLrel. 02, Created)
DT 01-FEB-1997 (TEMBLrel. 02, Last sequence update)
DT 01-JUN-2003 (TEMBLrel. 24, Last annotation update)
DE Hypothetical protein F22H10.6.
GN ORFNames=F22H10.6;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=9069613; PubMed=9851916;
RA Wilson R.;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology, the C. elegans Sequencing Consortium."
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Langston Y., Hawkins J.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Wilson R.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; J070845; AAB09103.1; -.
DR PIR; T30122; T30122.
DR WormPep; F22H10.6; CE09575.
KW Hypothetical protein.
SQ SEQUENCE 219 AA; 25258 MW; 2091CC121B35F5FDA CRC64;

Query Match 89.2%; Score 33; DB 2; Length 219;
Best Local Similarity 85.7%; Pred. No. 63;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSSNLS 7
Db 22 FSSNLS 28

RESULT 8
O9CDQ1 PRELIMINARY; PRT; 368 AA.
ID O9CDQ1
AC O9CDQ1;
DT 01-JUN-2001 (TEMBLrel. 17, Created)
DT 01-JUN-2001 (TEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TEMBLrel. 24, Last annotation update)
DE Hypothetical protein YweB.
GN Name=YweB; OrderedlocusNames=IL2167;
OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
OX NCBI_TaxID=1360;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IL1403;
RX MEDLINE=21235186; PubMed=11337471;
RA Bolotin A., Winkler P., Manger S., Jallion O., Malame K.,
RA Weisenbach J., Ehrlich S.D., Sorokin A.;
RT "The complete genome sequence of the lactic acid bacterium Lactococcus
RT lactis ssp. lactis IL1403."
RL Genome Res. 11:731-753(2001).
DR EMBL; AB006445; AAK06265.1; -.
DR PIR; G86895; G86895.
```

```
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 368 AA; 41726 MW; C1243C3B9F140DD CRC64;

Query Match 89.2%; Score 33; DB 2; Length 368;
Best Local Similarity 85.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSSNLS 7
Db 121 FSSNLS 127

RESULT 9
O8RR04 PRELIMINARY; PRT; 391 AA.
ID O8RR04
AC O8RR04;
DT 01-JUN-2002 (TEMBLrel. 21, Created)
DT 01-JUN-2002 (TEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
DE DNA gyrase subunit B (Ec 5.99.1.3) (Fragment).
GN Name=gyrB;
OS Cytophaga sp. T-588.
OC Bacteria; Bacteroidetes; Sphingobacteriales; Sphingobacteriales;
OC Flexibacteraceae; Cytophaga.
OX NCBI_TaxID=173740;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22431356; PubMed=12542710;
RA Matsuo Y., Suzuki M., Kasai H., Shizuri Y., Harayama S.;
RT "Isolation and phylogenetic characterization of bacteria capable of
RT inducing differentiation in the green alga Monostroma oxyspermum."
RL Environ. Microbiol. 5:25-35(2003).
CC -1- FUNCTION: DNA gyrase negatively supercoils closed circular double-
CC stranded DNA in an ATP-dependent manner and also catalyzes the
CC interconversion of other topological isomers of double-stranded
CC DNA rings, including catenanes and knotted rings (By similarity).
CC -1- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining
CC of double-stranded DNA.
CC -1- SIMILARITY: Belongs to the type II topoisomerase family.
DR EMBL; AB073038; BAB88340.1; -.
DR HSSP; P06982; 1A76.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0003918; F:DNA topoisomerase (ATP-hydrolyzing) activity; IEA.
DR GO; GO:0018853; F:isomerase activity; IEA.
DR GO; GO:0006265; P:DNA topological change; IEA.
DR InterPro; IPR003594; ATPbind_ATPase.
DR InterPro; IPR001241; DNA_topoisom.
DR Pfam; PF00204; DNA_gyraseB; 1.
DR Pfam; PF02518; HATPase_c1.
DR PRINTS; PR00418; TP12FAMILY.
DR SMART; SM00433; TOP2c; 1.
DR PROSITE; PS00177; TOPOISOMERASE_II; 1.
KW ATP-binding; Isomerase; Topoisomerase.
FT NON_TER 1
FT NON_TER 391
SQ SEQUENCE 391 AA; 43486 MW; 0C5B029383468759 CRC64;

Query Match 89.2%; Score 33; DB 2; Length 391;
Best Local Similarity 85.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YSSNLS 7
Db 158 YSSNLS 164

RESULT 10
O845X4 PRELIMINARY; PRT; 470 AA.
ID O845X4
AC O845X4;
DT 01-JUN-2003 (TEMBLrel. 24, Created)
DT 01-JUN-2003 (TEMBLrel. 24, Last sequence update)
```



```

DT 01-MAR-2004 (TRENBLREL. 26, Last annotation update)
DE DNA gyrase B subunit (Fragment).
GN Name=gyrB;
OS Cellulophaga fucicola.
OC Bacteriia; Bacteroidetes; Flavobacteriia; Flavobacteriales;
OC Flavobacteriaceae; Cellulophaga.
OX NCBI_TaxID=76595;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=LMG18536;
RX MEDLINE=22431356; PubMed=12542710;
RA Matsuo Y., Suzuki M., Kaeai H., Shizuri Y., Harayama S.;
RT Isolation and phylogenetic characterization of bacteria capable of
RT inducing differentiation in the green alga Monostroma oxyspermum;
RL Environ. Microbiol. 5:25-35(2003).
CC -1- FUNCTION: DNA gyrase negatively supercoils closed circular double-
CC stranded DNA in an ATP-dependent manner and also catalyzes the
CC interconversion of other topological isomers of double-stranded
CC DNA rings, including catenanes and knotted rings (by similarity).
CC -1- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining
CC of double-stranded DNA.
CC -1- SIMILARITY: Belongs to the type II topoisomerase family.
DR EMBL; AB071140; F:ATP binding; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0003918; P:DNA topoisomerase (ATP-hydrolyzing) activity; IEA.
DR GO; GO:0006304; P:DNA modification; IEA.
DR GO; GO:0006265; P:DNA topological change; IEA.
DR InterPro; IPR003594; ATPbind_ATPase.
DR InterPro; IPR011558; DNA_gyrase_B.
DR InterPro; IPR001241; DNA_topoisom.
DR InterPro; IPR006171; Toprim_dom.
DR Pfam; PF00204; DNA_gyraseB_1.
DR Pfam; PF02518; HATPase_c1.
DR Pfam; PF01751; Toprim_1.
DR PRINTS; PR00418; TP12FAMILY.
DR ProDom; PD149633; DNA_gyrase_B; 1.
DR SMART; SM00433; TOP2c; 1.
DR PROSITE; PS00177; TOPOISOMERASE II; 1.
KM ATP-binding; Isomerase; Topoisomerase.
FT NON_TER 1
FT NON_TER 470 474
SQ SEQUENCE 470 AA; 52527 MW; DF6BAE2EFD21A7D6 CRC64;

Query Match      89.2%; Score 33; DB 2; Length 470;
Best Local Similarity 85.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLS 7
DB 165 YESNLS 171

RESULT 11
Q9AJIO PRELIMINARY; PRT; 474 AA.
AC Q9AJIO;
DT 01-JUN-2001 (TRENBLREL. 17, Created)
DT 01-JUN-2001 (TRENBLREL. 17, Last sequence update)
DT 01-MAR-2004 (TRENBLREL. 26, Last annotation update)
DE DNA gyrase B subunit (Fragment).
GN Name=gyrB;
OS marine CFB-group bacterium MBIC04478.
OC Bacteria; Bacteroidetes.
OX NCBI_TaxID=135558;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=MBIC4478;
RA Suzuki M., Takadera T., Harayama S., Yamamoto S.;
RT Submitted (Aug-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: DNA gyrase negatively supercoils closed circular double-
CC stranded DNA in an ATP-dependent manner and also catalyzes the
CC interconversion of other topological isomers of double-stranded

```

```

CC DNA rings, including catenanes and knotted rings (by similarity).
CC -1- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining
CC of double-stranded DNA.
CC -1- SIMILARITY: Belongs to the type II topoisomerase family.
DR EMBL; AB047186; BAB40409.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0003918; P:DNA topoisomerase (ATP-hydrolyzing) activity; IEA.
DR GO; GO:0006304; P:DNA modification; IEA.
DR GO; GO:0006265; P:DNA topological change; IEA.
DR InterPro; IPR003594; ATPbind_ATPase.
DR InterPro; IPR011558; DNA_gyrase_B.
DR InterPro; IPR001241; DNA_topoisom.
DR InterPro; IPR006171; Toprim_dom.
DR Pfam; PF00204; DNA_gyraseB_1.
DR Pfam; PF02518; HATPase_c1.
DR Pfam; PF01751; Toprim_1.
DR PRINTS; PR00418; TP12FAMILY.
DR ProDom; PD149633; DNA_gyrase_B; 1.
DR SMART; SM00433; TOP2c; 1.
DR PROSITE; PS00177; TOPOISOMERASE II; 1.
KM ATP-binding; Isomerase; Topoisomerase.
FT NON_TER 1
FT NON_TER 474 474
SQ SEQUENCE 474 AA; 52920 MW; 1E1E631B9CEDFCC2 CRC64;

Query Match      89.2%; Score 33; DB 2; Length 474;
Best Local Similarity 85.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLS 7
DB 164 YESNLS 170

RESULT 12
Q9ETS8 PRELIMINARY; PRT; 474 AA.
AC Q9ETS8;
DT 01-MAR-2001 (TRENBLREL. 16, Created)
DT 01-MAR-2001 (TRENBLREL. 16, Last sequence update)
DT 05-JUL-2004 (TRENBLREL. 27, Last annotation update)
DE DNA gyrase B subunit (Fragment).
GN Name=gyrB;
OS Tenacibaculum ovoliticum.
OC Bacteria; Bacteroidetes; Flavobacteriia; Flavobacteriales;
OC Flavobacteriaceae; Tenacibaculum.
OX NCBI_TaxID=104270;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=IFO15992, and IAM14318;
RX MEDLINE=21477783; PubMed=11594591;
RA Suzuki M., Nakagawa Y., Harayama S., Yamamoto S.;
RT "Phylogenetic analysis and taxonomic study of marine Cytophaga-like
RT bacteria: proposal for Tenacibaculum gen. nov. with Tenacibaculum
RT maritimum comb. nov. and Tenacibaculum ovoliticum comb. nov.", and
RT description of Tenacibaculum mesophilum sp. nov. and Tenacibaculum
RT amylophilum sp. nov.";
RU Int. J. Syst. Evol. Microbiol. 51:1639-1652(2001).
CC -1- FUNCTION: DNA gyrase negatively supercoils closed circular double-
CC stranded DNA in an ATP-dependent manner and also catalyzes the
CC interconversion of other topological isomers of double-stranded
CC DNA rings, including catenanes and knotted rings (by similarity).
CC -1- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining
CC of double-stranded DNA.
CC -1- SIMILARITY: Belongs to the type II topoisomerase family.
DR EMBL; AB034230; BAB12489.1; -.
DR EMBL; AB034230; BAB12489.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0003918; P:DNA topoisomerase (ATP-hydrolyzing) activity; IEA.
DR GO; GO:0006304; P:DNA modification; IEA.
DR GO; GO:0006265; P:DNA topological change; IEA.

```

DR InterPro: IPR003594; ATPbind_ATPase.
DR InterPro: IPR011558; DNA_gyrase_B.
DR InterPro: IPR001241; DNA_topoisomII.
DR InterPro: IPR006171; Toprim_dom.
DR Pfam: PR00204; DNA_gyraseB; 1.
DR Pfam: PR02518; HATPase_c; 1.
DR PRINTS: PR00418; TP12FAMILY.
DR ProDom: PD149633; DNA_gyrase_B; 1.
DR SMART: SM00433; TOP2c; 1.
DR PROSITE: PS00177; TOPOISOMERASE_II; 1.
DR ATP-binding; Isomerase; Topoisomerase.
FT NON_TER 1 1
SQ SEQUENCE 474 AA; 53026 MW; 8AEFA02ABE986E3 CRC64;

Query Match 89.2%; Score 33; DB 2; Length 474;
Best Local Similarity 85.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLHS 7
DB 164 YSNNLHS 170

RESULT 13
Q9ETV9 PRELIMINARY; PRT; 474 AA.
AC Q9ETV9;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE DNA gyrase B subunit (Fragment).
GN Name=gyrB;
OS Cytophaga lytica.
OC Bacteria; Bacteroidetes; Flavobacteriia; Flavobacteriales;
OC Flavobacteriaceae; Cellulophaga.
NCBI_TaxId=979;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MBIC1544, and IFO16022;
RX MEDLINE=21477783; PubMed=11594591;
RA Suzuki M., Nakagawa Y., Hareyama S., Yamamoto S.;
RT "Phylogenetic analysis and taxonomic study of marine Cytophaga-like
bacteria: proposal for Tenacibaculum gen. nov. with Tenacibaculum
maritimum comb. nov. and Tenacibaculum ovolyticum comb. nov., and
RT description of Tenacibaculum mesophilum sp. nov. and Tenacibaculum
RT amyolyticum sp. nov.";
RL Int. J. Syst. Evol. Microbiol. 51:1639-1652(2001).
CC -!- FUNCTION: DNA gyrase negatively supercoils closed circular double-
stranded DNA in an ATP-dependent manner and also catalyzes the
CC interconversion of other topological isomers of double-stranded
CC DNA rings, including catenanes and knotted rings (By similarity).
CC -!- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining
CC of double-stranded DNA.
CC -!- SIMILARITY: Belongs to the type II topoisomerase family.
DR EMBL: AB034215; BAB12476.1; -.
DR EMBL: AB034215; BAB12473.1; -.
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:0003677; F:DNA binding; IEA.
DR GO: GO:0003918; F:DNA topoisomerase (ATP-hydrolyzing) activity; IEA.
DR GO: GO:0006265; P:DNA topological change; IEA.
DR InterPro: IPR003594; ATPbind_ATPase.
DR InterPro: IPR011558; DNA_gyrase_B.
DR InterPro: IPR001241; DNA_topoisomII.
DR InterPro: IPR006171; Toprim_dom.
DR Pfam: PF00204; DNA_gyraseB; 1.
DR Pfam: PF02518; HATPase_c; 1.
DR PRINTS: PR00418; TP12FAMILY.
DR PROSITE: PS00177; TOPOISOMERASE_II; 1.
DR ATP-binding; Isomerase; Topoisomerase.
FT NON_TER 1 1
SQ SEQUENCE 474 AA; 53068 MW; 7FEFA02ABE986F9 CRC64;

Query Match 89.2%; Score 33; DB 2; Length 474;
Best Local Similarity 85.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLHS 7
DB 164 YSNNLHS 170

DR PROSITE: PS00177; TOPOISOMERASE_II; 1.
DR ATP-binding; Isomerase; Topoisomerase.
FT NON_TER 1 1
SQ SEQUENCE 474 AA; 53160 MW; 792A989704B43027 CRC64;

Query Match 89.2%; Score 33; DB 2; Length 474;
Best Local Similarity 85.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLHS 7
DB 164 YSNNLHS 170

RESULT 14
Q9F1Y8 PRELIMINARY; PRT; 474 AA.
AC Q9F1Y8;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE DNA gyrase B subunit (Fragment).
GN Name=gyrB;
OS Tenacibaculum ovolyticum.
OC Bacteria; Bacteroidetes; Flavobacteriia; Flavobacteriales;
OC Flavobacteriaceae; Tenacibaculum.
NCBI_TaxId=104270;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IFO15993;
RX MEDLINE=21477783; PubMed=11594591;
RA Suzuki M., Nakagawa Y., Hareyama S., Yamamoto S.;
RT "Phylogenetic analysis and taxonomic study of marine Cytophaga-like
bacteria: proposal for Tenacibaculum gen. nov. with Tenacibaculum
maritimum comb. nov. and Tenacibaculum ovolyticum comb. nov., and
RT description of Tenacibaculum mesophilum sp. nov. and Tenacibaculum
RT amyolyticum sp. nov.";
RL Int. J. Syst. Evol. Microbiol. 51:1639-1652(2001).
CC -!- FUNCTION: DNA gyrase negatively supercoils closed circular double-
stranded DNA in an ATP-dependent manner and also catalyzes the
CC interconversion of other topological isomers of double-stranded
CC DNA rings, including catenanes and knotted rings (By similarity).
CC -!- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining
CC of double-stranded DNA.
CC -!- SIMILARITY: Belongs to the type II topoisomerase family.
DR EMBL: AB034232; BAB12490.1; -.
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:0003677; F:DNA binding; IEA.
DR GO: GO:0003918; F:DNA topoisomerase (ATP-hydrolyzing) activity; IEA.
DR GO: GO:0006265; P:DNA topological change; IEA.
DR GO: GO:0006265; P:DNA topological change; IEA.
DR InterPro: IPR003594; ATPbind_ATPase.
DR InterPro: IPR011558; DNA_gyrase_B.
DR InterPro: IPR001241; DNA_topoisomII.
DR InterPro: IPR006171; Toprim_dom.
DR Pfam: PF00204; DNA_gyraseB; 1.
DR Pfam: PF02518; HATPase_c; 1.
DR PRINTS: PR00418; TP12FAMILY.
DR ProDom: PD149633; DNA_gyrase_B; 1.
DR SMART: SM00433; TOP2c; 1.
DR PROSITE: PS00177; TOPOISOMERASE_II; 1.
DR ATP-binding; Isomerase; Topoisomerase.
FT NON_TER 1 1
SQ SEQUENCE 474 AA; 53068 MW; 7FEFA02ABE986F9 CRC64;

Query Match 89.2%; Score 33; DB 2; Length 474;
Best Local Similarity 85.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLHS 7

Db 164 YSENHLS 170

RESULT 15

ID 09FIY9 PRELIMINARY; PRT; 474 AA.

AC 09FIY9; 01-MAR-2001 (TREMBlrel. 16, Created)

DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)

DE 01-MAR-2004 (TREMBlrel. 26, Last annotation update)

DE DNA gyrase B subunit (Fragment).

GN Name=gyrB;

OS Tenacibaculum maritimum.

OC Bacteria; Bacteroidetes; Flavobacteriales; Flavobacteriaceae; Tenacibaculum.

CC NCBI_TaxID=107401;

CC [1]

CC SEQUENCE FROM N.A.

CC STRAIN=ATCC43398;

CC MEDLINE=2147783; PubMed=11594591;

CC Suzuki M., Nakagawa Y., Harayama S., Yamamoto S.;

CC "Phylogenetic analysis and taxonomic study of marine Cytophaga-like bacteria: proposal for Tenacibaculum gen. nov. with Tenacibaculum maritimum comb. nov. and Tenacibaculum ovolyticum comb. nov.", and description of Tenacibaculum mesophilum sp. nov. and Tenacibaculum amylolyticum sp. nov.;"

CC Int. J. Syst. Evol. Microbiol. 51:1639-1652(2001).

CC -I- FUNCTION: DNA gyrase negatively supercoils closed circular double-stranded DNA in an ATP-dependent manner and also catalyzes the interconversion of other topological isomers of double-stranded DNA rings, including catenanes and knotted rings (By similarity).

CC -I- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining of double-stranded DNA.

CC -I- SIMILARITY: Belongs to the type II topoisomerase family.

CC EMBL; AB034228; BAB12487.1; -.

CC DR GO; GO:0005524; F:ATP binding; IEA.

CC DR GO; GO:0003677; F:DNA binding; IEA.

CC DR GO; GO:0003918; F:DNA topoisomerase (ATP-hydrolyzing) activity; IEA.

CC DR GO; GO:0006304; P:DNA modification; IEA.

CC DR GO; GO:0006265; P:DNA topological change; IEA.

CC DR InterPro; IPR003594; ATPbind_ATPase.

CC DR InterPro; IPR011558; DNA_gyrase_B.

CC DR InterPro; IPR001241; DNA_topoisom.

CC DR InterPro; IPR006171; Toprim_dom.

CC DR Pfam; PF00204; DNA_gyraseB_1.

CC DR Pfam; PF02518; HATase_C_1.

CC DR Pfam; PF01751; Toprim_1.

CC DR PRINTS; PR00418; TP12FAMILY.

CC DR ProDom; PD149633; DNA_gyrase_B_1.

CC DR SMART; SM00433; TOP2C_1.

CC DR PROSITE; PS00177; TOPOISOMERASE_II; 1.

CC KM ATP-binding; Isomerase; Topoisomerase.

CC FT NON_TER 1

CC FT TER 1

CC SEQUENCE 474 AA; 52888 MW; 47D1F2DB02B996E CRC64;

Query Match 89.2%; Score 33; DB 2; Length 474;

Best Local Similarity 85.7%; Pred. No. 1.5e+02;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSENHLS 7

Db 164 YSENHLS 170

RESULT 16

ID 09FI20 PRELIMINARY; PRT; 474 AA.

AC 09FI20; 01-MAR-2001 (TREMBlrel. 16, Created)

DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)

DE 01-MAR-2004 (TREMBlrel. 26, Last annotation update)

DE DNA gyrase B subunit (Fragment).

GN Name=gyrB;

OS Tenacibaculum maritimum.

OC Bacteria; Bacteroidetes; Flavobacteriales; Flavobacteriaceae; Tenacibaculum.

CC NCBI_TaxID=107401;

CC [1]

CC SEQUENCE FROM N.A.

CC STRAIN=JFO16015;

CC MEDLINE=2147783; PubMed=11594591;

CC Suzuki M., Nakagawa Y., Harayama S., Yamamoto S.;

CC "Phylogenetic analysis and taxonomic study of marine Cytophaga-like bacteria: proposal for Tenacibaculum gen. nov. with Tenacibaculum maritimum comb. nov. and Tenacibaculum ovolyticum comb. nov.", and description of Tenacibaculum mesophilum sp. nov. and Tenacibaculum amylolyticum sp. nov.;"

CC Int. J. Syst. Evol. Microbiol. 51:1639-1652(2001).

CC -I- FUNCTION: DNA gyrase negatively supercoils closed circular double-stranded DNA in an ATP-dependent manner and also catalyzes the interconversion of other topological isomers of double-stranded DNA rings, including catenanes and knotted rings (By similarity).

CC -I- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining of double-stranded DNA.

CC -I- SIMILARITY: Belongs to the type II topoisomerase family.

CC EMBL; AB034228; BAB12486.1; -.

CC DR GO; GO:0005524; F:ATP binding; IEA.

CC DR GO; GO:0003677; F:DNA binding; IEA.

CC DR GO; GO:0003918; F:DNA topoisomerase (ATP-hydrolyzing) activity; IEA.

CC DR GO; GO:0006304; P:DNA modification; IEA.

CC DR GO; GO:0006265; P:DNA topological change; IEA.

CC DR InterPro; IPR003594; ATPbind_ATPase.

CC DR InterPro; IPR011558; DNA_gyrase_B.

CC DR InterPro; IPR001241; DNA_topoisom.

CC DR InterPro; IPR006171; Toprim_dom.

CC DR Pfam; PF00204; DNA_gyraseB_1.

CC DR Pfam; PF02518; HATase_C_1.

CC DR Pfam; PF01751; Toprim_1.

CC DR PRINTS; PR00418; TP12FAMILY.

CC DR ProDom; PD149633; DNA_gyrase_B_1.

CC DR SMART; SM00433; TOP2C_1.

CC DR PROSITE; PS00177; TOPOISOMERASE_II; 1.

CC KM ATP-binding; Isomerase; Topoisomerase.

CC FT NON_TER 1

CC FT TER 1

CC SEQUENCE 474 AA; 52960 MW; 4D738B7455D49FA8 CRC64;

Query Match 89.2%; Score 33; DB 2; Length 474;

Best Local Similarity 85.7%; Pred. No. 1.5e+02;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSENHLS 7

Db 164 YSENHLS 170

RESULT 17

ID 09FAV1 PRELIMINARY; PRT; 474 AA.

AC 09FAV1; 01-MAR-2001 (TREMBlrel. 16, Created)

DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)

DE 01-OCT-2003 (TREMBlrel. 25, Last annotation update)

DE DNA gyrase B subunit (Fragment).

GN Name=gyrB;

OS Psychroflexus gondwanensis.

OC Bacteria; Bacteroidetes; Flavobacteriales; Flavobacteriaceae; Psychroflexus.

CC NCBI_TaxID=251;

CC [1]

CC SEQUENCE FROM N.A.

CC STRAIN=DSM5423;

CC MEDLINE=2147783; PubMed=11594591;

CC Suzuki M., Nakagawa Y., Harayama S., Yamamoto S.;

RT "Phylogenetic analysis and taxonomic study of marine Cytophaga-like
RT bacteria: proposal for Tenacibaculum gen. nov. with Tenacibaculum
RT maritimum comb. nov. and Tenacibaculum ovolyticum comb. nov., and
RT description of Tenacibaculum mesophilum sp. nov. and Tenacibaculum
RT amylolyticum sp. nov.;"
RT Int. J. Syst. Evol. Microbiol. 51:1639-1652(2001).
CC -1- FUNCTION: DNA gyrase negatively supercoils closed circular double-
CC stranded DNA in an ATP-dependent manner and also catalyzes the
CC interconversion of other topological isomers of double-stranded
CC DNA rings, including catenanes and knotted rings (By similarity).
CC -1- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining
CC of double-stranded DNA.
CC -1- SIMILARITY: Belongs to the type II topoisomerase family.
CC EMBL: AB034216; BAB12484.1; -.
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:0003677; F:DNA binding; IEA.
DR GO: GO:0003918; F:DNA topoisomerase (ATP-hydrolyzing) activity; IEA.
DR GO: GO:0006265; P:DNA modification; IEA.
DR GO: GO:0006265; P:DNA topological change; IEA.
DR InterPro: IPR003594; ATPbind_ATPase.
DR InterPro: IPR011558; DNA_gyrase_B.
DR InterPro: IPR001241; DNA_topoisomII.
DR InterPro: IPR006171; Toprim_dom.
DR Pfam: PF00204; DNA_gyraseB; 1.
DR Pfam: PF02518; HATPase_c; 1.
DR Pfam: PF01751; Toprim; 1.
DR PRINTS: PR00418; TP12FAMILY.
DR ProDom: PD149633; DNA_gyrase_B; 1.
DR SMART: SM00433; TOP2c; 1.
DR PROSITE: PS00177; TOPOISOMERASE_II; 1.
DR ATP-binding; Isomerase; Topoisomerase.
KW NON_TER 1
FT 474 474
SQ SEQUENCE 474 AA; 53686 MW; 417E2D2C2C8DFDB CRC64;

Query Match 89.2%; Score 33; DB 2; Length 474;
Best Local Similarity 85.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
1 YSSNLHS 7
|||
Db 164 YSENLS 170

RESULT 18
O9FAV9 PRELIMINARY; PRT; 474 AA.
ID O9FAV9; PRT; 474 AA.
AC O9FAV9; 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE DNA gyrase B subunit (Fragment).
GN Name-gyrB;
OS Cytophaga lytica.
OC Bacteria; Bacteroidetes; Flavobacteriia; Flavobacteriales;
OC Flavobacteriaceae; Cellulophaga.
OX NCBI_TaxID=979;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IFO15986;
RX MEDLINE=21477783; PubMed=11594591;
RA Suzuki M., Nakagawa Y., Harayama S., Yamamoto S.;
RT "Phylogenetic analysis and taxonomic study of marine Cytophaga-like
RT bacteria: proposal for Tenacibaculum gen. nov. with Tenacibaculum
RT maritimum comb. nov. and Tenacibaculum ovolyticum comb. nov., and
RT description of Tenacibaculum mesophilum sp. nov. and Tenacibaculum
RT amylolyticum sp. nov.;"
RT Int. J. Syst. Evol. Microbiol. 51:1639-1652(2001).
CC -1- FUNCTION: DNA gyrase negatively supercoils closed circular double-
CC stranded DNA in an ATP-dependent manner and also catalyzes the
CC interconversion of other topological isomers of double-stranded
CC DNA rings, including catenanes and knotted rings (By similarity).
CC -1- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining
CC of double-stranded DNA.
CC -1- SIMILARITY: Belongs to the type II topoisomerase family.
CC EMBL: AB034216; BAB12474.1; -.
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:0003677; F:DNA binding; IEA.
DR GO: GO:0003918; F:DNA topoisomerase (ATP-hydrolyzing) activity; IEA.
DR GO: GO:0006265; P:DNA modification; IEA.
DR GO: GO:0006265; P:DNA topological change; IEA.
DR InterPro: IPR003594; ATPbind_ATPase.
DR InterPro: IPR011558; DNA_gyrase_B.
DR InterPro: IPR001241; DNA_topoisomII.

CC of double-stranded DNA.
CC -1- SIMILARITY: Belongs to the type II topoisomerase family.
CC EMBL: AB034217; BAB12475.1; -.
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:0003677; F:DNA binding; IEA.
DR GO: GO:0003918; F:DNA topoisomerase (ATP-hydrolyzing) activity; IEA.
DR GO: GO:0006265; P:DNA modification; IEA.
DR GO: GO:0006265; P:DNA topological change; IEA.
DR InterPro: IPR003594; ATPbind_ATPase.
DR InterPro: IPR011558; DNA_gyrase_B.
DR InterPro: IPR001241; DNA_topoisomII.
DR InterPro: IPR006171; Toprim_dom.
DR Pfam: PF00204; DNA_gyraseB; 1.
DR Pfam: PF02518; HATPase_c; 1.
DR Pfam: PF01751; Toprim; 1.
DR PRINTS: PR00418; TP12FAMILY.
DR ProDom: PD149633; DNA_gyrase_B; 1.
DR SMART: SM00433; TOP2c; 1.
DR PROSITE: PS00177; TOPOISOMERASE_II; 1.
DR ATP-binding; Isomerase; Topoisomerase.
KW NON_TER 1
FT 474 474
SQ SEQUENCE 474 AA; 53133 MW; E1B3FE15802A948B CRC64;

Query Match 89.2%; Score 33; DB 2; Length 474;
Best Local Similarity 85.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
1 YSSNLHS 7
|||
Db 164 YSENLS 170

RESULT 19
O9FAW0 PRELIMINARY; PRT; 474 AA.
ID O9FAW0; PRT; 474 AA.
AC O9FAW0; 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE DNA gyrase B subunit (Fragment).
GN Name-gyrB;
OS Cytophaga lytica.
OC Bacteria; Bacteroidetes; Flavobacteriia; Flavobacteriales;
OC Flavobacteriaceae; Cellulophaga.
OX NCBI_TaxID=979;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IAM14306;
RX MEDLINE=21477783; PubMed=11594591;
RA Suzuki M., Nakagawa Y., Harayama S., Yamamoto S.;
RT "Phylogenetic analysis and taxonomic study of marine Cytophaga-like
RT bacteria: proposal for Tenacibaculum gen. nov. with Tenacibaculum
RT maritimum comb. nov. and Tenacibaculum ovolyticum comb. nov., and
RT description of Tenacibaculum mesophilum sp. nov. and Tenacibaculum
RT amylolyticum sp. nov.;"
RT Int. J. Syst. Evol. Microbiol. 51:1639-1652(2001).
CC -1- FUNCTION: DNA gyrase negatively supercoils closed circular double-
CC stranded DNA in an ATP-dependent manner and also catalyzes the
CC interconversion of other topological isomers of double-stranded
CC DNA rings, including catenanes and knotted rings (By similarity).
CC -1- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining
CC of double-stranded DNA.
CC -1- SIMILARITY: Belongs to the type II topoisomerase family.
CC EMBL: AB034216; BAB12474.1; -.
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:0003677; F:DNA binding; IEA.
DR GO: GO:0003918; F:DNA topoisomerase (ATP-hydrolyzing) activity; IEA.
DR GO: GO:0006265; P:DNA modification; IEA.
DR GO: GO:0006265; P:DNA topological change; IEA.
DR InterPro: IPR003594; ATPbind_ATPase.
DR InterPro: IPR011558; DNA_gyrase_B.
DR InterPro: IPR001241; DNA_topoisomII.

DR InterPro; IPR006171; Toprim_dom.
DR Pfam; PF00204; DNA_gyraseB; 1.
DR Pfam; PF02518; HATPase_c; 1.
DR Pfam; PF01751; Toprim_1.
DR PRINTS; PR00418; TP12FAMILY.
DR PRODOM; PD149633; DNA_gyrase_B; 1.
DR SMART; SM00433; TOP2c; 1.
DR PROSITE; PS00177; TOPOISOMERASE_II; 1.
DR ATP-binding; Isomerase; Topoisomerase.
FT NON_TER 1 1
SQ SEQUENCE 474 AA; 53147 MW; 2601AA18DCDC7E CRC64;

Query Match
Best Local Similarity 89.2%; Score 33; DB 2; Length 474;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLS 7
DB 164 YSENLS 170

RESULT 20
Q9PAM1 PRELIMINARY; PRT; 474 AA.
ID Q9PAM1;
AC Q9PAM1;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE DNA gyrase B subunit (Fragment).
GN Name=gyrB;
OS Cytophaga lytica.
OC Bacteria; Bacteroidetes; Flavobacteriia; Flavobacteriales;
OC Flavobacteriaceae; Cellulophaga.
OX NCBI_Taxid=979;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IFO16021;
RX MEDLINE=2147783; PubMed=11594591;
RA Suzuki M., Nakagawa Y., Harayama S., Yamamoto S.;
RT "Phylogenetic analysis and taxonomic study of marine Cytophaga-like
bacteria: proposal for Tenacibaculum gen. nov. with Tenacibaculum
maritimum comb. nov. and Tenacibaculum ovolyticum comb. nov., and
description of Tenacibaculum mesophilum sp. nov. and Tenacibaculum
amolyticum sp. nov.";
RT Int. J. Syst. Evol. Microbiol. 51:1639-1652(2001).
RL Int. J. Syst. Evol. Microbiol. 51:1639-1652(2001).
CC -1- FUNCTION: DNA gyrase negatively supercoils closed circular double-
stranded DNA in an ATP-dependent manner and also catalyzes the
interconversion of other topological isomers of double-stranded
DNA rings, including catenanes and knotted rings (By similarity).
CC -1- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining
of double-stranded DNA.
CC -1- SIMILARITY: Belongs to the type II topoisomerase family.
DR EMBL; AB034214; BAB12472.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0003918; F:DNA topoisomerase (ATP-hydrolyzing) activity; IEA.
DR GO; GO:0006304; P:DNA modification; IEA.
DR GO; GO:0006265; P:DNA topological change; IEA.
DR InterPro; IPR003594; ATPbind_ATPase.
DR InterPro; IPR011558; DNA_gyrase_B.
DR InterPro; IPR001241; DNA_topoisom.
DR InterPro; IPR006171; Toprim_dom.
DR Pfam; PF00204; DNA_gyraseB; 1.
DR Pfam; PF02518; HATPase_c; 1.
DR Pfam; PF01751; Toprim_1.
DR PRINTS; PR00418; TP12FAMILY.
DR PRODOM; PD149633; DNA_gyrase_B; 1.
DR SMART; SM00433; TOP2c; 1.
DR PROSITE; PS00177; TOPOISOMERASE_II; 1.
DR ATP-binding; Isomerase; Topoisomerase.
FT NON_TER 1 1
SQ SEQUENCE 474 AA; 53119 MW; 38D059D7E0FE1E93 CRC64;

Query Match
Best Local Similarity 89.2%; Score 33; DB 2; Length 474;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLS 7
DB 164 YSENLS 170

SQ SEQUENCE 474 AA; 53001 MW; 1F874F9A8626182D CRC64;

Query Match
Best Local Similarity 89.2%; Score 33; DB 2; Length 474;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLS 7
DB 164 YSENLS 170

RESULT 21
Q9PAM2 PRELIMINARY; PRT; 474 AA.
ID Q9PAM2;
AC Q9PAM2;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE DNA gyrase B subunit (Fragment).
GN Name=gyrB;
OS Cytophaga lytica.
OC Bacteria; Bacteroidetes; Flavobacteriia; Flavobacteriales;
OC Flavobacteriaceae; Cellulophaga.
OX NCBI_Taxid=979;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IFO16020;
RX MEDLINE=2147783; PubMed=11594591;
RA Suzuki M., Nakagawa Y., Harayama S., Yamamoto S.;
RT "Phylogenetic analysis and taxonomic study of marine Cytophaga-like
bacteria: proposal for Tenacibaculum gen. nov. with Tenacibaculum
maritimum comb. nov. and Tenacibaculum ovolyticum comb. nov., and
description of Tenacibaculum mesophilum sp. nov. and Tenacibaculum
amolyticum sp. nov.";
RT Int. J. Syst. Evol. Microbiol. 51:1639-1652(2001).
RL Int. J. Syst. Evol. Microbiol. 51:1639-1652(2001).
CC -1- FUNCTION: DNA gyrase negatively supercoils closed circular double-
stranded DNA in an ATP-dependent manner and also catalyzes the
interconversion of other topological isomers of double-stranded
DNA rings, including catenanes and knotted rings (By similarity).
CC -1- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining
of double-stranded DNA.
CC -1- SIMILARITY: Belongs to the type II topoisomerase family.
DR EMBL; AB034213; BAB12471.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0003918; F:DNA topoisomerase (ATP-hydrolyzing) activity; IEA.
DR GO; GO:0006304; P:DNA modification; IEA.
DR GO; GO:0006265; P:DNA topological change; IEA.
DR InterPro; IPR003594; ATPbind_ATPase.
DR InterPro; IPR011558; DNA_gyrase_B.
DR InterPro; IPR001241; DNA_topoisom.
DR InterPro; IPR006171; Toprim_dom.
DR Pfam; PF00204; DNA_gyraseB; 1.
DR Pfam; PF02518; HATPase_c; 1.
DR Pfam; PF01751; Toprim_1.
DR PRINTS; PR00418; TP12FAMILY.
DR PRODOM; PD149633; DNA_gyrase_B; 1.
DR SMART; SM00433; TOP2c; 1.
DR PROSITE; PS00177; TOPOISOMERASE_II; 1.
DR ATP-binding; Isomerase; Topoisomerase.
FT NON_TER 1 1
SQ SEQUENCE 474 AA; 53119 MW; 38D059D7E0FE1E93 CRC64;

Query Match
Best Local Similarity 89.2%; Score 33; DB 2; Length 474;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLS 7
DB 164 YSENLS 170

```

RESULT 22
Q9FAM4 PRELIMINARY; PRT; 480 AA.
ID Q9FAM4;
AC Q9FAM4;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE DNA gyrase B subunit (Fragment).
GN Name=gyrB;
OS Capnocytophaga canimorsus.
OC Bacteria; Bacteroidetes; Flavobacteriia; Flavobacteriales;
OC Flavobacteriaceae; Capnocytophaga.
NCBI_TaxId=28188;
RX STRAIN=ATCC35979;
MEDLINE=21477783; PubMed=11594591;
RA Suzuki M., Nakagawa Y., Harayama S., Yamamoto S.;
RT "Phylogenetic analysis and taxonomic study of marine Cytophaga-like
RT bacteria: proposal for Tenacibaculum gen. nov. with Tenacibaculum
RT maritimum comb. nov. and Tenacibaculum ovoidelicum comb. nov., and
RT description of Tenacibaculum mesophilum sp. nov. and Tenacibaculum
RT amylophilum sp. nov.";
RL Int. J. Syst. Evol. Microbiol. 51:1639-1652(2001).
CC -I- FUNCTION: DNA gyrase negatively supercoils closed circular double-
CC stranded DNA in an ATP-dependent manner and also catalyzes the
CC interconversion of other topological isomers of double-stranded
CC DNA rings, including catenanes and knotted rings (by similarity).
CC -I- CATALYTIC ACTIVITY: ATP-dependant breakage, passage and rejoining
CC of double-stranded DNA.
CC -I- SIMILARITY: Belongs to the type II topoisomerase family.
DR EMBL; AB034211; BAB12469.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0003918; F:DNA topoisomerase (ATP-hydrolyzing) activity; IEA.
DR GO; GO:0006304; F:DNA modification; IEA.
DR GO; GO:0006265; F:DNA topological change; IEA.
DR InterPro; IPR003594; ATPbind_ATPase.
DR InterPro; IPR011558; DNA_gyrase_B.
DR InterPro; IPR001241; DNA_topoisom.
DR InterPro; IPR006171; Toprim_dom.
DR Pfam; PF00204; DNA_gyraseB_1.
DR Pfam; PF02518; HATPase_c_1.
DR Pfam; PF01751; Toprim_1.
DR PRINTS; PR00418; TP12FAMILY.
DR PRODOM; PD149633; DNA_gyrase_B_1.
DR SMART; SM00433; TOP2c_1.
DR PROSITE; PS00177; TOPOISOMERASE_II_1.
DR ATP-binding; Isomerase; Topoisomerase.
FT NON_TER 1
FT NON_TER 480
SQ SEQUENCE 480 AA; 53889 MW; 5F1F48BD18CE052 CRC64;

Query Match 89.2%; Score 33; DB 2; Length 480;
Best Local Similarity 85.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLS 7
DB 164 YSSNLS 170

RESULT 23
Q7PX57 PRELIMINARY; PRT; 817 AA.
ID Q7PX57;
AC Q7PX57;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE AgCP12123 (Fragment).
GN Name=agcG5541; ORFNames=ENSNNG00000011502;
OS Anopheles gambiae str. PST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

```

```

OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.
NCBI_TaxId=180454;
RX STRAIN=PEST;
RC SEQUENCE FROM N.A.
RA Anopheles Genome Sequencing Consortium;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -I- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAA01008987; EAA01793.1; -.
FT NON_TER 1
FT NON_TER 817
SQ SEQUENCE 817 AA; 87412 MW; F898FB958B2995 CRC64;

Query Match 89.2%; Score 33; DB 2; Length 817;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLS 6
DB 589 YSSNLS 594

RESULT 24
Q9S950 PRELIMINARY; PRT; 169 AA.
ID Q9S950;
AC Q9S950;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE CEL2-CELLULOSE 2 (Fragment).
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamids; Solanales; Solanaceae; Solanum.
NCBI_TaxId=4081;
RX STRAIN=96291721; PubMed=8754682;
RA del Campillo E., Bennett A.B.;
RT "Pedicle breaklength and cellulase gene expression during tomato
RT flower abscission.";
RL Plant Physiol. 111:813-820(1996).
DR GO; GO:0004553; F:hydrolyase activity, hydrolyzing O-glycosyl . . .; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR01701; Glyco_hydro_9.
DR InterPro; IPR008928; Glyco_trans_6np.
DR Pfam; PF00759; Glyco_hydro_9_1.
FT NON_TER 1
FT NON_TER 169
FT NON_TER 169
SQ SEQUENCE 169 AA; 18674 MW; CE8AB3AC5637C481 CRC64;

Query Match 86.5%; Score 32; DB 2; Length 169;
Best Local Similarity 85.7%; Pred. No. 78;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLS 7
DB 143 YSSNLS 149

RESULT 25
Q70Y33 PRELIMINARY; PRT; 172 AA.
ID Q70Y33;
AC Q70Y33;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative endo-1,4,-beta-glucanase (Fragment).
GN Name=cel;
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;

```

OC lamidae; Solanales; Solanaceae; Solanum.
 OX NCBI_TaxID=4081;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=fruit;
 RA Saisprasad G.V.S., Lalitha A.;
 RL Submitted (Aug-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ505749; CAD44274.1; -
 DR InterPro; IPR001701; Glyco_hydro_9.
 DR InterPro; IPR008928; Glyco_trans_6hp.
 DR Pfam; PF00759; Glyco_hydro_9; 1.
 FT NON_TER 1
 FT NON_TER 172
 SQ SEQUENCE 172 AA; 19004 MW; F8584877ABEB83F9 CRC64;
 Query Match 86.5%; Score 32; DB 2; Length 172;
 Best Local Similarity 85.7%; Pred. No. 80;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 YSSNLS 7
 Db 144 YSSSLHS 150
 RESULT 26
 CAD44274 PRELIMINARY; PRT; 172 AA.
 AC CAD44274;
 DT 02-MAR-2004 (TREMBlrel. 27, Created)
 DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
 DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)
 DE Putative endo-1,4,-beta-glucanase (Fragment).
 GN CEL.
 OS Lycopersicon esculentum (Tomato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; lamidae; Solanales; Solanaceae; Solanum; Lycopersicon.
 OX NCBI_TaxID=4081;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Arka vikas; TISSUE=fruit;
 RA Saisprasad G.V.S., Lalitha A.;
 RT "Isolation, cloning and characterization of endo-1,4,-beta-glucanase
 RT gene from ripening tomato fruit (Lycopersicon esculentum cv. Arka
 RT vikas)";
 RL Submitted (Aug-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ505749; CAD44274.1; -
 FT NON_TER 1
 FT NON_TER 172
 SQ SEQUENCE 172 AA; 19004 MW; F8584877ABEB83F9 CRC64;
 Query Match 86.5%; Score 32; DB 2; Length 172;
 Best Local Similarity 85.7%; Pred. No. 80;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 YSSNLS 7
 Db 144 YSSSLHS 150
 RESULT 27
 Q43751 PRELIMINARY; PRT; 325 AA.
 AC Q43751;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Cellulase (EC 3.2.1.4) (Fragment).
 GN Name=cc3;
 OS Capsicum annuum (Bell pepper).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC lamidae; Solanales; Solanaceae; Capsicum.

OX NCBI_TaxID=4072;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=leaf abscission zones;
 RA Ferrarese L., Trainotti L., Moretto P., De Laureto P.P., Rascio N.,
 RT "Differential ethylene-inducible expression of cellulase in pepper
 RT plants";
 RL Mol. Biol. 29:735-747(1995).
 DR EMBL; X83711; CA58686.1; -
 DR PIR; S61447; S61447.
 DR GO; GO:000810; F:cellulase activity, IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism, IEA.
 DR InterPro; IPR001701; Glyco_hydro_9.
 DR InterPro; IPR008928; Glyco_trans_6hp.
 DR Pfam; PF00759; Glyco_hydro_9; 1.
 KW Glycosylase; Hydrolyase.
 FT NON_TER 1
 FT NON_TER 325
 SQ SEQUENCE 325 AA; 36087 MW; CE2040A6C7B17937 CRC64;
 Query Match 86.5%; Score 32; DB 2; Length 325;
 Best Local Similarity 85.7%; Pred. No. 1.6e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 YSSNLS 7
 Db 144 YSSSLHS 150
 RESULT 28
 Q22124 PRELIMINARY; PRT; 331 AA.
 AC Q22124;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE C. elegans SRU-48 protein.
 GN Name=sru-48;
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RX MEDLINE=9069613; PubMed=9851916;
 RA Wilson R.;
 RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology. The C. elegans Sequencing Consortium.";
 RL Science 282:2012-2018(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Geisel C., Gattung S.;
 RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Waterston R.;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U41272; AA82450.2; -
 DR PIR; T29924; T29924.
 DR InterPro; IPR003839; DUF215.
 DR Pfam; PF02688; DUF215; 1.
 SQ SEQUENCE 331 AA; 37829 MW; 7FC40A485B9F837 CRC64;
 Query Match 86.5%; Score 32; DB 2; Length 331;
 Best Local Similarity 85.7%; Pred. No. 1.7e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Oy 1 YSSNLS 7
 Db 144 YSSSLHS 150

Db 325 YRSNLS 331

RESULT 29

Q8ES05 PRELIMINARY; PRT; 478 AA.

AC Q8ES05; 01-MAR-2003 (TrEMBLrel. 23, Created)

DT 01-MAR-2003 (TrEMBLrel. 23, last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, last annotation update)

DE Prolyl-tRNA synthetase.

GN OrderedCusNames=OB0566;

OS Oceanobacillus thelyensis.

OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Oceanobacillus.

NCBI_TaxID=182710;

NCBI_TaxID=182710;

RC STRAIN=HTEB31;

RP SEQUENCE FROM N.A.

RX MEDLINE=22220767; PubMed=1235376;

RA Takami H., Takaki Y., Uchiyama I.;

RT "Genome sequence of Oceanobacillus thelyensis isolated from the Iheya Ridge and its unexpected adaptive capabilities to extreme environments."

RT Nucleic Acids Res. 30:33927-33935(2002).

CC -1. SIMILARITY: Belongs to class-II aminoacyl-tRNA synthetase family.

DR EMBL; AB004594; BAC12522.1; -.

DR HSSP; Q93N97; 1HC7.

DR GO; GO:0005737; C:cyclopasam; IEA.

DR GO; GO:0005524; P:ATP binding; IEA.

DR GO; GO:0004827; F:proline-tRNA ligase activity; IEA.

DR GO; GO:0006433; P:prolyl-tRNA aminoacylation; IEA.

DR GO; GO:0006412; P:protein biosynthesis; IEA.

DR InterPro; IPR004154; HGTP anticodon.

DR InterPro; IPR002314; tRNA-synt 2b.

DR InterPro; IPR006195; tRNA_ligase_II.

DR Pfam; PF03129; HGTP_anticodon; 1.

DR Pfam; PF00587; tRNA-synt 2b; 1.

DR PRINTS; PRO1046; TRNASYNTHPRO.

DR TIGRFAMs; TIGR00408; pros_fam_I.1.

DR PROSITE; PS00862; AA_TRNA_LIGASE_II; 1.

KW Aminoacyl-tRNA synthetase; Complete proteome.

SQ SEQUENCE 478 AA; 54750 MW; 5E37D535328D880 CRC64;

Query Match 86.5%; Score 32; DB 2; Length 478;

Best Local Similarity 71.4%; Pred. No. 2.5e+02;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YRSNLS 7

Db 125 YSNINHS 131

RESULT 30

Q6DBD4 PRELIMINARY; PRT; 480 AA.

AC Q6DBD4; 01-OCT-2004 (TrEMBLrel. 28, Created)

DT 01-OCT-2004 (TrEMBLrel. 28, last sequence update)

DT 01-OCT-2004 (TrEMBLrel. 28, last annotation update)

DE At5g16410.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

OC euroside II; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TaxID=3702;

NCBI_TaxID=3702;

RN [1]

RP SEQUENCE FROM N.A.

RA Cheuk R., Chen C.J., Kim C.J., Shinn P., Ecker J.R.;

RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; BR015088; AAT71960.1; -.

SQ SEQUENCE 480 AA; 53687 MW; 4984BFD029021C5A CRC64;

Query Match 86.5%; Score 32; DB 2; Length 480;

Best Local Similarity 85.7%; Pred. No. 2.5e+02;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSNLS 7

Db 5 YSSSLHS 11

RESULT 31

Q9PFE4 PRELIMINARY; PRT; 481 AA.

AC Q9PFE4; 01-MAR-2001 (TrEMBLrel. 16, Created)

DT 01-MAR-2001 (TrEMBLrel. 16, last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, last annotation update)

DE Similarity to N-hydroxycinnamoyl/benzoyltransferase.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

OC euroside II; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TaxID=3702;

NCBI_TaxID=3702;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=97471969; PubMed=9330910;

RA Sato S., Kotani H., Nakamura Y., Kaneko T., Asamizu E., Fukami M., Miyajima N., Tabata S.;

RT "Structural analysis of Arabidopsis thaliana chromosome 5. I. Sequence features of the 1.6 Mb regions covered by twenty physically assigned pl clones."

RL DNA Res. 4:215-230(1997).

DR EMBL; AB005242; BAB09608.1; -.

DR GO; GO:0016740; P:transferase activity; IEA.

DR InterPro; IPR003480; Transferase.

DR Pfam; PF02458; Transferase; 1.

KW Transferase.

SQ SEQUENCE 481 AA; 53819 MW; B7991EF5C4A339B7 CRC64;

Query Match 86.5%; Score 32; DB 2; Length 481;

Best Local Similarity 85.7%; Pred. No. 2.5e+02;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSNLS 7

Db 6 YSSSLHS 12

RESULT 32

Q96547 PRELIMINARY; PRT; 485 AA.

AC Q96547; 01-FEB-1997 (TrEMBLrel. 02, Created)

DT 01-FEB-1997 (TrEMBLrel. 02, last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, last annotation update)

DE Cellulase (Endo-beta-1,4-glucanase) (EC 3.2.1.4).

GN Name=ccl3;

OS Capsicum annuum (Bell pepper).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;

OC lamiales; Solanales; Solanaceae; Capsicum.

NCBI_TaxID=4072;

NCBI_TaxID=4072;

RN [1]

RP SEQUENCE FROM N.A.

RA Traenkle L., Ferrarese L., Casadoro G.;

RT "Different endo-beta-1,4-glucanases are expressed during abscission and fruit ripening in pepper and peach plants."

RL (in) Kanellis A.K., Chang C., Kende and Giersen D. (eds.);

RL BIOLOGY AND BIOTECHNOLOGY OF THE PLANT HORMONE ETHYLENE, pp.191-196, Kluwer Academic Publishers, Dordrecht (1998).

RN [2]

RP SEQUENCE FROM N.A.


```

RC TISSUE=Abcission zone;
RA Casadoro G.;
RL Submitted (Apr-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; X97189; CAA65827.1; -.
DR HSSP; 077044; 1KS8.
DR GO; GO:0008810; F:cellulase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR001701; Glyco_hydro_9.
DR InterPro; IPR008928; Glyco_trans_6np.
DR Pfam; PF00759; Glyco_hydro_9; 1.
DR PROSITE; PS00698; GLYCOSYL_HYDROL_F9_2; UNKNOWN_1.
KM Glycosidase; Hydrolase.
SQ SEQUENCE 485 AA; 53631 MW; A8BCCB32E3FFA18A CRC64;

Query Match
Best Local Similarity 86.5%; Score 32; DB 2; Length 485;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLS 7
DB 213 YSSLSHS 219

RESULT 33
Q42872 PRELIMINARY; PRT; 489 AA.
AC Q42872;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Endo-1,4-beta-glucanase precursor (EC 3.2.1.4).
GN Name=Cel2;
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Caslemart; TISSUE=Pericarp;
RX MEDLINE=95086382; PubMed=7994180;
RA Laebrook C.C., Gonzalez-Bosch C., Bennett A.B.;
RT "Two divergent endo-beta-1,4-glucanase genes exhibit overlapping
RT expression in ripening fruit and abscising flowers.";
RL Plant Cell 6:1485-1493(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Caslemart; TISSUE=Pericarp;
RA Brumwell D.A., Laebrook C.C., Bennett A.B.;
RT "Plant endo-1,4-beta-D-glucanases: structure, properties, and
RT physiological function.";
RL ACS Symp. Ser. 566:100-129(1994).
DR EMBL; U13055; AAA69909.1; -.
DR PIR; T06350; T06350.
DR HSSP; 077044; 1KS8.
DR GO; GO:0008810; F:cellulase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR001701; Glyco_hydro_9.
DR InterPro; IPR008928; Glyco_trans_6np.
DR Pfam; PF00759; Glyco_hydro_9; 1.
DR PROSITE; PS00698; GLYCOSYL_HYDROL_F9_2; UNKNOWN_1.
KM Glycosidase; Hydrolase; Signal.
FT SIGNAL 1 23 Potential.
FT CHAIN 24 489 endo-1,4-beta-glucanase.
SQ SEQUENCE 489 AA; 54118 MW; FFADA8C4675F685F CRC64;

Query Match
Best Local Similarity 86.5%; Score 32; DB 2; Length 489;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLS 7
DB 216 YSSLSHS 222

```

```

RESULT 34
Q93WZ0 PRELIMINARY; PRT; 500 AA.
AC Q93WZ0;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Endo-beta-1,4-glucanase precursor (EC 3.2.1.4).
GN Name=Cel2;
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Nematode-infected roots;
RX MEDLINE=21480065; PubMed=11595799;
RA Goellner M., Wang X., Davis B.L.;
RT "Endo-beta-1,4-glucanase expression in compatible plant-nematode
RT interactions.";
RL Plant Cell 13:2241-2255(2001).
DR EMBL; AF362948; AAL30453.1; -.
DR HSSP; 077044; 1KS8.
DR GO; GO:0008810; F:cellulase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR001701; Glyco_hydro_9.
DR InterPro; IPR008928; Glyco_trans_6np.
DR Pfam; PF00759; Glyco_hydro_9; 1.
DR PROSITE; PS00592; GLYCOSYL_HYDROL_F9_1; 1.
DR PROSITE; PS00698; GLYCOSYL_HYDROL_F9_2; UNKNOWN_1.
KM Glycosidase; Hydrolase; Signal.
FT SIGNAL 1 35 Potential.
FT CHAIN 36 500 endo-beta-1,4-glucanase.
SQ SEQUENCE 500 AA; 55075 MW; 28B48D421165798 CRC64;

Query Match
Best Local Similarity 86.5%; Score 32; DB 2; Length 500;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLS 7
DB 228 YSSLSHS 234

RESULT 35
Q83Z58 PRELIMINARY; PRT; 536 AA.
AC Q83Z58;
DT 01-JUN-2003 (TRENBLrel. 24, Created)
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE DNA gyrase subunit B (Fragment).
GN Name=gyrB;
OS Mesoplasma pleciace.
OC Bacteria; Firmicutes; Mollicutes; Entomoplasmatales;
OC Entomoplasmataceae; Mesoplasma.
OX NCBI_TaxID=228419;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 49582;
RA Knight T.F., Jr., Lawhorn I., Gasparich G.E.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
CC -1-SIMILARITY: Belongs to the type II topoisomerase family.
DR EMBL; AY257486; AAP13529.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0003916; F:DNA topoisomerase (ATP-hydrolyzing) activity; IEA.
DR GO; GO:0006304; P:DNA modification; IEA.
DR GO; GO:0006265; P:DNA topological change; IEA.
DR InterPro; IPR003594; ATPbind_ATPase.

```

```

DR InterPro; IPR011558; DNA_gyrase_B.
DR InterPro; IPR001241; DNA_topoisomI.
DR InterPro; IPR006171; Toprim_dom.
DR Pfam; PF00204; DNA_gyraseB; 1.
DR Pfam; PF02518; HATPase_C; 1.
DR Pfam; PF01751; Toprim_1.
DR PRINTS; PR00418; TP12FAMILY.
DR ProDom; PD149633; DNA_gyrase_B; 1.
DR SMART; SM00387; HATPase_C; 1.
DR SMART; SM00433; TOP2c; 1.
DR PROSITE; PS00177; TOPOISOMERASE_II; 1.
KM ATP-binding; Isomerase; Topoisomerase.
FT NON_TER
FT NON_TER
SQ SEQUENCE 536 AA; 60040 MW; E302FC23AE9C5D09 CRC64;

Query Match
Best Local Similarity 86.5%; Score 32; DB 2; Length 536;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLS 7
Db 235 YSSNLS 241

RESULT 36
Q0708M6 PRELIMINARY; PRT; 598 AA.
AC Q0708M6;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DE AGCP15336 (Fragment).
GN Name=agcG49789; ORFNames=ENSANG0000018304;
OS Anopheles gambiae str. PEST.
OC Neoptera; Endopterygota; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.
OK NCBI_TaxId=180454;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAAB01008944; EAA10074.1; -.
DR GO; GO:0042765; C:GPI-anchor transamidase complex; IEA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR007245; Gp116.
DR Pfam; PF04113; Gp116; 1.
FT NON_TER
FT NON_TER
SQ SEQUENCE 598 AA; 67546 MW; 260B7B630D02C13A CRC64;

Query Match
Best Local Similarity 86.5%; Score 32; DB 2; Length 598;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLS 7
Db 216 YSSNLS 222

RESULT 37
Q09RP84 PRELIMINARY; PRT; 615 AA.
AC Q09RP84;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE DNA gyrase beta subunit.
GN Name=gyrB;
OS Acholteplasma laidlawii.

```

```

OC Bacteria; Firmicutes; Mollicutes; Acholteplasmatales;
OC Acholteplasmataceae; Acholteplasma.
OX NCBI_TaxId=2148;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PG-AB;
RX MEDLINE=20242229; PubMed=10779957;
RA Taganov K.D., Gushchin A.E., Akopian T.A., Oparina N.Iu,
RA Abramycheva N.Iu, Govorun V.M.;
RT "Analysis of genes, coding for DNA gyrase from the mycoplasma
RT Acholteplasma laidlawii PG-AB."
RL Mol. Biol. (Mosk.) 34:292-299(2000).
CC -1- FUNCTION: DNA gyrase negatively supercoils closed circular double-
CC stranded DNA in an ATP-dependent manner and also catalyzes the
CC interconversion of other topological isomers of double-stranded
CC DNA rings, including catenanes and knotted rings (By similarity).
CC -1- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining
CC of double-stranded DNA.
CC -1- SIMILARITY: Belongs to the type II topoisomerase family.
DR EMBL; AF167102; AAD52967.1; -.
DR HSSP; P06982; 1A06.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0003918; F:DNA topoisomerase (ATP-hydrolyzing) activity; IEA.
DR GO; GO:0003918; F:DNA topoisomerase (ATP-hydrolyzing) activity; IEA.
DR GO; GO:0006304; P:DNA modification; IEA.
DR GO; GO:0006265; P:DNA topological change; IEA.
DR InterPro; IPR003594; ATPbind_ATPase.
DR InterPro; IPR002288; DNA_gyraseB.
DR InterPro; IPR011558; DNA_gyrase_B.
DR InterPro; IPR001241; DNA_topoisomI.
DR InterPro; IPR011557; Gyrase.
DR InterPro; IPR006171; Toprim_dom.
DR Pfam; PF00204; DNA_gyraseB; 1.
DR Pfam; PF00986; DNA_gyraseB_C; 1.
DR Pfam; PF02518; HATPase_C; 1.
DR Pfam; PF01751; Toprim_1.
DR PRINTS; PR00418; TP12FAMILY.
DR ProDom; PD149633; DNA_gyrase_B; 1.
DR SMART; SM00387; HATPase_C; 1.
DR SMART; SM00433; TOP2c; 1.
DR TIGRFAMs; TIGR01059; gyrB; 1.
DR PROSITE; PS00177; TOPOISOMERASE_II; 1.
KM ATP-binding; Isomerase; Topoisomerase.
SQ SEQUENCE 615 AA; 68900 MW; 4D9962C35BAB73FE CRC64;

Query Match
Best Local Similarity 86.5%; Score 32; DB 2; Length 615;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLS 7
Db 267 YSSNLS 273

RESULT 38
Q08RFN2 PRELIMINARY; PRT; 335 AA.
AC Q08RFN2;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE ABC transporter ATP-binding protein.
GN OrderedocusNames=FN0660;
OS Fusobacterium nucleatum (subsp. nucleatum).
OC Bacteria; Fusobacteriia; Fusobacteriales; Fusobacteriaceae;
OC Fusobacterium.
OX NCBI_TaxId=76856;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 25586;
RX MEDLINE=2186394; PubMed=11889109;
RA Kapralov V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A.,
RA Bhattacharya A., Bartman A., Gardner W., Greenkin G., Zhu L.,

```

RA Vastava O., Chu L., Kogan Y., Chaga O., Goltzman E., Bernal A.,
 RA Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R.,
 RA Fontein M., Kyrzides N.C., Overbeek R.;
 RT "Genome sequence and analysis of the oral bacterium *Fusobacterium*
 RT *nucleatum* strain ATCC 25586.";
 RL J. Bacteriol. 184:2005-2018(2002).
 CC -1 - SIMILARITY: Belongs to the ABC transporter family.
 DR EMBL; AE010577; MAL94856.1; -.
 DR HSSP; O58206; 1L2T.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004009; F:ATP-binding cassette (ABC) transporter acti. .; IEA.
 DR GO; GO:0000166; F:nucleotide binding; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR003593; AAA ATPase.
 DR InterPro; IPR003439; ABC transporter.
 DR Pfam; PF00005; ABC_tran; 1.
 DR ProDom; PD000006; ABC_transporter; 1.
 DR SMART; SM00382; AAA; 1.
 DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
 DR PROSITE; PS00893; ABC_TRANSPORTER_2; 1.
 KW ATP-binding; Complete proteome.
 KM SEQUENCE 335 AA; 37442 MW; E6ABF4100E7B4C3B CRC64;
 SQ
 Query Match 83.8%; Score 31; DB 2; Length 335;
 Best Local Similarity 71.4%; Pred. No. 2.9e+02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YSSNLHS 7
 DB 11 YSSNLHA 17
 RESULT 39
 ID Q9L906 PRELIMINARY; PRT; 347 AA.
 AC Q9L906;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Glycosyltransferase (Putative Beta-1,4-N-
 DE acetylglucosaminyltransferase).
 GN Name=cgta;
 OS Campylobacter jejuni.
 OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
 OC Campylobacteraceae; Campylobacter.
 OC NCBI_TaxId=197;
 CX [1]
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 43446;
 RX MEDLINE=20127862; PubMed=10660542;
 RA Gilbert M., Brisson J.R., Karwaski M.F., Michniewicz J.,
 RA Cunningham A.M., Wu Y., Young N.M., Wakarchuk W.W.;
 RT "Biosynthesis of ganglioside mimics in *Campylobacter jejuni* OH4384.
 RT Identification of the glycosyltransferase genes, enzymatic synthesis
 RT of model compounds, and characterization of nanomole amounts by 600-
 RT mhz (11h and (13)C NMR analysis.";
 RT J. Biol. Chem. 275:3896-3906(2000).
 RL [2]
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 43446;
 RA Gilbert M.;
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GB11;
 RX PubMed=14742567;
 RA Gilbert M., Godeschalck P.C., Karwaski M.F., Ang C.W., Van Belkum A.,
 RA Li J., Wakarchuk W.W., Erditz H.P.;
 RT "Evidence for Acquisition of the Lipooligosaccharide Biosynthesis
 RT locus in *Campylobacter jejuni* GB11, a strain isolated from a Patient
 RT with Guillain-Barre Syndrome, by Horizontal Exchange.";
 RL Infect. Immun. 72:1162-1165(2004).

DR EMBL; AF167344; AAF34142.1; -.
 DR EMBL; AY422197; AAR82873.1; -.
 DR GO; GO:0016740; P:transferase activity; IEA.
 DR InterPro; IPR010446; Cgta.
 DR Pfam; PF06306; Cgta; 1.
 KW Transferase.
 KM SEQUENCE 347 AA; 41818 MW; 24006D7CF9C180C4 CRC64;
 SQ
 Query Match 83.8%; Score 31; DB 2; Length 347;
 Best Local Similarity 71.4%; Pred. No. 2.9e+02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YSSNLHS 7
 DB 268 FSSNLHS 274
 RESULT 40
 ID Q9LAK4 PRELIMINARY; PRT; 347 AA.
 AC Q9LAK4;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Beta-1,4-N-acetylglucosaminyltransferase.
 DE Name=cgta;
 GN Name=cgta;
 OS Campylobacter jejuni.
 OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
 OC Campylobacteraceae; Campylobacter.
 OC NCBI_TaxId=197;
 CX [1]
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=OH4384;
 RX MEDLINE=20127862; PubMed=10660542;
 RA Gilbert M., Brisson J.R., Karwaski M.F., Michniewicz J.,
 RA Cunningham A.M., Wu Y., Young N.M., Wakarchuk W.W.;
 RT "Biosynthesis of ganglioside mimics in *Campylobacter jejuni* OH4384.
 RT Identification of the glycosyltransferase genes, enzymatic synthesis
 RT of model compounds, and characterization of nanomole amounts by 600-
 RT mhz (11h and (13)C NMR analysis.";
 RT J. Biol. Chem. 275:3896-3906(2000).
 RL EMBL; AF130984; AAF31769.1; -.
 DR GO; GO:0016740; P:transferase activity; IEA.
 DR InterPro; IPR010446; Cgta.
 DR Pfam; PF06306; Cgta; 1.
 KW Transferase.
 KM SEQUENCE 347 AA; 41661 MW; 1251286DF3261FFD CRC64;
 SQ
 Query Match 83.8%; Score 31; DB 2; Length 347;
 Best Local Similarity 71.4%; Pred. No. 2.9e+02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YSSNLHS 7
 DB 268 FSSNLHS 274

Search completed: December 17, 2004, 19:14:42
 Job time : 22.9213 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 17, 2004, 18:10:02 ; Search time 27.3539 Seconds
(without alignments)
118.029 Million cell updates/sec

Title: US-10-089-500-8

Perfect score: 56

Sequence: 1 HQYSKLPWT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_23Sep04:*

1: geneseqp1980s:***
2: geneseqp1990s:***
3: geneseqp2000s:***
4: geneseqp2001s:***
5: geneseqp2002s:***
6: geneseqp2003as:***
7: geneseqp2003bs:***
8: geneseqp2004s:***

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	56	100.0	9	4	AAB81984	Aab81984 Gangliosid
2	56	100.0	9	6	ABU11009	Abu11009 Modified
3	56	100.0	108	4	AAB81988	Aab81988 Gangliosid
4	56	100.0	108	4	AAB81986	Aab81986 Gangliosid
5	56	100.0	108	4	AAB81990	Aab81990 Gangliosid
6	56	100.0	108	6	ABU11011	Abu11011 Modified
7	56	100.0	108	6	ABU11013	Abu11013 Modified
8	56	100.0	128	2	AAR33257	Rat Immun
9	56	100.0	128	2	AAR53340	KM641 H c
10	56	100.0	128	2	AAV28368	PLM641 LA
11	56	100.0	128	3	AAB01628	Murine im
12	56	100.0	128	4	AAB81994	Aab81994 Gangliosid
13	56	100.0	128	4	AAB81995	Aab81995 Gangliosid
14	56	100.0	128	4	AAB81997	Aab81997 Gangliosid
15	56	100.0	128	4	AAB81978	Aab81978 Gangliosid
16	56	100.0	128	4	AAB81996	Aab81996 Gangliosid
17	56	100.0	128	4	AAB81999	Aab81999 Gangliosid
18	56	100.0	128	4	AAB81993	Aab81993 Gangliosid
19	56	100.0	128	4	AAB81992	Aab81992 Gangliosid
20	56	100.0	128	6	ABU11003	Abu11003 Modified
21	56	100.0	126	2	AAR12237	Mouse Mab
22	48	85.7	127	2	AAR12359	Light (ka
23	48	78.6	109	6	ADA89188	Human ant
24	43	76.8	215	5	ABP43158	Human ova
25						

26	42	75.0	107	8	AD007305	Ado07305 Human pro
27	42	75.0	107	8	AD007307	Ado07307 Human pro
28	41	73.2	113	4	AAB48936	Aab48936 Anti-TrkA
29	41	73.2	295	4	AAB48934	Aab48934 Anti-TrkA
30	40	71.4	9	3	AAB06354	Aab06354 Randomise
31	40	71.4	9	3	AAB06352	Aab06352 Randomise
32	40	71.4	107	2	AAR30770	Aar30770 Consensus
33	40	71.4	107	4	AAB62087	Aab62087 Human VI
34	40	71.4	107	4	AAB60400	Aab60400 Consensus
35	40	71.4	107	4	AAB61585	Aab61585 Human var
36	40	71.4	107	8	AD871454	Ad871454 Human ant
37	40	71.4	107	8	ADJ88008	Adj88008 Human var
38	40	71.4	107	8	ADN12054	Adn12054 Variable
39	40	71.4	107	8	ADP43328	Adp43328 Human mon
40	40	71.4	108	2	AAW04177	Aaw04177 Variant v
41	40	71.4	108	2	AAW00834	Aaw00834 Variable
42	40	71.4	108	2	AAW16620	Aaw16620 Anti-huma
43	40	71.4	108	2	AAW70622	Aaw70622 Human con
44	40	71.4	108	3	AAV82345	Aav82345 Human con
45	40	71.4	108	4	AAE12062	Aae12062 Human ant

ALIGNMENTS

RESULT 1
AAB81984 standard; peptide; 9 AA.

AC AAB81984;
DT 03-JUL-2001 (first entry)
DE Ganglioside GD3 specific antibody related peptide SEQ ID NO: 8.

KW Ganglioside; GD3; complementarity determining region; CDR; antibody;
KM cancer.

OS Mus musculus.

PN WO200123432-A1.

PD 05-APR-2001.

PF 29-SEP-2000; 2000WO-JP006774.

PR 30-SEP-1999; 99JP-00278291.

PR 06-APR-2000; 2000JP-00105088.

PA (KYOW) KYOWA HAKKO KOGYO KK.

PI Hanai N, Shitara K, Nakamura K, Niwa R;

DR WPI, 2001-266143/27.

XX New human type complementation-determining region-transplanted antibody
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
PT of e.g. tumors, with low antigenicity, little side effects but potent
PT activity in cancer.

XX Claim 4; Page 142; 183pp; Japanese.

XX The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumors, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention

XX Sequence 9 AA;

Query Match 100.0%; Score 56; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HQYSKLPWT 9
 DB 1 HQYSKLPWT 9

RESULT 2
 ABU11009 standard; peptide; 9 AA.
 AC ABU11009;
 DT 04-FEB-2003 (first entry)
 DE Modified ganglioside GD3 antibody associated peptide #6.
 XX Ganglioside GD3; anti-ganglioside GD3 antibody; tumour; melanoma.
 XX Mus musculus.
 OS WO200278739-A1.
 PN 10-OCT-2002.
 PD 29-MAR-2002; 2002WO-IP003170.
 PF 29-MAR-2001; 2001JP-00097483.
 PR (KYOW) KYOWA HAKKO KOGYO KK.
 PA Shitara K, Niwa R, Kanazawa J, Asada M;
 PI WPI; 2003-067410/06.
 DR Drug containing genetically-modified antibody against ganglioside GD3,
 XX its fragment, immunocompetent cell activators or/and antitumor agents in
 PT combination, applicable in treating malignant tumor like melanoma.
 PS Claim 6; Page 99; 121pp; Japanese.
 CC The invention describes drugs contain a genetically-modified antibody
 CC against ganglioside GD3 or its fragment and at least 1 of a substance
 CC capable of activating immunocompetent cells and a substance having an
 CC antitumor activity in combination. The drugs can be used to treat tumour
 CC like melanoma and can provide a treatment with enhanced therapeutic
 CC effect and little side-reactions, particularly to relieve problems of
 CC side-effects during the conventional single administration. This sequence
 CC represents a peptide associated with the anti- ganglioside GD3 antibody

SQ Sequence 9 AA;
 Query Match 100.0%; Score 56; DB 6; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.7e+06; Mismatches 0; Gaps 0;
 Matches 9; Conservative 0; Indels 0; Gaps 0;

QY 1 HQYSKLPWT 9
 DB 1 HQYSKLPWT 9

RESULT 3
 AAB81988 standard; protein; 108 AA.
 AC AAB81988;
 DT 03-JUL-2001 (first entry)
 DE Ganglioside GD3 specific antibody related protein SEQ ID NO: 54.
 XX Ganglioside; GD3; complementarity determining region; CDR; antibody;
 KM cancer.

OS Synthetic.
 XX WO200123432-A1.
 PN 05-APR-2001.
 PD 29-SEP-2000; 2000WO-IP006774.
 PF 30-SEP-1999; 99JP-00278291.
 PR 06-APR-2000; 2000JP-00105088.
 XX (KYOW) KYOWA HAKKO KOGYO KK.
 PA Hanai N, Shitara K, Nakamura K, Niwa R;
 PI WPI; 2001-266143/27.
 DR New human type complementation-determining region-transplanted antibody
 PT and derivatives against ganglioside GD3; useful in diagnosis and therapy
 PT of e.g. tumors, with low antigenicity, little side effects but potent
 XX activity in cancer.
 PS Claim 22; Page 172-173; 183pp; Japanese.
 CC The present invention describes a monoclonal antibody which can react
 CC specifically with ganglioside GD3. The antibody and its derivatives are
 CC useful in the diagnosis and therapy of tumours, particularly cancer
 CC diagnosis. The present sequence is a protein used in the exemplification
 CC of the invention

SQ Sequence 108 AA;
 Query Match 100.0%; Score 56; DB 4; Length 108;
 Best Local Similarity 100.0%; Pred. No. 0.043; Mismatches 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HQYSKLPWT 9
 DB 89 HQYSKLPWT 97

RESULT 4
 AAB81986 standard; protein; 108 AA.
 ID AAB81986;
 AC AAB81986;
 DT 03-JUL-2001 (first entry)
 DE Ganglioside GD3 specific antibody related protein SEQ ID NO: 10.
 XX Ganglioside; GD3; complementarity determining region; CDR; antibody;
 KM cancer.
 OS Synthetic.
 XX WO200123432-A1.
 PN 05-APR-2001.
 PD 29-SEP-2000; 2000WO-IP006774.
 PF 30-SEP-1999; 99JP-00278291.
 PR 06-APR-2000; 2000JP-00105088.
 XX (KYOW) KYOWA HAKKO KOGYO KK.
 PA Hanai N, Shitara K, Nakamura K, Niwa R;
 PI WPI; 2001-266143/27.
 DR New human type complementation-determining region-transplanted antibody
 PT and derivatives against ganglioside GD3; useful in diagnosis and therapy

PT of e.g. tumors, with low antigenicity, little side effects but potent
 PT activity in cancer.

XX Example 1, Page 143-144; 183pp; Japanese.

CC The present invention describes a monoclonal antibody which can react
 CC specifically with ganglioside GD3. The antibody and its derivatives are
 CC useful in the diagnosis and therapy of tumors, particularly cancer
 CC diagnosis. The present sequence is a protein used in the exemplification
 CC of the invention

XX Sequence 108 AA;

Query Match 100.0%; Score 56; DB 4; Length 108;
 Best Local Similarity 100.0%; Pred. No. 0.043;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HQYSKLPMT 9
 |||||
 DB 89 HQYSKLPMT 97

RESULT 5

ABAB1990
 ID AAB81990 standard; protein; 108 AA.

XX AAB81990;

XX 03-JUL-2001 (first entry)

DE Ganglioside GD3 specific antibody related protein SEQ ID NO: 56.

XX Ganglioside; GD3; complementarity determining region; CDR; antibody;

KW cancer.

XX Mus musculus.

XX WO200123432-A1.

XX 05-APR-2001.

XX 29-SEP-2000; 2000MO-JP006774.

XX 30-SEP-1999; 99JP-00278291.

XX 06-APR-2000; 2000JP-00105088.

XX (KYOW) KYOWA HAKKO KOGYO KK.

XX Hanai N, Shitara K, Nakamura K, Niwa R;

XX WPI; 2001-266143/27.

XX New human type complementation-determining region-transplanted antibody
 PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
 PT of e.g. tumors, with low antigenicity, little side effects but potent
 PT activity in cancer.

XX Claim 11, Page 174-175; 183pp; Japanese.

CC The present invention describes a monoclonal antibody which can react
 CC specifically with ganglioside GD3. The antibody and its derivatives are
 CC useful in the diagnosis and therapy of tumors, particularly cancer
 CC diagnosis. The present sequence is a protein used in the exemplification
 CC of the invention

XX Sequence 108 AA;

Query Match 100.0%; Score 56; DB 4; Length 108;
 Best Local Similarity 100.0%; Pred. No. 0.043;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HQYSKLPMT 9
 |||||

DB 89 HQYSKLPMT 97

RESULT 6

ABU11011
 ID ABU11011 standard; protein; 108 AA.

XX ABU11011;

XX 04-FEB-2003 (first entry)

DE Modified ganglioside GD3 antibody associated protein #4.

XX Ganglioside GD3; anti-ganglioside GD3 antibody; tumour; melanoma.

XX Synthetic.

XX WO200278739-A1.

XX 10-OCT-2002.

XX 29-MAR-2002; 2002MO-JP003170.

XX 29-MAR-2001; 2001JP-00097483.

XX (KYOW) KYOWA HAKKO KOGYO KK.

XX Shitara K, Niwa R, Kanazawa J, Asada M;

XX WPI; 2003-067410/06.

PT Drugs containing genetically-modified antibody against ganglioside GD3,
 PT its fragment, immunocompetent cell activators or/and anticancer agents in
 PT combination, applicable in treating malignant tumor like melanoma.

XX Claim 8, Page 100; 121pp; Japanese.

CC The invention describes drugs contain a genetically-modified antibody
 CC against ganglioside GD3 or its fragment and at least 1 of a substance
 CC capable of activating immunocompetent cells and a substance having an
 CC antitumor activity in combination. The drugs can be used to treat tumour
 CC like melanoma and can provide a treatment with enhanced therapeutic
 CC effect and little side-reactions, particularly to relieve problems of
 CC side-effects during the conventional single administration. This sequence
 CC represents a protein associated with the anti- ganglioside GD3 antibody

XX Sequence 108 AA;

Query Match 100.0%; Score 56; DB 6; Length 108;
 Best Local Similarity 100.0%; Pred. No. 0.043;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HQYSKLPMT 9
 |||||
 DB 89 HQYSKLPMT 97

RESULT 7

ABU11013
 ID ABU11013 standard; protein; 108 AA.

XX ABU11013;

XX 04-FEB-2003 (first entry)

DE Modified ganglioside GD3 antibody associated protein #5.

XX Ganglioside GD3; anti-ganglioside GD3 antibody; tumour; melanoma.

XX Mus musculus.

XX WO200278739-A1.

XX

PD 10-OCT-2002.
 XX
 PF 29-MAR-2002; 2002WO-JP003170.
 XX
 PR 29-MAR-2001; 2001JP-00097483.
 XX
 PA (KYOW) KYOWA HAKKO KOGYO KK.
 XX
 PI Shitara K, Niwa R, Kanazawa J, Asada M;
 XX
 DR WPI; 2003-067410/06.
 XX
 PT Drugs containing genetically-modified antibody against ganglioside GD3,
 PT its fragment, immunocompetent cell activators or/and antitumor agents in
 PT combination, applicable in treating malignant tumor like melanoma.
 XX
 PS Claim 7; Page 113; 121pp; Japanese.
 XX
 CC The invention describes drugs contain a genetically-modified antibody
 CC against ganglioside GD3 or its fragment and at least 1 of a substance
 CC capable of activating immunocompetent cells and a substance having an
 CC antitumor activity in combination. The drugs can be used to treat tumour
 CC like melanoma and can provide a treatment with enhanced therapeutic
 CC effect and little side-reactions, particularly to relieve problems of
 CC side-effects during the conventional single administration. This sequence
 CC represents a protein associated with the anti- ganglioside GD3 antibody
 CC
 SQ Sequence 108 AA;

Query Match 100.0%; Score 56; DB 6; Length 108;
 Best Local Similarity 100.0%; Pred. No. 0.043;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 HOYSKLPT 9
 |||||
 89 HOYSKLPT 97

RESULT 8

AAR33257
 ID AAR33257 standard; protein; 128 AA.

AC AAR33257;

DT 25-MAR-2003 (revised)

DT 12-JUL-1993 (first entry)

DE Rat immunoglobulin L chain variable region of pKM6411A2.

KW Promoter; variable; region; rat; immunoglobulin; heavy; H; chain;

KW humanised; chimeric; antibody; expression vector.

OS Rattus rattus.

PH Key Location/Qualifiers

PT Peptide 1..20

FT Protein /note= "Signal peptide"

FT 21..128

FT /note= "Mature protein"

PN EP533199-A2.

PD 24-MAR-1993.

PF 18-SEP-1992; 92EP-00116026.

PR 18-SEP-1991; 91JP-00238375.

PA (KYOW) KYOWA HAKKO KOGYO CO LTD.

PI Shitara K, Hanai N, Hasegawa M, Miyaji H, Kuwana Y;

DR WPI; 1993-095510/12.

DR N-PSDB; AAQ33258.

XX Humanised chimeric antibody produ. against ganglioside GD3 - for treating
 PT cancers, such as melanoma, neuroblastoma, etc.

PS Claim 6; Page 30-31; 63pp; English.

XX The sequences given in AAR33256-57 represent rat heavy and light chain
 CC variable regions respectively. The DNA sequences encoding these proteins
 CC were used in the construction of humanised chimeric antibody expression
 CC vectors. In these humanised antibodies none of the amino acids of the non
 CC human animal Ab variable region have been changed. (Updated on 25-MAR-
 CC 2003 to correct FN field.)

XX

SQ Sequence 128 AA;

Query Match 100.0%; Score 56; DB 2; Length 128;
 Best Local Similarity 100.0%; Pred. No. 0.051;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 HOYSKLPT 9
 |||||
 109 HOYSKLPT 117

RESULT 9

AAR53340
 ID AAR53340 standard; protein; 128 AA.

AC AAR53340;

DT 18-NOV-1994 (first entry)

DE KM641 H chain variable region.

KW Monoclonal antibody; Ab; ganglioside GM2; chimera; chimeric antibody;

KW expression vector; heavy; light; chain; hypervariable region; CDR;

KW constant region; hybridoma; Ig; immunoglobulin; promoter; enhancer.

OS Mus musculus.

PH Key Location/Qualifiers

PT Peptide 1..20

FT /label= sig_peptide

PN AU9346181-A.

PD 17-MAR-1994.

PF 07-SEP-1993; 93AU-00046181.

PR 07-SEP-1992; 92JP-00238452.

PA (KYOW) KYOWA HAKKO KOGYO KK.

PI Nakamura K, Koike M, Shitara K, Hanai N, Kuwana Y, Hasegawa M;

DR WPI; 1994-126857/16.

DR N-PSDB; AAQ45438.

XX Humanised antibody specific for ganglioside GM2 - used for producing a
 PT cytotoxic effect on cancers such as melanoma, neuroblastoma and glioma.

PS Example 2; Page 115-116; 191pp; English.

XX Example 2 describes the construction of the vector pCh641HA1 for
 CC chimeric human antibody H chain expression. mRNA from mouse anti-GD3
 CC monoclonal Ab KM641-producing cells was isolated and KM641 H and L chain
 CC cDNAs isolated. The base sequences of the Ig variable regions in KM641 H
 CC chain cDNA (pKM641HA3) and KM641 L chain cDNA (pKM641LA2) are given in
 CC AAQ45438-39. A KM641-derived chimeric human Ab H chain expression vector
 CC was constructed by joining the H chain variable region gene from
 CC pKM641HA3 to a vector for chimeric human Ab H chain expression using the

CC synthetic DNAs given in AAG63439 and AAG63440
XX
SQ Sequence 128 AA;

Query Match 100.0%; Score 56; DB 2; Length 128;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HOYSKLPWT 9
|||
Db 109 HOYSKLPWT 117

RESULT 10
AAY28368
ID AAY28368 standard; protein; 128 AA.

XX AAY28368;

DT 04-NOV-1999 (first entry)

DE PKM641 IAA2 immunoglobulin light chain.

XX antibody; nucleotide; genomic; hypervariable region; chimeric;
KM light chain; amino acid.

XX Mus sp.

OS US5939532-A.

XX 17-AUG-1999.

XX 07-JUN-1995; 95US-00483528.

XX 07-SEP-1993; 93US-00116778.

XX (KYOW) KYOWA HAKKO KOGYO KK.

XX Nakamura K, Hanai N, Kuwana Y, Hasegawa M, Koike M, Shitara K;

XX WPI; 1999-468416/39.

XX N-PSDB; AAX93481.

PT Chimeric human antibody expression vectors.

XX Example 1; Col 99; 188pp; English.

XX This immunoglobulin region was isolated from PKM641IA2.A methionine
CC codon, presumably the initiation codon ATG, was found in the vicinity of
CC the 5' terminus and the sequence has a full length leader sequence. The
CC chimeric human antibodies are useful in the treatment of cancer.
CC especially that which is of neural ectodermal origin. In contrast to
CC prior art constructs based on mouse monoclonal antibodies, the chimeric
CC human antibodies do not cause anti-mouse immunoglobulin production. The
CC chimeric human antibodies have a prolonged half-life and a reduced
CC frequency of adverse effects when compared to mouse monoclonal antibodies
SQ Sequence 128 AA;

Query Match 100.0%; Score 56; DB 2; Length 128;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HOYSKLPWT 9
|||
Db 109 HOYSKLPWT 117

RESULT 11
AAB01628
ID AAB01628 standard; protein; 128 AA.
XX
AC AAB01628;

XX 07-DEC-2000 (first entry)
DT
XX Murine immunoglobulin light chain variable region.
DE
XX Mouse; immunoglobulin; L chain; light chain; variable region; cancer;
KM humanised antibody.
XX

XX Mus sp.

PH Key Location/Qualifiers

FT Peptide 1..20 /label= signal_peptide

FT Protein 21..128 /label= mature_immunoglobulin_light_chain_V_region

XX EP1013761-A2.

XX 28-JUN-2000.

XX 18-SEP-1992; 99EP-00124345.

XX 18-SEP-1991; 91JP-00238375.

XX 18-SEP-1992; 92EP-00116026.

XX (KYOW) KYOWA HAKKO KOGYO KK.

XX Shitara K, Hanai N, Hasegawa M, Miyaji H, Kuwana Y;

XX WPI; 2000-402204/35.

XX N-PSDB; AAA51004.

PT New humanized chimera antibody KM-871 useful for treating cancer.

XX Claim 14; Page 28-29; 65pp; English.

XX The present sequence is a murine immunoglobulin light chain variable
CC region from plasmid KM-641. The coding sequence was used in the creation
CC of an expression vector, along with the sequence for a human antibody, to
CC produce humanised chimaeric antibodies, which can be used to treat
CC cancer. Humanised chimaeric antibodies are more effective than mouse
CC antibodies as they do not provoke a reaction in the human and side
CC effects, such as the formation of anti-mouse immunoglobulin antibody and
CC the rapid half-life of the immunoglobulins, do not occur
XX

SQ Sequence 128 AA;

Query Match 100.0%; Score 56; DB 3; Length 128;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HOYSKLPWT 9
|||
Db 109 HOYSKLPWT 117

RESULT 12
AAB81994
ID AAB81994 standard; protein; 128 AA.

XX AAB81994;

DT 03-JUL-2001 (first entry)

DE Ganglioside GD3 specific antibody related protein #3.

XX Ganglioside; GD3; complementarity determining region; CDR; antibody;

XX cancer.

XX Synthetic.

PN WO200123432-A1.
XX
PD 05-APR-2001.
XX
PF 29-SEP-2000; 2000WO-JP006774.
XX
PR 30-SEP-1999; 99JP-00278291.
PR 06-APR-2000; 2000JP-00105088.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Hanai N, Shitara K, Nakamura K, Niwa R;
XX
DR WPI; 2001-266143/27.
XX
N-PSDB; AAF86898.
XX
PT New human type complementation-determining region-transplanted antibody
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
PT of e.g. tumors, with low antigenicity, little side effects but potent
PT activity in cancer.
XX
PS Example 1; Page 155-156; 183jp; Japanese.
XX
CC The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumors, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention
XX
SQ Sequence 128 AA;
XX
Query Match 100.0%; Score 56; DB 4; Length 128;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HOYSKLPWT 9
DB 109 HOYSKLPWT 117
XX
RESULT 13
AAB81995
ID AAB81995 standard; protein; 128 AA.
XX
AC AAB81995;
XX
DT 03-JUL-2001 (first entry)
XX
DE Ganglioside GD3 specific antibody related protein #4.
XX
KW Ganglioside; GD3; complementarity determining region; CDR; antibody;
KW cancer.
XX
OS Synthetic.
XX
PN WO200123432-A1.
XX
PD 05-APR-2001.
XX
PF 29-SEP-2000; 2000WO-JP006774.
XX
PR 30-SEP-1999; 99JP-00278291.
PR 06-APR-2000; 2000JP-00105088.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Hanai N, Shitara K, Nakamura K, Niwa R;
XX
DR WPI; 2001-266143/27.
XX
N-PSDB; AAF86901.
XX
PT New human type complementation-determining region-transplanted antibody
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy

PT of e.g. tumors, with low antigenicity, little side effects but potent
PT activity in cancer.
XX
PS Example 1; Page 157-158; 183jp; Japanese.
XX
CC The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumors, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention
XX
SQ Sequence 128 AA;
XX
Query Match 100.0%; Score 56; DB 4; Length 128;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HOYSKLPWT 9
DB 109 HOYSKLPWT 117
XX
RESULT 14
AAB81997
ID AAB81997 standard; protein; 128 AA.
XX
AC AAB81997;
XX
DT 03-JUL-2001 (first entry)
XX
DE Ganglioside GD3 specific antibody related protein #6.
XX
KW Ganglioside; GD3; complementarity determining region; CDR; antibody;
KW cancer.
XX
OS Synthetic.
XX
PN WO200123432-A1.
XX
PD 05-APR-2001.
XX
PF 29-SEP-2000; 2000WO-JP006774.
XX
PR 30-SEP-1999; 99JP-00278291.
PR 06-APR-2000; 2000JP-00105088.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Hanai N, Shitara K, Nakamura K, Niwa R;
XX
DR WPI; 2001-266143/27.
XX
N-PSDB; AAF86907.
XX
PT New human type complementation-determining region-transplanted antibody
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
PT of e.g. tumors, with low antigenicity, little side effects but potent
PT activity in cancer.
XX
PS Example 1; Page 161-162; 183jp; Japanese.
XX
CC The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumors, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention
XX
SQ Sequence 128 AA;
XX
Query Match 100.0%; Score 56; DB 4; Length 128;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HOYSKLPWT 9

Db 109 HQYSKLPWT 117

RESULT 15

AAAB81978 standard; protein; 128 AA.

AC AAB81978;

DT 03-JUL-2001 (first entry)

DE Ganglioside GD3 specific antibody related protein SEQ ID NO: 2.

KW Ganglioside; GD3; complementarity determining region; CDR; antibody;

KM cancer.

OS Mus musculus.

PN WO200123432-A1.

PD 05-APR-2001.

PF 29-SEP-2000; 2000WO-JP006774.

PR 30-SEP-1999; 99JP-00278291.

PR 06-APR-2000; 2000JP-00105088.

XX (KYOW) KYOWA HAKKO KOGYO KK.

PI Hanai N, Shitara K, Nakamura K, Niwa R;

DR WPI: 2001-266143/27.

PT New human type complementation-determining region-transplanted antibody

PT and derivatives against ganglioside GD3; useful in diagnosis and therapy

PT of e.g. tumors, with low antigenicity, little side effects but potent

XX activity in cancer.

XX Example 1; Page 140; 183pp; Japanese.

CC The present invention describes a monoclonal antibody which can react

CC specifically with ganglioside GD3. The antibody and its derivatives are

CC useful in the diagnosis and therapy of tumors, particularly cancer

CC diagnosis. The present sequence is a protein used in the exemplification

CC of the invention

XX Sequence 128 AA;

SQ

Query Match 100.0%; Score 56; DB 4; Length 128;

Best Local Similarity 100.0%; Pred. No. 0.051; Mismatches 0; Indels 0; Gaps 0;

Matches 9; Conservative 0; Indels 0; Gaps 0;

QY 1 HQYSKLPWT 9

DB 109 HQYSKLPWT 117

RESULT 16

AAAB81996 standard; protein; 128 AA.

AC AAB81996;

DT 03-JUL-2001 (first entry)

DE Ganglioside GD3 specific antibody related protein #5.

KW Ganglioside; GD3; complementarity determining region; CDR; antibody;

KM cancer.

OS Synthetic.

PN WO200123432-A1.

PD 05-APR-2001.

PF 29-SEP-2000; 2000WO-JP006774.

PR 30-SEP-1999; 99JP-00278291.

PR 06-APR-2000; 2000JP-00105088.

XX (KYOW) KYOWA HAKKO KOGYO KK.

PI Hanai N, Shitara K, Nakamura K, Niwa R;

DR WPI: 2001-266143/27.

DR N-PSDB; AAF86904.

PT New human type complementation-determining region-transplanted antibody

PT and derivatives against ganglioside GD3; useful in diagnosis and therapy

PT of e.g. tumors, with low antigenicity, little side effects but potent

XX activity in cancer.

XX Example 1; Page 159-160; 183pp; Japanese.

PS

CC The present invention describes a monoclonal antibody which can react

CC specifically with ganglioside GD3. The antibody and its derivatives are

CC useful in the diagnosis and therapy of tumors, particularly cancer

CC diagnosis. The present sequence is a protein used in the exemplification

XX of the invention

XX Sequence 128 AA;

SQ

Query Match 100.0%; Score 56; DB 4; Length 128;

Best Local Similarity 100.0%; Pred. No. 0.051; Mismatches 0; Indels 0; Gaps 0;

Matches 9; Conservative 0; Indels 0; Gaps 0;

QY 1 HQYSKLPWT 9

DB 109 HQYSKLPWT 117

RESULT 17

AAAB81999 standard; protein; 128 AA.

AC AAB81999;

DT 03-JUL-2001 (first entry)

DE Ganglioside GD3 specific antibody related protein #8.

KW Ganglioside; GD3; complementarity determining region; CDR; antibody;

KM cancer.

OS Synthetic.

PN WO200123432-A1.

PD 05-APR-2001.

PF 29-SEP-2000; 2000WO-JP006774.

PR 30-SEP-1999; 99JP-00278291.

PR 06-APR-2000; 2000JP-00105088.

XX (KYOW) KYOWA HAKKO KOGYO KK.

PI Hanai N, Shitara K, Nakamura K, Niwa R;

DR WPI: 2001-266143/27.

DR N-PSDB; AAF86913.

PT New human type complementation-determining region-transplanted antibody

PT and derivatives against ganglioside GD3; useful in diagnosis and therapy

PT of e.g. tumors, with low antigenicity, little side effects but potent
XX activity in cancer.
PS Example 1; Page 166; 183pp; Japanese.
XX
CC The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumours, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention
XX
SQ Sequence 128 AA;
Query Match 100.0%; Score 56; DB 4; Length 128;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HOYSKLPWT 9
DB 109 HOYSKLPWT 117
RESULT 18
AAB81993
ID AAB81993 standard; protein; 128 AA.
XX
AC AAB81993;
XX
DT 03-JUL-2001 (first entry)
XX
DE Ganglioside GD3 specific antibody related protein #2.
XX
KW Ganglioside; GD3; complementarity determining region; CDR; antibody;
XX cancer.
OS Synthetic.
XX
PN WO200123432-A1.
XX
PD 05-APR-2001.
XX
PF 29-SEP-2000; 2000WO-JP006774.
XX
PR 30-SEP-1999; 99JP-00278291.
XX
PR 06-APR-2000; 2000JP-00105088.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Hanai N, Shitara K, Nakamura K, Niwa R;
XX
DR WPI; 2001-266143/27.
DR N-PSDB; AAF86895.
XX
XX New human type complementation-determining region-transplanted antibody
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
PT of e.g. tumors, with low antigenicity, little side effects but potent
PT activity in cancer.
XX
PS Example 1; Page 153; 183pp; Japanese.
XX
XX The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumours, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention
XX
SQ Sequence 128 AA;
Query Match 100.0%; Score 56; DB 4; Length 128;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HOYSKLPWT 9
DB 109 HOYSKLPWT 117

DB 109 HOYSKLPWT 117
RESULT 19
AAB81992
ID AAB81992 standard; protein; 128 AA.
XX
AC AAB81992;
XX
DT 03-JUL-2001 (first entry)
XX
DE Ganglioside GD3 specific antibody related protein #1.
XX
KW Ganglioside; GD3; complementarity determining region; CDR; antibody;
XX cancer.
OS Synthetic.
XX
PN WO200123432-A1.
XX
PD 05-APR-2001.
XX
PF 29-SEP-2000; 2000WO-JP006774.
XX
PR 30-SEP-1999; 99JP-00278291.
XX
PR 06-APR-2000; 2000JP-00105088.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Hanai N, Shitara K, Nakamura K, Niwa R;
XX
DR WPI; 2001-266143/27.
DR N-PSDB; AAF86892.
XX
XX New human type complementation-determining region-transplanted antibody
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
PT of e.g. tumors, with low antigenicity, little side effects but potent
PT activity in cancer.
XX
PS Example 1; Page 150-151; 183pp; Japanese.
XX
CC The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumours, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention
XX
SQ Sequence 128 AA;
Query Match 100.0%; Score 56; DB 4; Length 128;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HOYSKLPWT 9
DB 109 HOYSKLPWT 117
RESULT 20
AAB81998
ID AAB81998 standard; protein; 128 AA.
XX
AC AAB81998;
XX
DT 03-JUL-2001 (first entry)
XX
DE Ganglioside GD3 specific antibody related protein #7.
XX
KW Ganglioside; GD3; complementarity determining region; CDR; antibody;
XX cancer.
OS Synthetic.

```

XX PN WO200123432-A1.
XX
XX PD 05-APR-2001.
XX
XX PF 29-SEP-2000; 2000WO-JP006774.
XX
XX PR 30-SEP-1999; 99JP-00278291.
XX
XX PR 06-APR-2000; 2000JP-00105088.
XX
XX PA (KYOW ) KYOWA HAKKO KOGYO KK.
XX
XX PI Hanai N, Shitara K, Nakamura K, Niwa R;
XX
XX DR WPI; 2001-266143/27.
XX
XX DR N-PSDB; AAF86912.
XX
XX PT New human type complementation-determining region-transplanted antibody
XX PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
XX PT of e.g. tumors, with low antigenicity, little side effects but potent
XX PT activity in cancer.
XX
XX PS Example 3; Page 164-165; 183pp; Japanese.
XX
XX CC The present invention describes a monoclonal antibody which can react
XX CC specifically with ganglioside GD3. The antibody and its derivatives are
XX CC useful in the diagnosis and therapy of tumors, particularly cancer
XX CC diagnosis. The present sequence is a protein used in the exemplification
XX CC of the invention
XX
XX SQ Sequence 128 AA;

Query Match          100.0%; Score 56; DB 4; Length 128;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HOYSKLPWT 9
DB 109 HOYSKLPWT 117

RESULT 21
ABU11003
ID ABU11003 standard; protein; 128 AA.
XX
XX AC ABU11003;
XX
XX DT 04-FEB-2003 (first entry)
XX
XX DE Modified ganglioside GD3 antibody associated protein #2.
XX
XX KM Ganglioside GD3; anti-ganglioside GD3 antibody; tumour; melanoma.
XX
XX OS Mus musculus.
XX
XX PN WO200278739-A1.
XX
XX PD 10-OCT-2002.
XX
XX PF 29-MAR-2002; 2002WO-JP003170.
XX
XX PR 29-MAR-2001; 2001JP-00097483.
XX
XX PR (KYOW ) KYOWA HAKKO KOGYO KK.
XX
XX PA Shitara K, Niwa R, Kanazawa J, Asada M;
XX
XX PI WPI; 2003-067410/06.
XX
XX DR Drug containing genetically-modified antibody against ganglioside GD3,
XX PT its fragment, immunocompetent cell activators or/and antitumor agents in
XX PT combination, applicable in treating malignant tumor like melanoma.

```

```

PS Example 3; Page 98; 121pp; Japanese.
XX
XX CC The invention describes drugs contain a genetically-modified antibody
XX CC against ganglioside GD3 or its fragment and at least 1 of a substance
XX CC capable of activating immunocompetent cells and a substance having an
XX CC antitumor activity in combination. The drugs can be used to treat tumour
XX CC like melanoma and can provide a treatment with enhanced therapeutic
XX CC effect and little side-reactions, particularly to relieve problems of
XX CC side-effects during the conventional single administration. This sequence
XX CC represents a protein associated with the anti- ganglioside GD3 antibody
XX
XX SQ Sequence 128 AA;

Query Match          100.0%; Score 56; DB 6; Length 128;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HOYSKLPWT 9
DB 109 HOYSKLPWT 117

RESULT 22
AAR12237
ID AAR12237 standard; protein; 126 AA.
XX
XX AC AAR12237;
XX
XX DT 25-MAR-2003 (revised)
XX
XX DT 19-AUG-1991 (first entry)
XX
XX DE Mouse MAb 1C11 L chain V region.
XX
XX KM HIV-1; chimera.
XX
XX OS Mus sp.
XX
XX PN WO9107494-A.
XX
XX PD 30-MAY-1991.
XX
XX PF 13-NOV-1989; 89US-00433703.
XX
XX PR 13-NOV-1989; 89US-00433703.
XX
XX PA (XOMA ) XOMA CORP.
XX
XX PA (GREG ) GREEN CROSS CORP.
XX
XX PA (ZOMA-) ZOMA CORP.
XX
XX PI Better MD, Horwitz AH, Ghoshdastgi P, Robinson RR;
XX
XX DR WPI; 1991-178106/24.
XX
XX DR N-PSDB; AAQ12017.
XX
XX PT New chimeric mouse human antibodies - used in treatment, diagnosis and
XX PT prophylaxis of HIV infections.
XX
XX PS Disclosure; Fig 13; 108pp; English.
XX
XX CC The mouse VL gene product may be used to produce chimeric mouse- human
XX CC Abs against HIV-1 comprising human Ig constant regions and murine
XX CC variable regions. These novel sequence are useful in treatment, diagnosis
XX CC and prophylaxis of HIV infections, and may be produced by a bacterial,
XX CC yeast or mammalian expression system. (Updated on 25-MAR-2003 to correct
XX CC PA field.) (Updated on 25-MAR-2003 to correct PI field.)
XX
XX SQ Sequence 126 AA;

Query Match          85.7%; Score 48; DB 2; Length 126;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYSKLPWT 9

```

Db 110 QYSKLPWT 117
RESULT 23
AAR12359
ID AAR12359 standard; protein; 127 AA.
XX
XX AAR12359;
AC
XX
XX 25-MAR-2003 (revised)
DT 15-AUG-1991 (first entry)
XX
XX Light (kappa) chain variable region of murine IC11 immunoglobulin.
DE
XX Chimeric antibodies; immunconjugates; HIV; AIDS.
XX
XX Mus musculus.
OS
XX W09107493-A.
PN 30-MAY-1991.
PD
XX 13-NOV-1989; 89US-00433730.
XX
XX 13-NOV-1989; 89US-00433730.
PR
XX 13-NOV-1989; 89US-00433730.
XX
XX (XOMA) XOMA CORP.
PA (GREC) GREEN CROSS CORP.
XX
XX Better MD, Horwitz AH, Ghoshdastgi P, Robinson R;
PI
XX
XX WPI; 1991-178105/24.
DR N-PSDB; AAQ12061.
XX
XX New chimeric mouse-human antibodies - used to detect, kill and remove HIV
PT -1 antigen from sample.
PT
XX
XX Disclosure; Fig 13; 107pp; English.
XX
XX This is the light (kappa) - chain variable (V) region of a mouse
CC monoclonal antibody (MAb), IC11, and is specific for an HIV-1 viral
CC antigen. It is used in the construction of a chimeric MAb comprising
CC heavy and light chains having murine V regions and human C regions. The
CC chimeric MAbs are more effective than murine MAb IC11 since they have an
CC increased compatibility in humans. The heavy and light chain V-regions
CC are joined by manipulating their respective joining (J) regions, to
CC generate restriction enzyme recognition sites. The chimeric MAbs can be
CC used as immunconjugates, in association with e.g. toxins for HIV
CC treatment. They can also be used in diagnosis of HIV. See also AAQ12056-
CC 60 and AAQ12062-63. (Updated on 25-MAR-2003 to correct PA field.)
CC (Updated on 25-MAR-2003 to correct PI field.) (Updated on 25-MAR-2003 to
CC correct DR field.)
XX
XX Sequence 127 AA;
SQ
Query Match 85.7%; Score 48; DB 2; Length 127;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 QYSKLPWT 9
Db 110 QYSKLPWT 117
RESULT 24
ADA89188
ID ADA89188 standard; protein; 109 AA.
XX
XX ADA89188;
AC
XX
XX 20-NOV-2003 (first entry)
DT
XX

DE Human antibody 2B2 light chain amino acid sequence SEQ ID NO:32.
XX
XX Immunoglobulin; Ig; heavy chain variable domain;
XX light chain variable domain; major histocompatibility complex; MHC;
XX gp100; MUC1; TAX; hTERT; cytoskeletal; gene therapy; cancerous disorder;
XX cancer.
XX
XX Synthetic.
OS
XX Homo sapiens.
XX
XX W02003070752-A2.
PN 28-AUG-2003.
PD
XX
XX 20-FEB-2003; 2003WO-US005128.
XX
XX 20-FEB-2002; 2002US-0358994P.
PR
XX
XX (DYAX-) DYAX CORP.
PA (TECR) TECHNION RES & DEV FOUND LTD.
XX
XX Hoogenboom HRJM, Reiter Y;
PI
XX
XX WPI; 2003-663847/62.
DR N-PSDB; ADA89187.
XX
XX New protein comprising an immunoglobulin heavy chain variable (VH) domain
PT and an immunoglobulin light chain variable (VL) domain, useful for
PT preparing a composition for treating or preventing a cancerous disorder.
XX
XX Disclosure; Fig 7A; 224pp; English.
XX
XX The present invention describes a protein comprising an immunoglobulin
CC (Ig) heavy chain variable (VH) domain and an Ig light chain variable (VL)
CC domain. The protein binds a complex comprising a major histocompatibility
CC complex (MHC) and a peptide, does not substantially bind the MHC in the
CC absence of the bound peptide, and does not substantially bind the peptide
CC in the absence of the MHC. The peptide is a peptide fragment of gp100,
CC in the absence of the MHC. Also described: (1) a pharmaceutical composition
CC comprising the novel protein and a carrier; (2) a cytotoxic T cell
CC comprising one or more nucleic acids for expressing the Ig that binds a
CC complex having an MHC and a peptide, does not substantially bind the MHC
CC in the absence of the bound peptide, and does not substantially bind the
CC peptide in the absence of the MHC; (3) an isolated nucleic acid
CC comprising a first segment that encodes the Ig variable domain; (4) a
CC host cell comprising heterologous nucleic acid sequences that encodes the
CC novel protein; (5) a transgenic animal whose genome includes heterologous
CC nucleic acid sequences that encode the protein; (6) identifying the
CC protein that specifically binds the MHC-peptide complex; (7) expressing
CC an antigen-binding protein; (8) ablating or killing a target cell that
CC displays a peptide on a surface MHC molecule; (9) treating or preventing
CC a cancerous disorder in a subject; and (10) detecting an MHC-peptide
CC complex in a sample. A protein of the invention has cytoskeletal activity,
CC and can be used in gene therapy. The protein is useful for preparing a
CC composition for treating or preventing a cancerous disorder. The present
CC sequence represents the light chain of an antibody which binds to an MHC-
CC peptide complex where the peptide component in as peptide fragment of
XX gp100.
XX
XX Sequence 109 AA;
SQ
Query Match 78.6%; Score 44; DB 6; Length 109;
Best Local Similarity 77.8%; Pred. No. 5.7;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 HOYSKLPWT 9
Db 90 HOYGLPWT 98
RESULT 25
ABP43158
ID ABP43158 standard; protein; 215 AA.

XX 09-OCT-2003; 2003WO-US032214.
PF 10-OCT-2002; 2002US-0417979P.
XX (INTE-) INTEGRIGEN INC.
XX Smider V, Larrick JW;
XX MPI; 2004-340921/31.
DR N-PSDB; ADO07304.
XX
PT Novel recombinant catalytic polypeptide useful for cleaving target
PT proteins or for treating or preventing cancers, comprises a human
PT antibody light chain operably joined to a heterologous antibody heavy
PT chain.
XX
PS Claim 62; SEQ ID NO 24; 92pp; English.
XX
CC The present sequence is the protein sequence of a human light chain
CC variable region (VL), denoted A26-JK1, that is preferred for use in
CC recombinant catalytic polypeptides of the invention. VL genes encoding
CC potentially catalytic variable regions were cloned by PCR from human
CC genomic DNA following analysis of the human kappa repertoire for genes
CC containing putative serine protease triads. Several genes were
CC identified, including A26. Catalytic polypeptides of the invention
CC comprise a human antibody light chain operably joined to a heterologous
CC antibody heavy chain. The light chain has a serine protease dyad and
CC endopeptidase activity, and the heavy chain has a predetermined
CC specificity for a target protein. By joining 2 heterologous human
CC antibody chains, one of which supplies the catalytic activity to a
CC hydrolyse polypeptides and the other the binding specificity for a target
CC protein, the invention provides for the construction of a repertoire of
CC proteases with customized protein substrate specificities of potentially
CC unlimited number and thus makes possible the effective treatment and/or
CC prevention of any medical condition attributable to the presence or
CC overexpression of an identified protein. The invention also provides
CC nucleic acids encoding the catalytic antibodies (which can be used for
CC gene therapy), host cells, transgenic non-human animals, and methods of
CC cleaving a target protein (in vitro or in vivo) using a recombinant
CC catalytic polypeptide. It also provides a library of recombinant
CC catalytic polypeptides with altered enzymatic activity, and a method of
CC altering the enzymatic activity of the recombinant catalytic polypeptides
CC by mutating at least one complementarily determining region of the heavy
CC chain.
CC
CC
SQ Sequence 107 AA:
Query Match 75.0%; Score 42; DB 8; Length 107;
Best Local Similarity 77.8%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 HQSKLPMT 9
Db 89 HQSSLPMT 97
RESULT 27
ADO07307
ID ADO07307 standard; protein; 107 AA.
XX
AC ADO07307;
XX
DT 15-JUL-2004 (first entry)
XX
DE Human proteolytic A10-JK1 light chain, used in catalytic antibody.
XX
KM Catalytic antibody; human; antibody; protease; gene therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 1..23

FT /label= FR1
FT /note= "Framework region 1"
FT 1
FT /note= "Possible Glu component of catalytic triad"
FT 24..34
FT /label= CDR1
FT /note= "Complementarity determining region 1"
FT 26
FT /note= "Possible Ser component of catalytic triad"
FT 28
FT /note= "Possible Ser component of catalytic triad"
FT 31
FT /note= "Possible Ser component of catalytic triad"
FT 32
FT /note= "Possible Ser component of catalytic triad"
FT 34
FT /note= "Possible His component of catalytic triad"
FT 35..49
FT /label= FR2
FT /note= "Framework region 2"
FT 50..56
FT /label= CDR2
FT /note= "Complementarity determining region 2"
FT 52
FT /note= "Possible Ser component of catalytic triad"
FT 54
FT /note= "Possible Ser component of catalytic triad"
FT 56
FT /note= "Possible Ser component of catalytic triad"
FT 57..88
FT /label= FR3
FT /note= "Framework region 3"
FT 89..95
FT /label= CDR3
FT /note= "Complementarity determining region 3"
FT 89
FT /note= "Possible His component of catalytic triad"
FT 91
FT /note= "Possible Ser component of catalytic triad"
FT 92
FT /note= "Possible Ser component of catalytic triad"
FT 93
FT /note= "Possible Ser component of catalytic triad"
FT
PN WO2004033658-A2.
XX
PD 22-APR-2004.
XX
PF 09-OCT-2003; 2003WO-US032214.
XX
PR 10-OCT-2002; 2002US-0417979P.
XX
PA (INTE-) INTEGRIGEN INC.
XX
PI Smider V, Larrick JW;
XX
XX MPI; 2004-340921/31.
DR N-PSDB; ADO07306.
XX
PT Novel recombinant catalytic polypeptide useful for cleaving target
PT proteins or for treating or preventing cancers, comprises a human
PT antibody light chain operably joined to a heterologous antibody heavy
PT chain.
XX
PS Claim 62; SEQ ID NO 26; 92pp; English.
XX
CC The present sequence is the protein sequence of a human light chain
CC variable region (VL), denoted A10-JK1, that is preferred for use in
CC recombinant catalytic polypeptides of the invention. VL genes encoding
CC potentially catalytic variable regions were cloned by PCR from human
CC genomic DNA following analysis of the human kappa repertoire for genes
CC containing putative serine protease triads. Several genes were
CC identified, including A10. Catalytic polypeptides of the invention

CC comprise a human antibody light chain operably joined to a heterologous
CC antibody heavy chain. The light chain has a serine protease dyad and
CC antipeptidase activity, and the heavy chain has a predetermined
CC specificity for a target protein. By joining 2 heterologous human
CC antibody chains, one of which supplies the catalytic activity to
CC hydrolyse polypeptides and the other the binding specificity for a target
CC protein, the invention provides for the construction of a repertoire of
CC proteases with customised protein substrate specificities of potentially
CC unlimited number and thus makes possible the effective treatment and/or
CC prevention of any medical condition attributable to the presence or
CC overexpression of an identified protein. The invention also provides
CC nucleic acids encoding the catalytic antibodies (which can be used for
CC gene therapy), host cells, transgenic non-human animals, and methods of
CC cleaving a target protein (in vitro or in vivo) using a recombinant
CC catalytic polypeptide. It also provides a library of recombinant
CC catalytic polypeptides with altered enzymatic activity, and a method of
CC altering the enzymatic activity of the recombinant catalytic polypeptides
CC by mutating at least one complementarily determining region of the heavy
CC chain.

SQ Sequence 107 AA;

Query Match 75.0%; Score 42; DB 8; Length 107;
Best Local Similarity 77.8%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 HOYSKLPMT 9
||| |||
Db 89 HOSSSLPMT 97

RESULT 28
AAB48936
ID AAB48936 standard; protein; 113 AA.

AC AAB48936;

DT 16-MAR-2001 (first entry)

DE Anti-TrkA murine monoclonal antibody MNAC13 light chain variable region.

KW Murine monoclonal antibody MNAC13; light chain variable region; VL;

KW human TrkA antagonist; NGF receptor; nerve growth factor;

KW neurological pathology; acute pain; chronic pain; analgesic; neuroma;

KW cancer; TrkA-expressing tumour; gene therapy; in vivo imaging; diagnosis.

XX Mus sp.

XX WO20007344-A2.

XX 07-DEC-2000.

XX 26-MAY-2000; 2000WO-IT000218.

XX 26-MAY-1999; 99IT-RM000333.

XX (SIRS-) SIRS SOC ITAL RICERCA SCI SRL.

XX Novak MM;

XX WPI; 2001-061515/07.

XX N-PSDB; AAC87642.

XX Monoclonal antibody and its derivatives specific to high affinity

XX tyrosine kinase receptor of nerve growth factor useful for treating and

XX diagnosing neuropathological disorders such as pain, neuromas, TrkA

XX expressing neoplastic tumors.

XX Claim 2; Page; 33pp; English.

CC chain variable region (VL) as given in AAB48936, and a heavy chain
CC variable region (VH) as given in AAB48937. The invention also encompasses
CC synthetic derivatives of monoclonal antibody MNAC13, such as the single
CC chain antibody, scFvMNAC13 (AAB48934), which comprises the VL and VH
CC regions of MNAC13 in one polypeptide chain. The invention additionally
CC relates to pharmaceutical compositions comprising the antibody or
CC antibody derivatives of the invention, engineered eukaryotic cells able
CC to express the MNAC13 antibody or its derivatives, and a diagnostic
CC composition comprising the antibody or its derivatives for in vivo
CC imaging. NGF antagonist (inhibitor of binding of NGF to TrkA receptor The
CC MNAC13 monoclonal antibody and its derivatives are useful for treating
CC neurological pathologies such as acute or chronic pain, neuromas, and
CC TrkA-expressing neoplastic tumors. A composition comprising MNAC13 or
CC its derivatives with a diagnostically acceptable carrier is useful for in
CC vivo imaging diagnostics. The present sequence represents the light chain
CC variable region of the anti-TrkA murine monoclonal antibody MNAC13. Note:
CC The present sequence is derived from that of the single chain antibody
CC scFvMNAC13 shown on pages 32-33 and the information given in claim 2

SQ Sequence 113 AA;

Query Match 73.2%; Score 41; DB 4; Length 113;
Best Local Similarity 66.7%; Pred. No. 20;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 HOYSKLPMT 9
||| |||
Db 89 HOSSSLPMT 97

RESULT 29
AAB48934
ID AAB48934 standard; protein; 295 AA.

AC AAB48934;

DT 16-MAR-2001 (first entry)

DE Anti-TrkA single chain antibody scFvMNAC13.

KW Single chain antibody; murine monoclonal antibody MNAC13; scFvMNAC13;

KW human TrkA antagonist; NGF receptor; nerve growth factor;

KW neurological pathology; acute pain; chronic pain; analgesic; neuroma;

KW cancer; TrkA-expressing tumour; gene therapy; in vivo imaging; diagnosis.

XX Mus sp.

XX Synthetic.

XX WO20007344-A2.

XX 07-DEC-2000.

XX 26-MAY-2000; 2000WO-IT000218.

XX 26-MAY-1999; 99IT-RM000333.

XX (SIRS-) SIRS SOC ITAL RICERCA SCI SRL.

XX Novak MM;

XX WPI; 2001-061515/07.

XX N-PSDB; AAC87642.

XX Monoclonal antibody and its derivatives specific to high affinity

XX tyrosine kinase receptor of nerve growth factor useful for treating and

XX diagnosing neuropathological disorders such as pain, neuromas, TrkA

XX expressing neoplastic tumors.

XX Claim 8; Page 32-33; 33pp; English.

XX The invention relates to a murine monoclonal antibody, MNAC13, which

XX recognises the human nerve growth factor (NGF) receptor tyrosine kinase,

XX TrkA, and acts as an antagonist of NGF/TrkA binding. MNAC13 has a light

CC chain variable region (VL) as given in AAB48936, and a heavy chain
CC variable region (VH) as given in AAB48937. The invention also encompasses
CC synthetic derivatives of monoclonal antibody MNAC13, such as the single
CC chain antibody, scFvMNAC13 (AAB48934), which comprises the VL and VH
CC regions of MNAC13 in one polypeptide chain. The invention additionally
CC relates to pharmaceutical compositions comprising the antibody or
CC antibody derivatives of the invention, engineered eukaryotic cells able
CC to express the MNAC13 antibody or its derivatives, and a diagnostic
CC composition comprising the antibody or its derivatives for in vivo
CC imaging. NGF antagonist (inhibitor of binding of NGF to TrkA receptor. The
CC MNAC13 monoclonal antibody and its derivatives are useful for treating
CC neurological pathologies such as acute or chronic pain, neuromas, and
CC TrkA-expressing neoplastic tumours. A composition comprising MNAC13 or
CC its derivatives with a diagnostically acceptable carrier is useful for in
CC vivo imaging diagnostics. The present sequence represents the anti-TrkA
CC single chain antibody scFvMNAC13
XX

SO Sequence 295 AA;

Query Match 73.2%; Score 41; DB 4; Length 295;
Best Local Similarity 66.7%; Pred. No. 53;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HOYSKLPMT 9
Db ||:|||||
110 HQWSSYPWT 118

RESULT 30
AAB06354
ID AAB06354 standard; peptide; 9 AA.
XX
AC AAB06354;
XX
DT 17-OCT-2000 (first entry)
XX

DE Randomised VL3 sequence of anti-VEGF antibody variant Y0241-5.
XX

XX Humanised; antibody variant; phage display; randomised library;
KW cytostatic; antiarthritic; antipsoriatic; antidiabetic; antiinflammatory;
KW antiarteriosclerotic; vascular endothelial growth factor; VEGF;
KW breast cancer; lung cancer; retinoblastoma; rheumatoid arthritis;
KW psoriasis; atherosclerosis; diabetic retinopathy;
KW complementarity determining region; CDR.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX WO200029584-A1.
PN
XX
PD 25-MAY-2000.
XX
PF 16-NOV-1999; 99WO-US027153.
XX
PR 18-NOV-1998; 98US-0108945P.
XX
XX (GETH) GENENTECH INC.
PA
XX Chen YM, Lowman HB, Muller Y;
PI
XX WPI; 2000-387797/33.
DR

XX Antibody variants with higher binding affinity than native antibodies
PT useful for diagnosis, prevention and treatment of neoplastic and non-
PT neoplastic diseases comprises amino acid insertion in hypervariable
PT region.
XX
XX Example 1; Page 58; 110pp; English.
PS
XX The present sequence is the randomised VL3 region of a variant of anti-
CC vascular endothelial growth factor (VEGF) antibody from phage library YC-
CC 89. A large number of antibody variants containing randomised peptide
CC inserts within the complementarity determining regions (CDRs) were

CC prepared by phage display. Libraries were subjected to eight rounds of
CC selection to isolate variants with an antigen binding affinity at least
CC two-fold stronger than the binding affinity of parent antibody for the
CC target VEGF antibody. The anti-VEGF antibody variants may be useful in
CC diagnostic assays for detecting expression of VEGF in cells, tissue or
CC serum. They may also be used in the prevention and treatment of
CC neoplastic diseases such as breast cancer, lung cancer and
CC retinoblastoma, and non-neoplastic diseases including rheumatoid
CC arthritis, psoriasis, atherosclerosis, and diabetic and other
CC proliferative retinopathies
XX

SO Sequence 9 AA;

Query Match 71.4%; Score 40; DB 3; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSKLPMT 9
Db |||:|||||
2 QYSSVPMT 9

RESULT 31
AAB06352
ID AAB06352 standard; peptide; 9 AA.
XX
AC AAB06352;
XX
DT 17-OCT-2000 (first entry)
XX

DE Randomised VL3 sequence of anti-VEGF antibody variant Y0241-3.
XX

XX Humanised; antibody variant; phage display; randomised library;
KW cytostatic; antiarthritic; antipsoriatic; antidiabetic; antiinflammatory;
KW antiarteriosclerotic; vascular endothelial growth factor; VEGF;
KW breast cancer; lung cancer; retinoblastoma; rheumatoid arthritis;
KW psoriasis; atherosclerosis; diabetic retinopathy;
KW complementarity determining region; CDR.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX WO200029584-A1.
PN
XX
PD 25-MAY-2000.
XX
PF 16-NOV-1999; 99WO-US027153.
XX
PR 18-NOV-1998; 98US-0108945P.
XX
XX (GETH) GENENTECH INC.
PA
XX Chen YM, Lowman HB, Muller Y;
PI
XX WPI; 2000-387797/33.
DR

XX Antibody variants with higher binding affinity than native antibodies
PT useful for diagnosis, prevention and treatment of neoplastic and non-
PT neoplastic diseases comprises amino acid insertion in hypervariable
PT region.
XX
XX Example 1; Page 58; 110pp; English.
PS
XX The present sequence is the randomised VL3 region of a variant of anti-
CC vascular endothelial growth factor (VEGF) antibody from phage library YC-
CC 89. A large number of antibody variants containing randomised peptide
CC inserts within the complementarity determining regions (CDRs) were
CC prepared by phage display. Libraries were subjected to eight rounds of
CC selection to isolate variants with an antigen binding affinity at least
CC two-fold stronger than the binding affinity of parent antibody for the
CC target VEGF antibody. The anti-VEGF antibody variants may be useful in
CC diagnostic assays for detecting expression of VEGF in cells, tissue or
CC serum. They may also be used in the prevention and treatment of

CC neoplastic diseases such as breast cancer, lung cancer and
 CC retinoblastoma, and non-neoplastic diseases including rheumatoid
 CC arthritis, psoriasis, atherosclerosis, and diabetic and other
 CC proliferative retinopathies

SO Sequence 9 AA;

Query Match 71.4%; Score 40; DB 3; Length 9;
 Best Local Similarity 75.0%; Pred. No. 1.7e+06;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QVSKLPMT 9
 ||:||||
 DB 2 QVSNVPMT 9

RESULT 32
 AAR30770
 ID AAR30770 standard; protein; 107 AA.

AC AAR30770;
 XX
 DT 25-MAR-2003 (revised)
 DT 12-MAY-1993 (first entry)
 XX
 DE Consensus humanised murine anti-CD3 MAb UCHT1 VL domain hUK1.
 XX
 KM Humanisation; rapid; monoclonal antibody; mxCd3; light chain.

OS Synthetic.

PN WO9222653-A1.

PD 23-DEC-1992.

XX 15-JUN-1992; 92WO-US005126.

XX 14-JUN-1991; 91US-00715272.

XX (GETH) GENENTECH INC.

PI Carter PJ, Presta LG;

DR WPI; 1993-018139/02.

PT Humanisation of antibodies - by molecular modelling of the variable
 PT domains and alteration by gene conversion mutagenesis.

XX Disclosure; Fig 5; 126pp; English.

CC The sequence is that of a consensus sequence hUK1 of the most abundant
 CC human subgroup, namely VL K1 upon which is based the humanised variants
 CC of the light chain variable domain of murine anti-CD3 monoclonal antibody
 CC UCHT1 (mxCd3, Shalaby 1992). (Updated on 25-MAR-2003 to correct PN
 CC field.)

SO Sequence 107 AA;

Query Match 71.4%; Score 40; DB 2; Length 107;
 Best Local Similarity 75.0%; Pred. No. 28;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QVSKLPMT 9
 ||:||||
 DB 90 QVNSLPMT 97

RESULT 33
 AAB62087
 ID AAB62087 standard; protein; 107 AA.

AC AAB62087;
 XX

DT 29-MAY-2001 (first entry)
 XX
 DE Human VL consensus framework hunkappal.

XX ErbB2 receptor; anti-ErbB2 antibody; tumour; cancer; breast cancer;
 KM leukemia; cytostatic; carcinoma.

OS Homo sapiens.

PN WO200115730-A1.

PD 08-MAR-2001.

PF 25-AUG-2000; 2000WO-US023391.

PR 27-AUG-1999; 99US-0151018P.

PR 23-JUN-2000; 2000US-0213822P.

PA (GETH) GENENTECH INC.
 PI Baughman SA, Shak S;

DR WPI; 2001-235058/24.

PT Treating a human patient with a disorder characterized by overexpression
 PT of ErbB2 receptor such as a tumor or cancer (e.g. metastatic breast
 PT carcinoma) comprises administering several dosages of an anti-ErbB2
 PT antibody.

PS Disclosure; Fig 5A; 71pp; English.

XX The invention relates to treating cancer in a human susceptible to or
 CC diagnosed with a disorder characterized by overexpression of ErbB2
 CC receptor. The method comprises administering an initial dose of at least
 CC approx.5 mg/kg of the anti-ErbB2 antibody, and administering subsequent
 CC doses of the antibody in approximately the same amount or less than the
 CC initial dose. The method is useful for treating a disorder characterized
 CC by overexpression of ErbB2 receptor, particularly a benign or malignant
 CC tumour, or a cancer. The cancer is selected from breast cancer
 CC (particularly metastatic breast carcinoma), leukemia, squamous cell
 CC cancer, small-cell lung cancer, non-small cell lung cancer, pancreatic
 CC cancer, gastrointestinal cancer, glioblastoma, cervical cancer, ovarian
 CC cancer, liver cancer, bladder cancer, hepatoma, colon cancer, colorectal
 CC cancer, endometrial carcinoma, salivary gland carcinoma, kidney cancer,
 CC liver cancer, prostate cancer, vulval cancer, thyroid cancer, hepatic
 CC carcinoma and various types of head and neck cancer. The present sequence
 CC represents the human variable light chain consensus framework hunkappal
 CC (light kappa subgroup I)

SO Sequence 107 AA;

Query Match 71.4%; Score 40; DB 4; Length 107;
 Best Local Similarity 75.0%; Pred. No. 28;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QVSKLPMT 9
 ||:||||
 DB 90 QVNSLPMT 97

RESULT 34
 AAB60400
 ID AAB60400 standard; protein; 107 AA.

AC AAB60400;

DT 24-APR-2001 (first entry)

DE Consensus human light chain kappa subgroup I framework, SEQ ID NO:5.

XX Anti-ErbB2 monoclonal antibody 2C4; HER2; humanised; VL;
 KM light chain variable region; cancer; cytostatic; EGFR-expressing cancer;
 KM epidermal growth factor receptor; colon cancer; rectal cancer; tumour;

KW colorectal cancer; non-small cell lung cancer; metastatic breast cancer;
 XX affinity purification; kappa subgroup 1 framework.
 OS Homo sapiens.
 OS Synthetic.
 XX WO200100245-A2.
 PN 04-JAN-2001.
 PD 23-JUN-2000; 2000WO-US017366.
 PF 25-JUN-1999; 99US-0141316P.
 PR (GETH) GENENTECH INC.
 PA (GETH) GENENTECH INC.
 PI Adams CM, Presta LG, Sliwkowsky M;
 XX WPI; 2001-080862/09.
 DR Treating cancer in a human, where the cancer expresses epidermal growth
 XX factor receptor (EGFR), comprises administering an antibody which binds
 PT ErbB2.
 PS Example 3; Fig 7A; 89pp; English.
 XX The invention relates to a method for treating cancer in a human patient,
 CC wherein the cancer expresses epidermal growth factor receptor (EGFR),
 CC comprising administering an antibody which binds ErbB2 (HER2; AAB60408).
 CC In particular, the anti-ErbB2 antibody is the murine monoclonal antibody
 CC 2C4 (AAB60396, AAB60397) or a humanised version of 2C4 (AAB60398,
 CC AAB60399). The invention also encompasses an isolated nucleic acid
 CC encoding a humanised ErbB2-binding antibody; vectors and host cells
 CC comprising such nucleic acids; the recombinant production of a humanised
 CC ErbB2-binding antibody; and an immun conjugate comprising a humanised
 CC ErbB2-binding antibody and a cytotoxic drug. The ErbB2-binding antibodies
 CC act by antagonising ErbB receptors, and as inhibitors of transforming
 CC growth factor alpha (TGF-alpha)-activated mitogen activated protein
 CC kinase (MAPK). The method of the invention is used for treating cancer,
 CC especially colon cancer, rectal cancer, colorectal cancer, lung cancer
 CC (especially non-small cell lung cancer), or breast cancer (especially
 CC metastatic breast cancer). The antibodies may also have non-therapeutic
 CC uses e.g., as affinity purification agents. Using an antibody which binds
 CC to ErbB2 to treat cancer is preferable to the use of EGFR-targeted
 CC drugs, as EGFR is also highly expressed in other tissues such as the
 CC liver and skin, where the active drug will also bind, with skin toxicity
 CC having been observed for EGFR-targeted drugs. Antibodies which bind
 CC ErbB2 are anticipated to have a better safety profile than such drugs.
 CC The present sequence represents the consensus human light chain kappa
 CC subgroup 1 framework used to humanise the anti-ErbB2 antibody 2C4
 CC XX
 SQ Sequence 107 AA;
 Query Match 71.4%; Score 40; DB 4; Length 107;
 Best Local Similarity 75.0%; Pred. No. 28;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 2 QYSLPMT 9
 XX ||:||||
 Db 90 QYNSLPMT 97
 RESULT 35
 AAB61585
 ID AAB61585 standard; protein; 107 AA.
 XX
 AC AAB61585;
 XX
 DT 04-APR-2001 (first entry)
 XX
 DE Human variable light chain consensus sequence.
 XX
 KW ErbB2; cytosolic; prostate cancer; receptor tyrosine kinase; human;

KW antibody; ErbB receptor; monoclonal antibody 2C4; variable light chain.
 XX
 OS Homo sapiens.
 XX
 PN WO200100238-A1.
 XX 04-JAN-2001.
 PD 23-JUN-2000; 2000WO-US017423.
 PF 25-JUN-1999; 99US-0141315P.
 PR (GETH) GENENTECH INC.
 PA (SLOK) SLOAN KETTERING INST CANCER RES.
 PI Agus DB, Scher HI, Sliwkowski MX;
 XX WPI; 2001-159131/16.
 DR Treating prostate cancer in a human comprises administering an antibody
 XX which binds ErbB2 and blocks ligand activation of an ErbB receptor.
 PT
 PS Example 3; Fig 7; 93pp; English.
 XX The ErbB family of receptor tyrosine kinases are important mediators of
 CC cell growth, differentiation and survival. The receptor family includes
 CC four distinct members including Epidermal Growth Factor Receptor (EGFR or
 CC ErbB1), HER2 (ErbB2 or p185^{neu}), HER3 (ErbB3) and Her4 (ErbB4 or tyro2).
 CC The present invention relates to a method for treating prostate cancer.
 CC The method comprises administering an antibody which binds ErbB2 and
 CC blocks ligand activation of an ErbB receptor. Preferably, the antibody
 CC blocks binding of monoclonal antibody 2C4 to ErbB2 and/or blocks TGF-
 CC alpha activation of mitogen-activated protein kinase (MAPK). The present
 CC sequence is the consensus framework for the human variable light chain.
 CC This sequence was used in a sequence alignment homology with the variable
 CC light chain of antibody 2C4 (see AAB61581)
 CC XX
 SQ Sequence 107 AA;
 Query Match 71.4%; Score 40; DB 4; Length 107;
 Best Local Similarity 75.0%; Pred. No. 28;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 2 QYSLPMT 9
 XX ||:||||
 Db 90 QYNSLPMT 97
 RESULT 36
 ADE71454
 ID ADE71454 standard; protein; 107 AA.
 XX
 AC ADE71454;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Human antibody variable light chain framework.
 XX
 KW Cytostatic; ErbB2 antagonist; tyrosine kinase inhibitor; cancer; ErbB2;
 KW ErbB2 antibody; carcinoma; lymphoma; blastoma; sarcoma; liposarcoma;
 KW neuroendocrine tumour; mesothelioma; schwannoma; meningioma;
 KW adenocarcinoma; melanoma; leukaemia; lymphoid malignancy;
 KW squamous cell cancer; epithelial squamous cell cancer; lung cancer;
 KW small-cell lung cancer; non-small cell lung cancer;
 KW adenocarcinoma of the lung; squamous carcinoma of the lung;
 KW cancer of the peritoneum; hepatocellular cancer; gastric cancer;
 KW stomach cancer; gastrointestinal cancer; pancreatic cancer; glioblastoma;
 KW cervical cancer; ovarian cancer; liver cancer; bladder cancer; hepatoma;
 KW breast cancer; colon cancer; rectal cancer; colorectal cancer;
 KW endometrial carcinoma; uterine carcinoma; salivary gland carcinoma;
 KW kidney cancer; renal cancer; prostate cancer; vulval cancer;
 KW thyroid cancer; hepatic carcinoma; anal carcinoma; penile carcinoma;
 KW testicular cancer; oesophageal cancer; tumour of the biliary tract;

XX head and neck cancer; human antibody; variable light chain framework.
OS Homo sapiens.
XX US2003086924-A1.
PN 08-MAY-2003.
PD 10-OCT-2002; 2002US-00268501.
PF 25-JUN-1999; 99US-0141316P.
PR 23-JUN-2000; 2000US-00602812.
XX (GETH) GENENTECH INC.
PA S11KOWSKI MX;
XX S11KOWSKI MX;
XX WPI; 2004-020226/02.
DR
XX
XX Treating cancer (e.g. carcinoma, lymphoma or sarcoma) that expresses
PT ErbB2 by administering to a patient an anti-ErbB2 antibody, and
PT optionally an epidermal growth factor receptor-targeted drug or a
PT tyrosine kinase inhibitor.
XX
XX Example 3; SEQ ID NO 5; 56pp; English.
PS
XX The invention describes a method of treating cancer that expresses ErbB2
CC comprising administering to a patient an antibody that binds ErbB2.
CC Specifically claimed are antibodies that bind ErbB2, particularly
CC monoclonal antibody 2C4 or humanised 2C4, or monoclonal antibody 4D5 or
CC humanised 4D5. The methods are useful for treating cancer in a patient,
CC particularly a human. The cancer includes carcinoma, lymphoma, blastoma,
CC sarcoma, liposarcoma, neuroendocrine tumour, mesothelioma, schwannoma,
CC meningioma, adenocarcinoma, melanoma, leukaemia, lymphoid malignancy,
CC squamous cell cancer, epithelial squamous cell cancer, lung cancer, small
CC cell lung cancer, non-small cell lung cancer, adenocarcinoma of the
CC lung, squamous carcinoma of the lung, cancer of the peritoneum,
CC hepatocellular cancer, gastric or stomach cancer, gastrointestinal
CC cancer, pancreatic cancer, glioblastoma, cervical cancer, ovarian cancer,
CC liver cancer, bladder cancer, hepatoma, breast cancer, colon cancer,
CC rectal cancer, colorectal cancer, endometrial or uterine carcinoma,
CC salivary gland carcinoma, kidney or renal cancer, prostate cancer, vulval
CC cancer, thyroid cancer, hepatic carcinoma, anal carcinoma, penile
CC carcinoma, testicular cancer, esophageal cancer, a tumour of the biliary
CC tract, or head and neck cancer. This is the amino acid sequence of human
CC antibody variable light chain framework that was used to produce a
CC humanised antibody.
XX
XX Sequence 107 AA;
SQ
XX
XX Query Match 71.4%; Score 40; DB 8; Length 107;
XX Best Local Similarity 75.0%; Pred. No. 28;
XX Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0.
QY 2 QYSLPWT 9
XX ||: ||||
XX 90 QYNSLPWT 97
DB
RESULT 37
ADJ88008
ID ADJ88008 standard; protein; 107 AA.
XX
XX ADJ88008;
AC
XX 06-MAY-2004 (first entry)
DT
XX
XX Human variable light chain consensus peptide.
DE
XX
XX Cancer; ErbB2; gene therapy; human.
KW
XX
XX Homo sapiens.
OS Unidentified.

PN	US2004013667-A1.	
XX		
PD	22-JAN-2004.	
XX		
PF	27-JUN-2003; 2003US-00608626.	
XX		
PR	25-JUN-1999; 99US-0141316P.	
PR	23-JUN-2000; 2000US-00602812.	
PR	10-OCT-2002; 2002US-00268501.	
XX		
PA	(GETH) GENENTECH INC.	
XX		
PI	Kalsey SM, Sliwowski MX;	
XX		
DR	WPI; 2004-121529/12.	
XX		
PT	Treating cancer that expresses ErbB2 e.g., breast, colon, rectal or	
PT	colorectal cancer comprises administering an antibody that binds to ErbB2	
PT	to a patient.	
XX		
PS	Example 3; SEQ ID NO 5; 56bp; English.	
XX		
CC	The present invention relates to methods for treating cancer such as	
CC	carcinoma, lymphoma, blastoma, medulloblastoma, retinoblastoma, sarcoma,	
CC	liposarcoma, synovial cell sarcoma, neuroendocrine tumour, carcinoid	
CC	tumour, gastrinoma, islet cell cancer, mesothelioma, schwannoma, acoustic	
CC	neuroma, meningioma, adenocarcinoma, melanoma, leukaemia, lymphoid	
CC	malignancy, squamous cell cancer, epithelial squamous cell cancer, lung	
CC	cancer, small-cell lung cancer, non-small cell lung cancer,	
CC	adenocarcinoma of the lung, squamous carcinoma of the lung, cancer of the	
CC	peritoneum, hepatocellular cancer, gastric or stomach cancer,	
CC	gastrointestinal cancer, pancreatic cancer, glioblastoma, cervical	
CC	cancer, ovarian cancer, liver cancer, bladder cancer, hepatoma, breast	
CC	cancer, colon cancer, rectal cancer, colorectal cancer, endometrial or	
CC	uterine carcinoma, salivary gland carcinoma, kidney or renal cancer,	
CC	prostate cancer, vulvar cancer, thyroid cancer, hepatic carcinoma, anal	
CC	carcinoma, penile carcinoma, testicular cancer, oesophageal cancer, a	
CC	tumour of the biliary tract or head and neck cancer with anti-ErbB2	
CC	antibodies. The invention is also useful in gene therapy. The present	
CC	sequence is human variable light chain consensus peptide.	
XX		
SO	Sequence 107 AA;	
Query Match	71.4%;	Score 40; DB: 8; Length 107;
Best Local Similarity	75.0%;	Pred. No. 28;
Matches	6; Conservative	1; Mismatches 1; Indels 0; Gaps 0;
QY	2 QYSLPMT 9	
	:	
Db	90 QYNLPLPMT 97	
RESULT 38		
IDN	ADN12054	
ID	ADN12054 standard; protein; 107 AA.	
XX		
AC	ADN12054;	
XX		
DT	17-JUN-2004 (first entry)	
XX		
XX	Variable light chain consensus sequence.	
XX		
KW	tumor; anti-HER2 antibody; HER2/HER3; HER2/HER1; Cytostatic; cancer.	
XX		
OS	Homo sapiens.	
XX		
PN	WO2004008099-A2.	
XX		
PN	22-JAN-2004.	
XX		
PD	11-JUL-2003; 2003WO-US021590.	
XX		

PR 15-JUL-2002; 2002US-0396290P.
PR 20-JUN-2003; 2003US-0480043P.
XX
XX (GETH) GENENTECH INC.
XX
XX Koll H, Bossemmaier B, Mueller H, Sliwkowski MX, Kelsey SM,
XX WPI; 2004-156546/15.
XX
XX Identifying a tumor responsive to treatment with an anti-HER2 antibody,
PT useful in treating cancer, comprises detecting the presence of a
DR HER2/HER3 and/or HER2/HER1 protein complex.
XX
XX Disclosure; SEQ ID NO 5; 105pp; English.
XX
XX The present invention relates to identifying a tumor responsive to
CC treatment with an anti-HER2 antibody involves detecting the presence of
CC an HHR2/HER3 and/or HHR2/HER1 protein complex in a sample of the tumor.
CC The method is useful in identifying a tumor as responsive to treatment
CC with an anti-HER2 antibody. The methods and antibodies are useful in
CC treating a condition or disorder including tumor or cancer, e.g. breast,
CC prostate, lung, colorectal or ovarian cancer. The present sequence
CC represents a variable light chain consensus sequence.
XX
XX

SQ Sequence 107 AA;

Query Match 71.4%; Score 40; DB 8; Length 107;
Best Local Similarity 75.0%; Pred. No. 28;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSLPWT 9
Db 90 QYNSLPWT 97
||:||||

RESULT 39

ADP43328
ID ADP43328 standard; protein; 107 AA.

AC ADP43328;

XX
XX 26-AUG-2004 (first entry)

DE Human monoclonal variable light kappa chain antibody SegID 5.

XX human; variable light kappa chain; antibody;
XX epidermal growth factor receptor; ErbB; ErbB2;
XX transforming growth factor alpha; benign hyperproliferative disorder;
XX psoriasis; endometriosis; scleroderma; vascular disease; atherosclerosis;
XX restenosis; colon polyps; fibroadenoma; respiratory disease;
XX chronic bronchitis; cystic fibrosis; cystostatic; antipsoriatic;
XX gynaecological; dermatological; vasotrophic; antiarteriosclerotic;
XX cardiant; antianginal; antidiabetic; hypotensive; antiasthmatic;
XX anti-allergic; anti-inflammatory; antitussive.
XX

OS Homo sapiens.

PN WO2004048525-A2.

PD 10-JUN-2004.

PF 21-NOV-2003; 2003WO-US037367.

PR 21-NOV-2002; 2002US-0428027P.

XX (GETH) GENENTECH INC.

XX Sliwkowski MX, Brunetta FG;

XX WPI; 2004-450361/42.

PT Treating non-malignant disease or disorder such as psoriasis, epidermal
PT endometriosis, involving abnormal activation or production of

PT growth factor receptor or ErbB ligand by administering antibody that
PT binds ErbB2 to mammal.

XX Example 3; SEQ ID NO 5; 74pp; English.

XX This invention refers to a novel method for treating a non-malignant
CC disease that involves abnormal activation or production of an epidermal
CC growth factor receptor (ErbB) receptor or an ErbB ligand. Specifically,
CC it refers to the use of humanised murine anti-ErbB2 antibodies to block
CC ligand activation of the ErbB receptor, where the ErbB ligand is a
CC transforming growth factor alpha that promotes mitogen-activated protein
CC kinase (MAPK). The present invention describes conjugating the monoclonal
CC murine antibody 2C4, or more particularly the humanised antibody 574, to
CC a cytotoxic or therapeutic agent such that it can be used to treat a
CC benign hyperproliferative disorder, psoriasis, endometriosis,
CC scleroderma, vascular disease (such as atherosclerosis or restenosis),
CC colon polyps, fibroadenoma or respiratory disease (such as chronic
CC bronchitis or cystic fibrosis). Accordingly, they exhibit cytostatic,
CC antipsoriatic, gynaecological, dermatological, vasotrophic, hypotensive,
CC antiarteriosclerotic, cardiant, antianginal, anti-allergic, hypotensive,
CC antiasthmatic, anti-allergic, anti-inflammatory and antitussive activities.
CC This polypeptide sequence is the human variable light kappa chain protein
CC used to humanise the murine anti-ErbB2 proteins of the invention.
XX
XX

SQ Sequence 107 AA;

Query Match 71.4%; Score 40; DB 8; Length 107;
Best Local Similarity 75.0%; Pred. No. 28;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSLPWT 9
Db 90 QYNSLPWT 97
||:||||

RESULT 40

AAW04177
ID AAW04177 standard; protein; 108 AA.

AC AAW04177;

XX
XX 19-MAY-1997 (first entry)

DE Variant variable light chain of Fas ligand antibody NOK-1.

XX Variable region; light chain; human; Fas ligand; monoclonal; antibody;
XX NOK-1; hybridoma; inhibition; apoptosis; assay; diagnosis; disease;
XX hepatitis; infectious mononucleosis; systemic lupus erythematosus;
XX variant.
XX

OS Mus musculus.

PN WO9629350-A1.

PD 26-SEP-1996.

PF 21-MAR-1996; 96WO-JP000734.

PR 20-MAR-1995; 95JP-00087420.

XX 27-OCT-1995; 95JP-00303492.

XX (SUME) SUMITOMO ELECTRIC IND CO.

XX Kayagaki N, Yagita H, Okumura K, Nakata M;

XX WPI; 1996-443140/44.

XX N-PADB; AAT39350.

PT Monoclonal antibody specifically recognising the Fas ligand - useful for
PT the detection of Fas ligands either on cell surface or in solution.

XX Claim 20; Page 80-81; 133pp; Japanese.

CC The present sequence is a variant light chain variable region of the anti
CC -human Fas ligand monoclonal antibody (Mab) NOK-1. NOK-1 is produced by
CC the hybridoma NOK-1 (PERM BP-5044), which was prepared by immunising mice
CC with transformed human Fas ligand expressing COS cells, and fusing spleen
CC cells isolated from the mice with myeloma P3x63Ag8.653 (ATCC CRL-1580)
CC cells. The Mab recognises the human Fas ligand on the cell surface or in
CC solution, and can be used to inhibit the apoptosis inducing cell surface
CC Fas ligand/Fas reaction. The Mab can also be used for a Fas ligand assay
CC in biological samples (e.g. human blood), especially for disease
CC diagnosis, e.g. hepatitis, infectious mononucleosis and systemic lupus
CC erythematosus.

XX Sequence 108 AA;

Query Match 71.4%; Score 40; DB 2; Length 108;

Best Local Similarity 75.0%; Pred. No. 29;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSKLPWT 9

DB 90 QYSEFPWT 97

Search completed: December 17, 2004, 18:29:07
Job time : 29.3539 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 17, 2004, 18:13:27 ; Search time 5.46067 seconds
(without alignments)
109.302 Million cell updates/sec

Title: US-10-089-500-8
Perfect score: 56
Sequence: 1 HQYSKLPWT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 6631800 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/prodata1/1aa/5A_COMB.pep:*
2: /cgn2_6/prodata1/1aa/5B_COMB.pep:*
3: /cgn2_6/prodata1/1aa/6A_COMB.pep:*
4: /cgn2_6/prodata1/1aa/6B_COMB.pep:*
5: /cgn2_6/prodata1/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/prodata1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	56	100.0	128	4	US-09-225-322B-10
2	56	100.0	128	4	US-09-225-322B-19
3	56	100.0	128	4	US-09-764-304-10
4	56	100.0	128	4	US-09-764-304-19
5	40	71.4	9	4	US-09-440-781-24
6	40	71.4	9	4	US-09-440-781-26
7	40	71.4	107	2	US-07-934-373C-18
8	40	71.4	107	3	US-08-437-642B-18
9	40	71.4	107	4	US-08-146-206C-18
10	40	71.4	107	4	US-08-648-067A-14
11	40	71.4	107	4	US-09-705-686-18
12	40	71.4	107	4	US-09-705-392A-18
13	40	71.4	107	5	PCT-US93-07832-18
14	40	71.4	108	3	US-08-974-899-3
15	40	71.4	108	3	US-09-065-059-3
16	40	71.4	108	4	US-09-795-798-3
17	39	69.6	9	2	US-08-560-558B-31
18	39	69.6	9	4	US-09-217-268B-31
19	39	69.6	9	4	US-09-440-781-25
20	39	69.6	110	4	US-09-440-781-94
21	39	69.6	110	4	US-09-440-781-95
22	39	69.6	113	1	US-08-497-112-18
23	39	69.6	114	2	US-08-560-558B-27
24	39	69.6	114	4	US-09-217-268B-27
25	39	69.6	114	4	US-09-217-268B-35
26	39	69.6	116	1	US-08-497-312-14
27	38	67.9	191	4	US-09-270-767-37260

28	38	67.9	191	4	US-09-270-767-52477	Sequence 52477, A
29	38	67.9	249	2	US-08-797-689-18	Sequence 18, Appl
30	38	67.9	249	4	US-09-984-186-18	Sequence 18, Appl
31	38	67.9	572	6	5200183-5	Patent No. 5200183
32	38	67.9	573	6	5215909-12	Patent No. 5215909
33	38	67.9	602	3	US-08-446-100-1	Sequence 1, Appl
34	38	67.9	602	3	US-08-446-100-2	Sequence 2, Appl
35	38	67.9	602	3	US-08-446-100-3	Sequence 3, Appl
36	38	67.9	602	3	US-08-446-100-4	Sequence 4, Appl
37	38	67.9	602	3	US-08-446-100-5	Sequence 5, Appl
38	38	67.9	602	3	US-08-446-100-6	Sequence 6, Appl
39	38	67.9	602	3	US-08-446-100-7	Sequence 7, Appl
40	38	67.9	602	3	US-08-446-100-8	Sequence 8, Appl
41	38	67.9	602	3	US-08-446-100-9	Sequence 9, Appl
42	38	67.9	602	3	US-08-446-100-10	Sequence 10, Appl
43	38	67.9	602	3	US-08-446-100-11	Sequence 11, Appl
44	38	67.9	602	3	US-08-446-100-12	Sequence 12, Appl
45	38	67.9	602	3	US-08-446-100-13	Sequence 13, Appl

ALIGNMENTS

```

RESULT 1
US-09-225-322B-10
; Sequence 10, Application US/09225322B
; Patent No. 6437098
; GENERAL INFORMATION:
; APPLICANT: SHITTARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KOMANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/09/225,322B
; CURRENT FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 10
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CDNA KM-641
US-09-225-322B-10

Query Match          100.0%; Score 56; DB 4; Length 128;
Best Local Similarity 100.0%; Pred. No. 0.0042;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      1 HQYSKLPWT 9
Db      109 HQYSKLPWT 117

RESULT 2
US-09-225-322B-19
; Sequence 19, Application US/09225322B
; Patent No. 6437098
; GENERAL INFORMATION:
; APPLICANT: SHITTARA, KENYA
; APPLICANT: HANAI, NOBUO

```

```
/ APPLICANT: HASEGAWA, MAMORU
/ APPLICANT: MIYAJI, HIROMASA
/ APPLICANT: KIWANA, YOSHIHISA
/ TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
/ FILE REFERENCE: 249-101
/ CURRENT APPLICATION NUMBER: US/09/225,322B
/ CURRENT FILING DATE: 1999-01-05
/ PRIOR APPLICATION NUMBER: US 08/454,680
/ PRIOR FILING DATE: 1995-05-31
/ PRIOR APPLICATION NUMBER: US 08/408,133
/ PRIOR FILING DATE: 1995-03-21
/ PRIOR APPLICATION NUMBER: US 08/292,178
/ PRIOR FILING DATE: 1994-08-17
/ PRIOR APPLICATION NUMBER: US07/947,674
/ PRIOR FILING DATE: 1992-09-17
/ PRIOR APPLICATION NUMBER: JP 3-238375
/ PRIOR FILING DATE: 1991-09-18
/ NUMBER OF SEQ ID NOS: 19
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO 19
/ LENGTH: 128
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:light chain
/ US-09-225-322B-19
```

```
Query Match          100.0%; Score 56; DB 4; Length 128;
Best Local Similarity 100.0%; Pred. No. 0.0042;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 HOYSKLPWT 9
Db      109 HOYSKLPWT 117
```

```
RESULT 3
/ US-09-764-304-10
/ Sequence 10, Application US/09764304
/ Patent No. 6495666
/ GENERAL INFORMATION:
/ APPLICANT: SHITTARA, KENYA
/ APPLICANT: HANAI, NOBUO
/ APPLICANT: HASEGAWA, MAMORU
/ APPLICANT: MIYAJI, HIROMASA
/ APPLICANT: KIWANA, YOSHIHISA
/ TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
/ FILE REFERENCE: 249-101
/ CURRENT APPLICATION NUMBER: US/09/764,304
/ CURRENT FILING DATE: 2001-01-19
/ EARLIER APPLICATION NUMBER: 09/225,322
/ EARLIER FILING DATE: 1999-01-05
/ EARLIER APPLICATION NUMBER: US 08/454,680
/ EARLIER FILING DATE: 1995-05-31
/ EARLIER APPLICATION NUMBER: US 08/408,133
/ EARLIER FILING DATE: 1995-03-21
/ EARLIER APPLICATION NUMBER: US 08/292,178
/ EARLIER FILING DATE: 1994-08-17
/ EARLIER APPLICATION NUMBER: US07/947,674
/ EARLIER FILING DATE: 1992-09-17
/ EARLIER APPLICATION NUMBER: JP 3-238375
/ EARLIER FILING DATE: 1991-09-18
/ NUMBER OF SEQ ID NOS: 19
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO 10
/ LENGTH: 128
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: CDNA KM-641
/ US-09-764-304-10
```

```
Query Match          100.0%; Score 56; DB 4; Length 128;
Best Local Similarity 100.0%; Pred. No. 0.0042;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 HOYSKLPWT 9
Db      109 HOYSKLPWT 117
```

```
RESULT 4
/ US-09-764-304-19
/ Sequence 19, Application US/09764304
/ Patent No. 6495666
/ GENERAL INFORMATION:
/ APPLICANT: SHITTARA, KENYA
/ APPLICANT: HANAI, NOBUO
/ APPLICANT: HASEGAWA, MAMORU
/ APPLICANT: MIYAJI, HIROMASA
/ APPLICANT: KIWANA, YOSHIHISA
/ TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
/ FILE REFERENCE: 249-101
/ CURRENT APPLICATION NUMBER: US/09/764,304
/ CURRENT FILING DATE: 2001-01-19
/ EARLIER APPLICATION NUMBER: 09/225,322
/ EARLIER FILING DATE: 1999-01-05
/ EARLIER APPLICATION NUMBER: US 08/454,680
/ EARLIER FILING DATE: 1995-05-31
/ EARLIER APPLICATION NUMBER: US 08/408,133
/ EARLIER FILING DATE: 1995-03-21
/ EARLIER APPLICATION NUMBER: US 08/292,178
/ EARLIER FILING DATE: 1994-08-17
/ EARLIER APPLICATION NUMBER: US07/947,674
/ EARLIER FILING DATE: 1992-09-17
/ EARLIER APPLICATION NUMBER: JP 3-238375
/ EARLIER FILING DATE: 1991-09-18
/ NUMBER OF SEQ ID NOS: 19
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO 19
/ LENGTH: 128
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: light chain
/ OTHER INFORMATION: variable region
/ US-09-764-304-19
```

```
Query Match          100.0%; Score 56; DB 4; Length 128;
Best Local Similarity 100.0%; Pred. No. 0.0042;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 HOYSKLPWT 9
Db      109 HOYSKLPWT 117
```

```
RESULT 5
/ US-09-440-781-24
/ Sequence 24, Application US/09440781
/ Patent No. 6632926
/ GENERAL INFORMATION:
/ APPLICANT: Yvonne Man-yea Chen et al.
/ TITLE OF INVENTION: ANTIBODY VARIANTS
/ FILE REFERENCE: P1469R1
/ CURRENT APPLICATION NUMBER: US/09/440,781
/ CURRENT FILING DATE: 1999-11-16
/ NUMBER OF SEQ ID NOS: 99
/ SEQ ID NO 24
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: artificial sequence
/ NAME/KEY: artificial
/ LOCATION: 1-9
```

OTHER INFORMATION: variant CDR sequence
US-09-440-781-24

Query Match 71.4%; Score 40; DB 4; Length 9;
Best Local Similarity 75.0%; Pred. No. 3.8e+05;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSLPMT 9
DB 2 QYSLPMT 9

RESULT 6
US-09-440-781-26

Sequence 26, Application US/09440781
Patent No. 6632926
GENERAL INFORMATION:
APPLICANT: Yvonne Man-yea Chen et al.
TITLE OF INVENTION: ANTIBODY VARIANTS
FILE REFERENCE: P1469R1
CURRENT APPLICATION NUMBER: US/09/440,781
CURRENT FILING DATE: 1999-11-16
NUMBER OF SEQ ID NOS: 99
SEQ ID NO 26
LENGTH: 9
TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
NAME/KEY: artificial
LOCATION: 1-9
OTHER INFORMATION: variant CDR sequence
US-09-440-781-26

Query Match 71.4%; Score 40; DB 4; Length 9;
Best Local Similarity 75.0%; Pred. No. 3.8e+05;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSLPMT 9
DB 2 QYSLPMT 9

RESULT 7
US-07-934-373C-18

Sequence 18, Application US/07934373C
Patent No. 5821337
GENERAL INFORMATION:
APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/934,373C
FILING DATE: 21-Aug-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA: 07/715272
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991

ATTORNEY/AGENT INFORMATION:

NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear

US-07-934-373C-18

Query Match 71.4%; Score 40; DB 2; Length 107;
Best Local Similarity 75.0%; Pred. No. 3.4;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSLPMT 9
DB 90 QYSLPMT 97

RESULT 8
US-08-437-642B-18

Sequence 18, Application US/08437642B
Patent No. 6054297
GENERAL INFORMATION:
APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/437,642B
FILING DATE: 09-May-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/934373
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA: 07/715272
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P2C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear

US-08-437-642B-18

Query Match 71.4%; Score 40; DB 3; Length 107;
Best Local Similarity 75.0%; Pred. No. 3.4;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QVSKLPMT 9
||:||||
Db 90 QVNSLPMT 97

RESULT 9
US-08-146-206C-18
; Sequence 18, Application US/08146206C
; Patent No. 6407213
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method for Making Humanized Antibodies
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPacIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/146.206C
FILING DATE: 17-No. 6407213-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-146-206C-18

Query Match 71.4%; Score 40; DB 4; Length 107;
Best Local Similarity 75.0%; Pred. No. 3.4;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QVSKLPMT 9
||:||||
Db 90 QVNSLPMT 97

RESULT 10
US-09-648-067A-14
; Sequence 14, Application US/09648067A
; Patent No. 6627196
; GENERAL INFORMATION:
; APPLICANT: Baughman, Sharon A.
; APPLICANT: Shak Steven
; TITLE OF INVENTION: Dosages for Treatment with Anti-ErbB2 Antibodies
; FILE REFERENCE: P1775R1
; CURRENT APPLICATION NUMBER: US/09/648.067A
; CURRENT FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,018

; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: US 60/213,822
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 15
; SEQ ID NO 14
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: VL consensus sequence
US-09-648-067A-14

Query Match 71.4%; Score 40; DB 4; Length 107;
Best Local Similarity 75.0%; Pred. No. 3.4;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QVSKLPMT 9
||:||||
Db 90 QVNSLPMT 97

RESULT 11
US-09-705-686-18
; Sequence 18, Application US/09705686
; Patent No. 6638055
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method for Making Humanized Antibodies
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPacIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/705.686
FILING DATE: 02-No. 6639055-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P1D3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-705-686-18

Query Match 71.4%; Score 40; DB 4; Length 107;
Best Local Similarity 75.0%; Pred. No. 3.4;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QVSKLPMT 9
||:||||
Db 90 QVNSLPMT 97

RESULT 12
US-09-705-392A-18
Sequence 18, Application US/09705392A
Patent No. 671971
GENERAL INFORMATION:
APPLICANT: Carter, Paul J.
Presta, Leonard G.
TITLE OF INVENTION: Method for Making Humanized Antibodies
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/705,392A
FILING DATE: 02-No. 671971-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P1D1 REVISED
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-705-392A-18
Query Match 71.4%; Score 40; DB 4; Length 107;
Best Local Similarity 75.0%; Pred. No. 3.4;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 2 QVSKLPWT 9
DB 90 QVNSLPWT 97
PCT-US93-07832-18
RESULT 13
Sequence 18, Application PC/TUS9307832
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07832
FILING DATE: 19930820
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/934373
FILING DATE: 21-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME:
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER: 709P2PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE:
TELEFAX: 415/952-9881
TELFX: 910/371-7168
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
PCT-US93-07832-18
Query Match 71.4%; Score 40; DB 5; Length 107;
Best Local Similarity 75.0%; Pred. No. 3.4;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 2 QVSKLPWT 9
DB 90 QVNSLPWT 97
RESULT 14
US-08-974-899-3
Sequence 3, Application US/08974899
Patent No. 6037454
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,899
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/031971
FILING DATE: 11/27/96
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1014R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994

TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-974-899-3

Query Match 71.4%; Score 40; DB 3; Length 108;
Best Local Similarity 75.0%; Pred. No. 3.4;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSLPWT 9
||:||||
DB 90 QYNSLPWT 97

RESULT 15
US-09-065-059-3
; Sequence 3, Application US/09065059
; Patent No. 6068841
; GENERAL INFORMATION:

APPLICANT: SEINO, Ken-ichiro
APPLICANT: KAYAGAKI, No. 6068841uhiko
APPLICANT: YAGITA, Hideo
APPLICANT: OKUMURA, Ko
APPLICANT: NAKATA, Motomi
TITLE OF INVENTION: THERAPEUTIC AGENT FOR HEPATITIS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDermott, Will & Emery
STREET: 99 Canal Center Plaza
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
ZIP: 22314

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/065,059
FILING DATE:

CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Bucca Ph.D., Daniel
REGISTRATION NUMBER: P-42,368
REFERENCE/DOCKET NUMBER: 50356-151
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-518-5100
TELEFAX: 703-684-1124
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-065-059-3

Query Match 71.4%; Score 40; DB 3; Length 108;
Best Local Similarity 75.0%; Pred. No. 3.4;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSLPWT 9
||:||||
DB 90 QYNSLPWT 97

RESULT 16
US-09-795-798-3
; Sequence 3, Application US/09795798

Patent No. 6703018
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; Jardiou, Paula M.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Minipain (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/795,798
FILING DATE: 28-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/974,899
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1014R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-795-798-3
SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Query Match 71.4%; Score 40; DB 4; Length 108;
Best Local Similarity 75.0%; Pred. No. 3.4;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSLPWT 9
||:||||
DB 90 QYNSLPWT 97

RESULT 17
US-08-560-558E-31
; Sequence 31, Application US/08560558E
; Patent No. 5891996
; GENERAL INFORMATION:

APPLICANT:
TITLE OF INVENTION: Humanized and chimeric monoclonal
antibodies that recognize epidermal growth factor receptor
TITLE OF INVENTION: EGF-R; diagnostic and therapeutic use.
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Allen C. Turner, TRASK, BRITT & ROSSA
STREET: P.O. Box 2250
CITY: Salt Lake City
STATE: Utah
COUNTRY: United States of America
ZIP: 84110

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: WINDOWS95
SOFTWARE: Wordperfect 5.1/5.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/560,558E

FILING DATE: No. 5891996ember 17, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Turner, Allen C.
REGISTRATION NUMBER: 33,041
REFERENCE/DOCKET NUMBER: 2720US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (801) 532-1922
TELEFAX: (801) 531-9168
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
US-08-560-558B-31

Query Match 69.6%; Score 39; DB 2; Length 9;
Best Local Similarity 75.0%; Pred. No. 3.8e+05;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSLPMT 9
DB 2 QYSHVPM 9

RESULT 18
US-09-217-268B-31
Sequence 31, Application US/09217268B
Patent No. 6506883
GENERAL INFORMATION:
APPLICANT: Mateo de Acosta del Rio, Christina M
APPLICANT: Rodriguez, Rolando P
APPLICANT: Frias, Ernesto M
TITLE OF INVENTION: Humanized and Chimeric Monoclonal Antibodies That Recognize Epide
TITLE OF INVENTION: Growth Factor Receptor (EGF-R); Diagnostic and Therapeutic Use
FILE REFERENCE: 2720.1US
CURRENT APPLICATION NUMBER: US/09/217,268B
CURRENT FILING DATE: 1998-12-21
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn version 3.1
SEQ ID NO 31
LENGTH: 9
TYPE: PRT
ORGANISM: Murine
FEATURE:
NAME/KEY: MISC FEATRE
OTHER INFORMATION: CDR of murine R3 antibody
US-09-217-268B-31

Query Match 69.6%; Score 39; DB 4; Length 9;
Best Local Similarity 75.0%; Pred. No. 3.8e+05;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSLPMT 9
DB 2 QYSHVPM 9

RESULT 19
US-09-440-781-25
Sequence 25, Application US/09440781
Patent No. 6632926
GENERAL INFORMATION:
APPLICANT: Yvonne Man-yea Chen et al.
TITLE OF INVENTION: ANTIBODY VARIANTS
FILE REFERENCE: P1469R1
CURRENT APPLICATION NUMBER: US/09/440,781
CURRENT FILING DATE: 1999-11-16
NUMBER OF SEQ ID NOS: 99
SEQ ID NO 25
LENGTH: 9

TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
NAME/KEY: artificial
LOCATION: 1-9
OTHER INFORMATION: variant CDR sequence
US-09-440-781-25

Query Match 69.6%; Score 39; DB 4; Length 9;
Best Local Similarity 75.0%; Pred. No. 3.8e+05;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSLPMT 9
DB 2 QYSHVPM 9

RESULT 20
US-09-440-781-94
Sequence 94, Application US/09440781
Patent No. 6632926
GENERAL INFORMATION:
APPLICANT: Yvonne Man-yea Chen et al.
TITLE OF INVENTION: ANTIBODY VARIANTS
FILE REFERENCE: P1469R1
CURRENT APPLICATION NUMBER: US/09/440,781
CURRENT FILING DATE: 1999-11-16
NUMBER OF SEQ ID NOS: 99
SEQ ID NO 94
LENGTH: 110
TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
NAME/KEY: artificial
LOCATION: 1-110
OTHER INFORMATION: humanized antibody light chain variable domain
US-09-440-781-94

Query Match 69.6%; Score 39; DB 4; Length 110;
Best Local Similarity 75.0%; Pred. No. 5.4;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSLPMT 9
DB 90 QYSTVPM 97

RESULT 21
US-09-440-781-95
Sequence 95, Application US/09440781
Patent No. 6632926
GENERAL INFORMATION:
APPLICANT: Yvonne Man-yea Chen et al.
TITLE OF INVENTION: ANTIBODY VARIANTS
FILE REFERENCE: P1469R1
CURRENT APPLICATION NUMBER: US/09/440,781
CURRENT FILING DATE: 1999-11-16
NUMBER OF SEQ ID NOS: 99
SEQ ID NO 95
LENGTH: 110
TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
NAME/KEY: artificial
LOCATION: 1-110
OTHER INFORMATION: humanized antibody light chain variable domain
US-09-440-781-95

Query Match 69.6%; Score 39; DB 4; Length 110;
Best Local Similarity 75.0%; Pred. No. 5.4;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSLPMT 9

Db 90 QYSHVPT 97

RESULT 22

US-08-497-312-18
; Sequence 18, Application US/08497312
; Patent No. 5712120
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Method for obtaining modified
; TITLE OF INVENTION: immunoglobulins with reduced immunogenicity of murine
; TITLE OF INVENTION: antibody variable domains, compositions containing them.
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: CENTRO DE INMUNOLOGIA MOLECULAR
; STREET: 215 Y 15, ATABEY PLAYA
; CITY: HAVANA
; STATE:
; COUNTRY: CUBA
; ZIP: 11600
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EBO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/497,312
; FILING DATE: 30-JUN-1995
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: CU 80/94
; FILING DATE: 30-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BOND, LAURENCE B.
; REGISTRATION NUMBER: 30,549
; REFERENCE/DOCKET NUMBER: 2629US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 801/531-1922
; TELEFAX: 801/531-9168
; TELEX: 388961 1PMO4UT
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
US-08-497-312-18

Query Match 69.6%; Score 39; DB 1; Length 113;
Best Local Similarity 75.0%; Pred. No. 5.6;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSHVPT 9
Db 95 QYSHVPT 102

RESULT 23

US-08-560-558E-27
; Sequence 27, Application US/08560558E
; Patent No. 5891996
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Humanized and chimeric monoclonal
; TITLE OF INVENTION: antibodies that recognize epidermal growth factor receptor
; TITLE OF INVENTION: EGF-R; diagnostic and therapeutic use.
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Allen C. Turner, TRASK, BRITT & ROSSA
; STREET: P.O. Box 2250
; CITY: Salt Lake City

STATE: Utah
COUNTRY: United States of America
ZIP: 84110

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Wordperfect 5.1/5.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/560,558E
FILING DATE: No. 5891996ember 17, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Turner, Allen C.
REGISTRATION NUMBER: 33,041
REFERENCE/DOCKET NUMBER: 2720US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (801) 532-1922
TELEFAX: (801) 531-9168
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHEICAL: NO
US-08-560-558E-27

Query Match 69.6%; Score 39; DB 2; Length 114;
Best Local Similarity 75.0%; Pred. No. 5.6;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSHVPT 9
Db 95 QYSHVPT 102

RESULT 24
US-09-217-268B-27
; Sequence 27, Application US/09217268B
; Patent No. 6506883
; GENERAL INFORMATION:
; APPLICANT: Mateo de Acosta del Rio, Christina M
; APPLICANT: Rodriguez, Rolando P
; APPLICANT: Frias, Ernesto M
; TITLE OF INVENTION: Humanized and Chimeric Monoclonal Antibodies That Recognize Epider
; TITLE OF INVENTION: Growth Factor Receptor (EGF-R); Diagnostic and Therapeutic Use
; FILE REFERENCE: 2720.1US
; CURRENT APPLICATION NUMBER: US/09/217,268B
; CURRENT FILING DATE: 1998-12-21
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 27
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Murine R3 antibody
; FEATURE:
; NAME/KEY: MISC FEATURE
; OTHER INFORMATION: Deduced amino acid sequence of VK of murine R3 antibody
US-09-217-268B-27

Query Match 69.6%; Score 39; DB 4; Length 114;
Best Local Similarity 75.0%; Pred. No. 5.6;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSHVPT 9
Db 95 QYSHVPT 102

RESULT 25
US-09-217-268B-35
; Sequence 35, Application US/09217268B

Patent No. 6506883
GENERAL INFORMATION:
APPLICANT: Mateo de Acosta del Rio, Christina M
APPLICANT: Rodriguez, Rolando P
TITLE OF INVENTION: Humanized and Chimeric Monoclonal Antibodies That Recognize Epide
FILE REFERENCE: 2720.1US
CURRENT APPLICATION NUMBER: US/09/217,268B
CURRENT FILING DATE: 1998-12-21
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Patentin version 3.1
SEQ ID NO 35
LENGTH: 114
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Amino acid sequence of humanized VK of murine R3 antibody contain
US-09-217-268B-35

Query Match
Best Local Similarity 69.6%; Score 39; DB 4; Length 114;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QXSKLPMT 9
Db 95 QYSHVPM 102

RESULT 26
US-08-497-312-14
Sequence 14, Application US/08497312
Patent No. 5712120
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Method for obtaining modified
TITLE OF INVENTION: Immunoglobulins with reduced immunogenicity of murine
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: CENTRO DE INMUNOLOGIA MOLECULAR
STREET: 215 Y 15, ATABEY PLAYA
CITY: HAVANA
STATE:
COUNTRY: CUBA
ZIP: 11600
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Releasee #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/497,312
FILING DATE: 30-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CU 80/94
FILING DATE: 30-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: BOND, LAURENCE B.
REGISTRATION NUMBER: 30,549
REFERENCE/DOCKET NUMBER: 2629US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 801/532-1922
TELEFAX: 801/531-9168
TELEX: 388961 1PM04UT
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein

HYPOTHETICAL: NO
US-08-497-312-14

Query Match
Best Local Similarity 69.6%; Score 39; DB 1; Length 116;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QXSKLPMT 9
Db 97 QYSHVPM 104

RESULT 27
US-09-270-767-37260
Sequence 37260, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 37260
LENGTH: 191
TYPE: PRT
ORGANISM: Drosophila melanogaster
FEATURE:
OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-37260

Query Match
Best Local Similarity 67.9%; Score 38; DB 4; Length 191;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HOYSKLPMT 9
Db 147 HRYSGRPM 155

RESULT 28
US-09-270-767-52477
Sequence 52477, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 52477
LENGTH: 191
TYPE: PRT
ORGANISM: Drosophila melanogaster
FEATURE:
OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-52477

Query Match
Best Local Similarity 67.9%; Score 38; DB 4; Length 191;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HOYSKLPMT 9
Db 147 HRYSGRPM 155

RESULT 29
US-08-797-689-18
Sequence 18, Application US/08797689

Patent No. 5876969
GENERAL INFORMATION:
APPLICANT: Fleer, Reinhard
APPLICANT: Fournier, Alain
APPLICANT: Guitton, Jean-Dominique
APPLICANT: Jung, Gerard
TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
TITLE OF INVENTION: CONTAINING SAID POLYPEPTIDES
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43
CITY: Collegeville
STATE: PA
COUNTRY: USA
ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: Word 5.1 (PatentIn)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/797,689
FILING DATE: 31-JAN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/256,927
FILING DATE: 28-JUL-1994
APPLICATION NUMBER: FR 92/01064
FILING DATE: 31-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR93/00085
FILING DATE: 28-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith Ph.D., Julie K.
REGISTRATION NUMBER: P-38,619
REFERENCE/DOCKET NUMBER: ST92006-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 454-3839
TELEFAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 249 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-797-689-18

Query Match 67.9%; Score 38; DB 2; Length 249;
Best Local Similarity 75.0%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QYSKLPWT 9
DB 232 QYSSYPWT 239

RESULT 30
US-09-984-186-18
Sequence 18, Application US/09984186
Patent No. 6686179
GENERAL INFORMATION:
APPLICANT: Fleer, Reinhard
APPLICANT: Fournier, Alain
APPLICANT: Guitton, Jean-Dominique
APPLICANT: Jung, Gerard
TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
CONTAINING SAID POLYPEPTIDES
NUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43
CITY: Collegeville
STATE: PA
COUNTRY: USA
ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: Word 5.1 (PatentIn)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/984,186
FILING DATE: 29-Oct-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/797,689
FILING DATE: 31-JAN-1997
APPLICATION NUMBER: US 08/256,927
FILING DATE: 28-JUL-1994
APPLICATION NUMBER: FR 92/01064
FILING DATE: 31-JAN-1992
APPLICATION NUMBER: PCT/FR93/00085
FILING DATE: 28-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith Ph.D., Julie K.
REGISTRATION NUMBER: P-38,619
REFERENCE/DOCKET NUMBER: ST92006-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 454-3808
TELEFAX: (610) 454-3839
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 249 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-984-186-18

Query Match 67.9%; Score 38; DB 4; Length 249;
Best Local Similarity 75.0%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QYSKLPWT 9
DB 232 QYSSYPWT 239

RESULT 31
5200183-5
Patent No. 5200183
APPLICANT: TANG, JORDAN J N; WANG, CHI-SUN
TITLE OF INVENTION: RECOMBINANT BLUE SALT ACTIVATED LIPASES
NUMBER OF SEQUENCES: 22
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/537,426
FILING DATE: 12-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 504,635
FILING DATE: 04-APR-1990
APPLICATION NUMBER: 122,410
FILING DATE: 19-NOV-1987
SEQ ID NO: 5;
LENGTH: 572
5200183-5

Query Match 67.9%; Score 38; DB 6; Length 572;
Best Local Similarity 75.0%; Pred. No. 47;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYSKLFW 8

Db 421 HRSSKLPW 428

RESULT 32
5215909-12
; Patent No. 5215909
; APPLICANT: SOREQ, HERMONA
; TITLE OF INVENTION: HUMAN CHOLINESTERASE GENES
; NUMBER OF SEQUENCES: 13
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/572,911
; FILING DATE: 15-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 87,724
; FILING DATE: 21-AUG-1987
; APPLICATION NUMBER: 875,737
; FILING DATE: 18-JUN-1986
; SEQ ID NO:12
; LENGTH: 573
5215909-12

Query Match 67.9%; Score 38; DB 6; Length 573;
Best Local Similarity 75.0%; Pred. No. 47;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HOYSKLPW 8
|: |||||
Db 424 HRSSKLPW 431

RESULT 33
US-08-446-100-1
; Sequence 1, Application US/08446100
; Patent No. 6001625
; GENERAL INFORMATION:
; APPLICANT: Broomfield, Clarence A
; APPLICANT: Millard, Charles B
; APPLICANT: Lockridge, Oksana
; TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hendricks and Assoc.
; STREET: 9669 A Main Street, P.O. Box 2509
; CITY: Fairfax
; STATE: VA
; COUNTRY: US
; ZIP: 22031
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,100
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hendricks, Glenna
; REGISTRATION NUMBER: 32,535
; REFERENCE/DOCKET NUMBER: Broomfield
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 425-4250
; TELEFAX: (703) 425-2767
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 602 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE: human esterases
; ORGANISM: human esterases
US-08-446-100-2

; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: human esterases
US-08-446-100-1

Query Match 67.9%; Score 38; DB 3; Length 602;
Best Local Similarity 75.0%; Pred. No. 50;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HOYSKLPW 8
|: |||||
Db 451 HRSSKLPW 458

RESULT 34
US-08-446-100-2
; Sequence 2, Application US/08446100
; Patent No. 6001625
; GENERAL INFORMATION:
; APPLICANT: Broomfield, Clarence A
; APPLICANT: Millard, Charles B
; APPLICANT: Lockridge, Oksana
; TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hendricks and Assoc.
; STREET: 9669 A Main Street, P.O. Box 2509
; CITY: Fairfax
; STATE: VA
; COUNTRY: US
; ZIP: 22031
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,100
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hendricks, Glenna
; REGISTRATION NUMBER: 32,535
; REFERENCE/DOCKET NUMBER: Broomfield
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 425-4250
; TELEFAX: (703) 425-2767
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 602 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE: human esterases
; ORGANISM: human esterases
US-08-446-100-2

Query Match 67.9%; Score 38; DB 3; Length 602;
Best Local Similarity 75.0%; Pred. No. 50;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HOYSKLPW 8
|: |||||
Db 451 HRSSKLPW 458

RESULT 35
US-08-446-100-3
; Sequence 3, Application US/08446100

```

; Patent No. 6001625
; GENERAL INFORMATION:
; APPLICANT: Broomfield, Clarence A
; APPLICANT: Millard, Charles B
; APPLICANT: Lockridge, Oksana
; TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESS: Hendricks and Assoc.
; STREET: 9669 A Main Street, P.O. Box 2509
; CITY: Fairfax
; STATE: VA
; COUNTRY: US
; ZIP: 22031
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,100
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hendricks, Glenna
; REGISTRATION NUMBER: 32,535
; REFERENCE/DOCKET NUMBER: broomfield
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 425-4250
; TELEFAX: (703) 425-2767
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 602 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: human esterases
;
US-08-446-100-3
;
Query Match 67.9%; Score 38; DB 3; Length 602;
Best Local Similarity 75.0%; Pred. No. 50;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HQYSKLPW 8
Db 451 HRSSKLPW 458

RESULT 36
US-08-446-100-4
; Sequence 4, Application US/08446100
; Patent No. 6001625
; GENERAL INFORMATION:
; APPLICANT: Broomfield, Clarence A
; APPLICANT: Millard, Charles B
; APPLICANT: Lockridge, Oksana
; TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESS: Hendricks and Assoc.
; STREET: 9669 A Main Street, P.O. Box 2509
; CITY: Fairfax
; STATE: VA
; COUNTRY: US
; ZIP: 22031
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,100
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hendricks, Glenna
; REGISTRATION NUMBER: 32,535
; REFERENCE/DOCKET NUMBER: broomfield
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 425-4250
; TELEFAX: (703) 425-2767
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 602 amino acids
; TYPE: amino acid
```

```

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,100
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hendricks, Glenna
; REGISTRATION NUMBER: 32,535
; REFERENCE/DOCKET NUMBER: broomfield
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 425-4250
; TELEFAX: (703) 425-2767
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 602 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: human esterases
;
US-08-446-100-4
;
Query Match 67.9%; Score 38; DB 3; Length 602;
Best Local Similarity 75.0%; Pred. No. 50;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HQYSKLPW 8
Db 451 HRSSKLPW 458

RESULT 37
US-08-446-100-5
; Sequence 5, Application US/08446100
; Patent No. 6001625
; GENERAL INFORMATION:
; APPLICANT: Broomfield, Clarence A
; APPLICANT: Millard, Charles B
; APPLICANT: Lockridge, Oksana
; TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESS: Hendricks and Assoc.
; STREET: 9669 A Main Street, P.O. Box 2509
; CITY: Fairfax
; STATE: VA
; COUNTRY: US
; ZIP: 22031
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,100
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hendricks, Glenna
; REGISTRATION NUMBER: 32,535
; REFERENCE/DOCKET NUMBER: broomfield
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 425-4250
; TELEFAX: (703) 425-2767
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 602 amino acids
; TYPE: amino acid
```

STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ANTI-SENSE: YES
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: human esterases
US-08-446-100-5

Query Match 67.9%; Score 38; DB 3; Length 602;
Best Local Similarity 75.0%; Pred. No. 50;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYSKLPW 8
|:|||||
DB 451 HRSSKLPW 458

RESULT 38
US-08-446-100-6
Sequence 6, Application US/08446100
Patent No. 6001625
GENERAL INFORMATION:
APPLICANT: Broomfield, Clarence A
APPLICANT: Millard, Charles B
APPLICANT: Lockridge, Oksana
TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hendricks and Assoc.
STREET: 9669 A Main Street, P.O. Box 2509
CITY: Fairfax
STATE: VA
COUNTRY: US
ZIP: 22031
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,100
FILING DATE: 19-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Hendricks, Glenna
REGISTRATION NUMBER: 32,535
REFERENCE/DOCKET NUMBER: Broomfield
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 425-4250
TELEFAX: (703) 425-2767
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 602 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ANTI-SENSE: YES
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: human esterases
US-08-446-100-6

Query Match 67.9%; Score 38; DB 3; Length 602;
Best Local Similarity 75.0%; Pred. No. 50;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYSKLPW 8
|:|||||
DB 451 HRSSKLPW 458

RESULT 39
US-08-446-100-7
Sequence 7, Application US/08446100
Patent No. 6001625
GENERAL INFORMATION:
APPLICANT: Broomfield, Clarence A
APPLICANT: Millard, Charles B
APPLICANT: Lockridge, Oksana
TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hendricks and Assoc.
STREET: 9669 A Main Street, P.O. Box 2509
CITY: Fairfax
STATE: VA
COUNTRY: US
ZIP: 22031
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,100
FILING DATE: 19-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Hendricks, Glenna
REGISTRATION NUMBER: 32,535
REFERENCE/DOCKET NUMBER: Broomfield
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 425-4250
TELEFAX: (703) 425-2767
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 602 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ANTI-SENSE: YES
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: human esterases
US-08-446-100-7

Query Match 67.9%; Score 38; DB 3; Length 602;
Best Local Similarity 75.0%; Pred. No. 50;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYSKLPW 8
|:|||||
DB 451 HRSSKLPW 458

RESULT 40
US-08-446-100-8
Sequence 8, Application US/08446100
Patent No. 6001625
GENERAL INFORMATION:
APPLICANT: Broomfield, Clarence A
APPLICANT: Millard, Charles B
APPLICANT: Lockridge, Oksana
TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hendricks and Assoc.
STREET: 9669 A Main Street, P.O. Box 2509
CITY: Fairfax
STATE: VA

```

; COUNTRY: US
; ZIP: 22031
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,100
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hendricks, Glenna
; REGISTRATION NUMBER: 32,535
; REFERENCE/DOCKET NUMBER: broomfield
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 425-4250
; TELEFAX: (703) 425-2767
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 602 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHEetical: YES
; ANTI-SENSE: YES
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: human esterases
;
US-08-446-100-8

```

```

Query Match 67.9%; Score 38; DB 3; Length 602;
Best Local Similarity 75.0%; Pred. No. 50;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 HQYSKLPW 8
   | : |||||
Db 451 HRSSKLPW 458

```

Search completed: December 17, 2004, 18:32:10
 Job time : 6.46067 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using SW model

Run on: December 17, 2004, 18:20:33 ; Search time 17.3933 seconds
(without alignments)
185.159 Million cell updates/sec

Title: US-10-089-500-8

Perfect score: 56

Sequence: 1 HQYSLRPMPT 9

Scoring table: BLOSUM62

Searched: 1589859 seqs, 357834939 residues

Total number of hits satisfying chosen parameters: 1589859

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA:
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	56	100.0	128 9 US-09-764-304-10	Sequence 10, Appl
2	56	100.0	128 9 US-09-764-304-19	Sequence 19, Appl
3	56	100.0	128 14 US-10-265-713-10	Sequence 10, Appl
4	56	100.0	128 14 US-10-265-713-19	Sequence 19, Appl
5	56	100.0	128 14 US-10-166-626-10	Sequence 10, Appl
6	56	100.0	128 14 US-10-166-626-19	Sequence 19, Appl
7	44	78.6	99 16 US-10-697-399-6	Sequence 6, Appl
8	44	78.6	109 14 US-10-371-942-32	Sequence 32, Appl
9	43	76.8	215 15 US-10-264-049-4290	Sequence 4290, Ap
10	40	71.4	9 15 US-10-624-153-24	Sequence 24, Appl
11	40	71.4	9 15 US-10-624-153-26	Sequence 26, Appl
12	40	71.4	93 15 US-10-424-599-159861	Sequence 159861,
13	40	71.4	107 14 US-10-268-501-5	Sequence 5, Appl

ALIGNMENTS

14	40	71.4	107 15 US-10-608-626-5	Sequence 5, Appl
15	40	71.4	107 15 US-10-600-152-14	Sequence 14, Appl
16	40	71.4	107 16 US-10-619-754-5	Sequence 5, Appl
17	40	71.4	107 17 US-10-835-641-18	Sequence 18, Appl
18	40	71.4	108 9 US-09-056-1608-12	Sequence 12, Appl
19	40	71.4	108 10 US-09-795-798-3	Sequence 3, Appl
20	40	71.4	108 14 US-10-234-671-12	Sequence 12, Appl
21	40	71.4	109 9 US-09-811-123-6	Sequence 6, Appl
22	40	71.4	110 14 US-10-044-896-4	Sequence 4, Appl
23	40	71.4	126 16 US-10-469-125-8	Sequence 8, Appl
24	40	71.4	153 9 US-09-187-693-62	Sequence 62, Appl
25	40	71.4	159 9 US-09-187-693-66	Sequence 66, Appl
26	39	69.6	9 9 US-09-056-1608-6	Sequence 6, Appl
27	39	69.6	9 9 US-09-217-2688-31	Sequence 31, Appl
28	39	69.6	9 9 US-10-234-671-6	Sequence 6, Appl
29	39	69.6	9 15 US-10-624-153-25	Sequence 25, Appl
30	39	69.6	64 17 US-10-425-115-293070	Sequence 293070,
31	39	69.6	103 16 US-10-379-392-100	Sequence 100, App
32	39	69.6	103 16 US-10-379-392-121	Sequence 121, App
33	39	69.6	103 16 US-10-379-392-123	Sequence 123, App
34	39	69.6	103 16 US-10-379-392-129	Sequence 129, App
35	39	69.6	103 16 US-10-379-392-131	Sequence 131, App
36	39	69.6	107 9 US-09-056-1608-13	Sequence 13, Appl
37	39	69.6	107 9 US-09-056-1608-15	Sequence 15, Appl
38	39	69.6	107 14 US-10-234-671-13	Sequence 13, Appl
39	39	69.6	107 14 US-10-234-671-15	Sequence 14, Appl
40	39	69.6	107 14 US-10-251-215-49	Sequence 49, Appl
41	39	69.6	107 16 US-10-723-434-1	Sequence 1, Appl
42	39	69.6	107 16 US-10-723-434-2	Sequence 2, Appl
43	39	69.6	107 16 US-10-723-434-3	Sequence 3, Appl
44	39	69.6	107 16 US-10-723-434-4	Sequence 4, Appl
45	39	69.6	107 16 US-10-723-434-5	Sequence 5, Appl

RESULT 1
US-09-764-304-10
; Sequence 10, Application US/09764304
; Patent No. US2002026036A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUMANA, YOSHIOHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/09/764,304
; EARLIER FILING DATE: 2001-01-19
; EARLIER APPLICATION NUMBER: 09/225,322
; EARLIER FILING DATE: 1999-01-05
; EARLIER APPLICATION NUMBER: US 08/454,680
; EARLIER FILING DATE: 1995-05-31
; EARLIER APPLICATION NUMBER: US 08/408,133
; EARLIER FILING DATE: 1995-03-21
; EARLIER APPLICATION NUMBER: US 08/292,178
; EARLIER FILING DATE: 1994-08-17
; EARLIER APPLICATION NUMBER: US07/947,674
; EARLIER FILING DATE: 1992-09-17
; EARLIER APPLICATION NUMBER: JP 3-238375
; EARLIER FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: CDNA KM-641
; US-09-764-304-10

Query Match 100.0%; Score 56; DB 9; Length 128;
Best Local Similarity 100.0%; Pred. No. 0.071;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HOYSKLPWT 9
Db 109 HOYSKLPWT 117

RESULT 2

US-09-764-304-19
; Sequence 19, Application US/09764304
; Patent No. US2002026036A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUMANA, YOSHITISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/09/764,304
; EARLIER FILING DATE: 2001-01-19
; EARLIER APPLICATION NUMBER: 09/225,322
; EARLIER FILING DATE: 1999-01-05
; EARLIER APPLICATION NUMBER: US 08/454,680
; EARLIER FILING DATE: 1995-05-31
; EARLIER APPLICATION NUMBER: US 08/408,133
; EARLIER FILING DATE: 1995-03-21
; EARLIER APPLICATION NUMBER: US 08/292,178
; EARLIER FILING DATE: 1994-08-17
; EARLIER APPLICATION NUMBER: US07/947,674
; EARLIER FILING DATE: 1992-09-17
; EARLIER APPLICATION NUMBER: JP 3-238375
; EARLIER FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: light chain
; OTHER INFORMATION: variable region
US-09-764-304-19

Query Match 100.0%; Score 56; DB 9; Length 128;
Best Local Similarity 100.0%; Pred. No. 0.071;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HOYSKLPWT 9
Db 109 HOYSKLPWT 117

RESULT 3

US-10-265-713-10
; Sequence 10, Application US/10265713
; Publication No. US20030095964A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUMANA, YOSHITISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/10/265,713
; CURRENT FILING DATE: 2002-10-08
; PRIOR APPLICATION NUMBER: US/09/225,322
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31

; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cDNA KM-641
US-10-265-713-10

QY 1 HOYSKLPWT 9
Db 109 HOYSKLPWT 117

RESULT 4

US-10-265-713-19
; Sequence 19, Application US/10265713
; Publication No. US20030095964A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUMANA, YOSHITISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/10/265,713
; CURRENT FILING DATE: 2002-10-08
; PRIOR APPLICATION NUMBER: US/09/225,322
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: light chain
US-10-265-713-19

Query Match 100.0%; Score 56; DB 14; Length 128;
Best Local Similarity 100.0%; Pred. No. 0.071;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HOYSKLPWT 9
Db 109 HOYSKLPWT 117

RESULT 5
US-10-166-626-10
; Sequence 10, Application US/10166626
; Publication No. US2003016876A1
; GENERAL INFORMATION:
; APPLICANT: SHITTARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUMANA, YOSHIOHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/10/166,626
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US/09/225,322B
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CDNA KM-641
US-10-166-626-10
Query Match 100.0%; Score 56; DB 14; Length 128;
Best Local Similarity 100.0%; Pred. No. 0.071;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HOYSKLPMT 9
Db 109 HOYSKLPMT 117

RESULT 6
US-10-166-626-19
; Sequence 19, Application US/10166626
; Publication No. US2003016876A1
; GENERAL INFORMATION:
; APPLICANT: SHITTARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUMANA, YOSHIOHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/10/166,626
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US/09/225,322B
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 19
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: light chain
US-10-166-626-19
Query Match 100.0%; Score 56; DB 14; Length 128;
Best Local Similarity 100.0%; Pred. No. 0.071;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HOYSKLPMT 9
Db 109 HOYSKLPMT 117

RESULT 7
US-10-697-399-6
; Sequence 6, Application US/10697399
; Publication No. US20040162413A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Huse, William D.
; APPLICANT: Vasselet, Alain P.
; APPLICANT: Marguis, David P.
; APPLICANT: Smith, Eric P.
; TITLE OF INVENTION: Methods of Optimizing Antibody Variable Region Binding Affinity
; FILE REFERENCE: AME-08122
; CURRENT APPLICATION NUMBER: US/10/697,399
; CURRENT FILING DATE: 2003-10-30
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-697-399-6
Query Match 78.6%; Score 44; DB 16; Length 99;
Best Local Similarity 87.5%; Pred. No. 6.4;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QVSKLPMT 9
Db 82 QVSKLPMT 89

RESULT 8
US-10-371-942-32
; Sequence 32, Application US/10371942
; Publication No. US20030223994A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Henricus Renertus Jacobus Mattheus
; APPLICANT: Reiter, Yoram
; TITLE OF INVENTION: MHC-PEPTIDE COMPLEX BINDING LIGANDS
; FILE REFERENCE: 10280-034001
; CURRENT APPLICATION NUMBER: US/10/371,942
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,994
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PasteSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-371-942-32
Query Match 78.6%; Score 44; DB 14; Length 109;
Best Local Similarity 77.8%; Pred. No. 7;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 HQYSKLPWT 9
|||:||||
Db 90 HQYGFLLPWT 98

RESULT 9
US-10-264-049-4290
; Sequence 4290, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA133P1
; CURRENT APPLICATION NUMBER: US/10/264,049
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 4290
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (168)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-10-264-049-4290

Query Match 76.8%; Score 43; DB 15; Length 215;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YSKLPWT 9
|||||:
Db 196 YSKLPWT 202

RESULT 10
US-10-624-153-24
; Sequence 24, Application US/10624153
; Publication No. US20040086502A1
; GENERAL INFORMATION:
; APPLICANT: CHEN, YVONNE M.
; APPLICANT: LOWMAN, HENRY B.
; APPLICANT: MULLER, YVES
; TITLE OF INVENTION: ANTIBODY VARIANTS
; FILE REFERENCE: P1469R1C1
; CURRENT APPLICATION NUMBER: US/10/624,153
; CURRENT FILING DATE: 2003-07-21
; PRIOR APPLICATION NUMBER: US 09/440,781
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: US 60/108,945
; PRIOR FILING DATE: 1998-11-18
; NUMBER OF SEQ ID NOS: 99
; SEQ ID NO 24
; LENGTH: 9
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
; FEATURE:
; NAME/KEY: artificial
; LOCATION: 1-9
; OTHER INFORMATION: variant CDR sequence
US-10-624-153-24

Query Match 71.4%; Score 40; DB 15; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.4e+06;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSKLPWT 9
|||:||||
Db 2 QYSNVPWT 9

RESULT 11
US-10-624-153-26
; Sequence 26, Application US/10624153
; Publication No. US20040086502A1
; GENERAL INFORMATION:
; APPLICANT: CHEN, YVONNE M.
; APPLICANT: LOWMAN, HENRY B.
; APPLICANT: MULLER, YVES
; TITLE OF INVENTION: ANTIBODY VARIANTS
; FILE REFERENCE: P1469R1C1
; CURRENT APPLICATION NUMBER: US/10/624,153
; CURRENT FILING DATE: 2003-07-21
; PRIOR APPLICATION NUMBER: US 09/440,781
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: US 60/108,945
; PRIOR FILING DATE: 1998-11-18
; NUMBER OF SEQ ID NOS: 99
; SEQ ID NO 26
; LENGTH: 9
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
; NAME/KEY: artificial
; LOCATION: 1-9
; OTHER INFORMATION: variant CDR sequence
US-10-624-153-26

Query Match 71.4%; Score 40; DB 15; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.4e+06;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSKLPWT 9
|||:||||
Db 2 QYSSVPWT 9

RESULT 12
US-10-424-599-159861
; Sequence 159861, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 159861
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MR3847_115373C.1.pap
US-10-424-599-159861

Query Match 71.4%; Score 40; DB 15; Length 93;
Best Local Similarity 66.7%; Pred. No. 29;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 56 HRLQKLPWT 64

RESULT 13

US-10-268-501-5

Sequence 5, Application US/10268501

Publication No. US20030086924A1

GENERAL INFORMATION:

APPLICANT: Sliwkowski, Mark X.

TITLE OF INVENTION: Treatment with Anti-ErbB2 Antibodies

FILE REFERENCE: P1467R2P1

CURRENT APPLICATION NUMBER: US/10/268,501

PRIOR FILING DATE: 2002-10-10

PRIOR APPLICATION NUMBER: US 09/602,812

PRIOR FILING DATE: 2000-06-23

PRIOR APPLICATION NUMBER: US 60/141,316

PRIOR FILING DATE: 1999-06-25

NUMBER OF SEQ ID NOS: 13

SEQ ID NO 5

LENGTH: 107

TYPE: PRT

ORGANISM: Artificial sequence

FEATURE:

OTHER INFORMATION: light chain consensus sequence

US-10-268-501-5

Query Match

Best Local Similarity 71.4%; Score 40; DB 14; Length 107;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSLPWT 9

Db 90 QYNSLPWT 97

RESULT 14

US-10-608-626-5

Sequence 5, Application US/10608626

Publication No. US20040013667A1

GENERAL INFORMATION:

APPLICANT: Kelsey, Stephen M.

APPLICANT: Sliwkowski, Mark X.

TITLE OF INVENTION: Treatment with Anti-ErbB2 Antibodies

FILE REFERENCE: P1467R2P2

CURRENT APPLICATION NUMBER: US/10/608,626

PRIOR FILING DATE: 2003-06-27

PRIOR APPLICATION NUMBER: US 10/268,501

PRIOR FILING DATE: 2002-10-10

PRIOR APPLICATION NUMBER: US 09/602,812

PRIOR FILING DATE: 2000-06-23

PRIOR APPLICATION NUMBER: US 60/141,316

PRIOR FILING DATE: 1999-06-25

NUMBER OF SEQ ID NOS: 13

SEQ ID NO 5

LENGTH: 107

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: light chain consensus sequence

US-10-608-626-5

Query Match

Best Local Similarity 71.4%; Score 40; DB 15; Length 107;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSLPWT 9

Db 90 QYNSLPWT 97

RESULT 15

US-10-600-152-14

Sequence 14, Application US/10600152

Publication No. US20040037824A1

GENERAL INFORMATION:

APPLICANT: Baughman, Sharon A.

APPLICANT: Shak Steven

TITLE OF INVENTION: Dosages for Treatment with Anti-ErbB2 Antibodies

FILE REFERENCE: P1775R1

CURRENT APPLICATION NUMBER: US/10/600,152

PRIOR FILING DATE: 2003-06-20

PRIOR APPLICATION NUMBER: 09/648,067

PRIOR FILING DATE: 2000-08-25

PRIOR APPLICATION NUMBER: US 60/151,018

PRIOR FILING DATE: 1999-08-27

PRIOR APPLICATION NUMBER: US 60/213,822

PRIOR FILING DATE: 2000-06-23

NUMBER OF SEQ ID NOS: 15

SEQ ID NO 14

LENGTH: 107

TYPE: PRT

ORGANISM: Artificial sequence

FEATURE:

OTHER INFORMATION: VL consensus sequence

US-10-600-152-14

Query Match

Best Local Similarity 71.4%; Score 40; DB 15; Length 107;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSLPWT 9

Db 90 QYNSLPWT 97

RESULT 16

US-10-619-754-5

Sequence 5, Application US/10619754

Publication No. US20040106161A1

GENERAL INFORMATION:

APPLICANT: Genentech, Inc.

APPLICANT: Koll, Hans

APPLICANT: Bosenmaier, Birgit

APPLICANT: Muller, Hans-Joachim

APPLICANT: Sliwkowski, Mark

APPLICANT: Kelsey, Stephen

TITLE OF INVENTION: Methods For Identifying Tumors That Are Responsive To Treatment With Anti-ErbB2 Antibodies

FILE REFERENCE: 39766-0114A

CURRENT APPLICATION NUMBER: US/10/619,754

PRIOR FILING DATE: 2003-07-14

PRIOR APPLICATION NUMBER: US 60/396,290

PRIOR FILING DATE: 2002-07-15

PRIOR APPLICATION NUMBER: US 60/480,043

PRIOR FILING DATE: 2003-06-20

NUMBER OF SEQ ID NOS: 6

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 5

LENGTH: 107

TYPE: PRT

ORGANISM: Homosapiens

US-10-619-754-5

Query Match

Best Local Similarity 71.4%; Score 40; DB 16; Length 107;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSLPWT 9

Db 90 QYNSLPWT 97

RESULT 17

US-10-835-641-18

Sequence 18, Application US/10835641

Publication No. US20040236078A1

GENERAL INFORMATION:
APPLICANT: Carter, Paul J.
Presta, Leonard G.
TITLE OF INVENTION: Method for Making Humanized Antibodies
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/835,641
FILING DATE: 30-Apr-2004
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/705,398
FILING DATE: 02-Nov-2000
APPLICATION NUMBER: 08/146206
FILING DATE: 17-Nov-1993
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709PID2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-10-835-641-18

Query Match 71.4%; Score 40; DB 17; Length 107;
Best Local Similarity 75.0%; Pred. No. 33;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSLPWT 9
DB 90 QYNSLPWT 97

RESULT 18
US-09-056-160B-12
Sequence 12, Application US/09056160B
Patent No. US20020032315A1
GENERAL INFORMATION:
APPLICANT: Baca, Manuel
APPLICANT: Wells, James A.
APPLICANT: Presta, Leonard G.
APPLICANT: Lowman, Henry B.
APPLICANT: Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,160B
FILING DATE: 06-Apr-1998
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/054,856
FILING DATE: 06-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Haasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: P1093R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1896
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-056-160B-12

Query Match 71.4%; Score 40; DB 9; Length 108;
Best Local Similarity 75.0%; Pred. No. 34;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSLPWT 9
DB 90 QYNSLPWT 97

RESULT 19
US-09-795-798-3
Sequence 3, Application US/09795798
Publication No. US20030207336A1
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
Jardieu, Paula M.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/795,798
FILING DATE: 28-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/974,899
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1014R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-795-798-3

Query Match 71.4%; Score 40; DB 10; Length 108;
Best Local Similarity 75.0%; Pred. No. 34;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QVSKLPMT 9
||:||||
Db 90 QVNSLPMT 97

RESULT 20
US-10-234-671-12

Sequence 12, Application US/10234671
Publication No. US20030190317A1

GENERAL INFORMATION:

APPLICANT: Baca, Manuel

Wellis, James A.

Presta, Leonard G.

Lowman, Henry B.

Chen, Yvonne M.

TITLE OF INVENTION: ANTI-VEGF ANTIBODIES

NUMBER OF SEQUENCES: 131

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Winpatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/234,671

FILING DATE: 03-Sep-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/056160

FILING DATE: 06-APR-1998

APPLICATION NUMBER: 60/126446

FILING DATE: 07-APR-1997

APPLICATION NUMBER: 60/054856

FILING DATE: 06-AUG-1997

ATTORNEY/AGENT INFORMATION:

NAME: Cui, Steven X.

REGISTRATION NUMBER: 44,637

REFERENCE/DOCKET NUMBER: P1093R2C1

TELEPHONE: 650/225-8674

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 108 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 12:

US-10-234-671-12

Query Match 71.4%; Score 40; DB 14; Length 108;
Best Local Similarity 75.0%; Pred. No. 34;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QVSKLPMT 9
||:||||
Db 90 QVNSLPMT 97

RESULT 21
US-09-811-123-6

Sequence 6, Application US/09811123
Patent No. US20020001587A1

GENERAL INFORMATION:

APPLICANT: Sharon Erickson

APPLICANT: Ralph Schwall

APPLICANT: Mark Sliwkowski

TITLE OF INVENTION: METHODS OF TREATMENT USING ANTI-ERBB

FILE REFERENCE: GENENT. 073A2

CURRENT APPLICATION NUMBER: US/09/811,123

CURRENT FILING DATE: 2001-03-16

PRIOR APPLICATION NUMBER: 60/238,327

PRIOR FILING DATE: 2000-10-05

PRIOR APPLICATION NUMBER: 09/602,530

PRIOR FILING DATE: 2000-06-23

NUMBER OF SEQ ID NOS: 11

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 6

LENGTH: 109

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Humanized Antibody Sequence

US-09-811-123-6

Query Match 71.4%; Score 40; DB 9; Length 109;
Best Local Similarity 75.0%; Pred. No. 34;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QVSKLPMT 9
||:||||
Db 90 QVNSLPMT 97

RESULT 22

US-10-044-896-4

Sequence 4, Application US/10044896

Publication No. US2003016628A1

GENERAL INFORMATION:

APPLICANT: Chuntharapal, Anan

APPLICANT: Kim, Jin K.

APPLICANT: Stewart, Timothy

APPLICANT: Presta, Leonard G.

TITLE OF INVENTION: ANTI-INTERFERON-ALPHA ANTIBODIES

FILE REFERENCE: GENENT. 074A

CURRENT APPLICATION NUMBER: US/10/044,896

CURRENT FILING DATE: 2002-01-09

PRIOR APPLICATION NUMBER: 60/270775

PRIOR FILING DATE: 2001-02-22

NUMBER OF SEQ ID NOS: 14

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 4

LENGTH: 110

TYPE: PRT

ORGANISM: Homo sapiens

US-10-044-896-4

Query Match 71.4%; Score 40; DB 14; Length 110;
Best Local Similarity 75.0%; Pred. No. 34;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QVSKLPMT 9
||:||||
Db 90 QVNSLPMT 97

RESULT 23
US-10-469-125-8

Sequence 8, Application US/10469125
Publication No. US20040143101A1

GENERAL INFORMATION:

APPLICANT: Solitis, Daniel A.

APPLICANT: Burch, Ronald M.

```

; APPLICANT: Shukla, Rajiv
; TITLE OF INVENTION: IMMUNOGLOBULIN CONSTRUCT CONTAINING ANTI-MUCIN VARIABLE DOMAIN SE
; TITLE OF INVENTION: FOR ELICITING AN ANTI-IDIOYPE ANTI-TUMOR RESPONSE
; FILE REFERENCE: 02755/100G273-US1
; CURRENT APPLICATION NUMBER: US/10/469,125
; CURRENT FILING DATE: 2003-08-25
; PRIOR APPLICATION NUMBER: US 60/281,182
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: PCT/US02/10304
; PRIOR FILING DATE: 2002-04-02
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-469-125-8

Query Match      71.4%; Score 40; DB 16; Length 126;
Best Local Similarity 75.0%; Pred. No. 39;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      2 QYSKLPWT 9
Db      109 QYNSLPWT 116

RESULT 24
US-09-187-693-62
; Sequence 62, Application US/09187693
; Patent No. US20020173629A1
; GENERAL INFORMATION:
; APPLICANT: Jakobovits, Aya
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Gallo, Michael
; APPLICANT: Jia, Xiao-Chi
; TITLE OF INVENTION: Human Monoclonal Antibodies to Epidermal
; TITLE OF INVENTION: Growth Factor Receptor
; FILE REFERENCE: Cell 4.20 CIP2
; CURRENT APPLICATION NUMBER: US/09/187,693
; CURRENT FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 09/162,280
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 08/851,362
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 62
; LENGTH: 153
; TYPE: PRT
; ORGANISM: human
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(153)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-187-693-62

Query Match      71.4%; Score 40; DB 9; Length 153;
Best Local Similarity 66.7%; Pred. No. 47;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 HOYSKLPWT 9
Db      91 HOYSTPWT 99

RESULT 25
US-09-187-693-66
; Sequence 66, Application US/09187693
; Patent No. US20020173629A1
; GENERAL INFORMATION:
; APPLICANT: Jakobovits, Aya
; APPLICANT: Yang, Xiao-Dong
```

```

; APPLICANT: Gallo, Michael
; APPLICANT: Jia, Xiao-Chi
; TITLE OF INVENTION: Human Monoclonal Antibodies to Epidermal
; TITLE OF INVENTION: Growth Factor Receptor
; FILE REFERENCE: Cell 4.20 CIP2
; CURRENT APPLICATION NUMBER: US/09/187,693
; CURRENT FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 09/162,280
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 08/851,362
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 66
; LENGTH: 159
; TYPE: PRT
; ORGANISM: human
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(159)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-187-693-66

Query Match      71.4%; Score 40; DB 9; Length 159;
Best Local Similarity 66.7%; Pred. No. 49;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 HOYSKLPWT 9
Db      88 HOYSTPWT 96

RESULT 26
US-09-056-160B-6
; Sequence 6, Application US/09056160B
; Patent No. US20020032315A1
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
; APPLICANT: Wells, James A.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Lowman, Henry B.
; APPLICANT: Chen, Yvonne M.
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/056,160B
; FILING DATE: 06-Apr-1998
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/054,856
; FILING DATE: 06-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Haasek, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: P1093R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1896
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
```

TYPE: Amino Acid
TOPOLOGY: Linear
US-09-056-160B-6

Query Match
Best Local Similarity 69.6%; Score 39; DB 9; Length 9;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSKLPWT 9
DB 2 QYSTVPWT 9

RESULT 27
US-09-217-268B-31
Sequence 31, Application US/09217268B
Patent No. US20020065398A1
GENERAL INFORMATION:
APPLICANT: Mateo de Acosta del Rio, Christina M
APPLICANT: Rodriguez, Rolando P
APPLICANT: Frias, Ernesto M
TITLE OF INVENTION: Humanized and Chimeric Monoclonal Antibodies That Recognize Epide
FILE REFERENCE: 2720.1US
CURRENT FILING DATE: 1998-12-21
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn version 3.1
SEQ ID NO 31
LENGTH: 9
TYPE: PRT
ORGANISM: Murine
FEATURE:
NAME/KEY: MISC FEATURE
OTHER INFORMATION: CDR of murine R3 antibody
US-09-217-268B-31

Query Match
Best Local Similarity 69.6%; Score 39; DB 9; Length 9;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSKLPWT 9
DB 2 QYSTVPWT 9

RESULT 28
US-10-234-671-6
Sequence 6, Application US/10234671
Publication No. US20030190317A1
GENERAL INFORMATION:
APPLICANT: Baca, Manuel
Wells, James A.
Prestia, Leonard G.
Lowman, Henry B.
Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94060

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/234,671
FILING DATE: 03-Sep-2002

CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/056160
FILING DATE: 06-APR-1998
APPLICATION NUMBER: 60/126446
FILING DATE: 07-APR-1997
APPLICATION NUMBER: 60/054856
FILING DATE: 06-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Cui, Steven X.
REGISTRATION NUMBER: 44,637
REFERENCE/DOCKET NUMBER: P1093R2C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Query Match
Best Local Similarity 69.6%; Score 39; DB 14; Length 9;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSKLPWT 9
DB 2 QYSTVPWT 9

RESULT 29
US-10-624-153-25
Sequence 25, Application US/10624153
Publication No. US20040086502A1
GENERAL INFORMATION:
APPLICANT: CHEN, YVONNE M.
APPLICANT: LOWMAN, HENRY B.
APPLICANT: MILLER, YVES
TITLE OF INVENTION: ANTIBODY VARIANTS
FILE REFERENCE: P1469R1C1
CURRENT APPLICATION NUMBER: US/10/624,153
CURRENT FILING DATE: 2003-07-21
PRIOR APPLICATION NUMBER: US 09/440,781
PRIOR FILING DATE: 1999-11-16
PRIOR APPLICATION NUMBER: US 60/108,945
PRIOR FILING DATE: 1998-11-18
NUMBER OF SEQ ID NOS: 99
SEQ ID NO 25
LENGTH: 9
TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
OTHER INFORMATION: sequence is synthesized
NAME/KEY: artificial
LOCATION: 1-9
OTHER INFORMATION: variant CDR sequence
US-10-624-153-25

Query Match
Best Local Similarity 69.6%; Score 39; DB 15; Length 9;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSKLPWT 9
DB 2 QYSTVPWT 9

RESULT 30
US-10-425-115-293070
Sequence 293070, Application US/10425115

```
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ. ID NOS: 369326
; SEQ. ID NO 293070
; LENGTH: 64
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_30360C.1.pep
US-10-425-115-293070
```

```
Query Match 69.6%; Score 39; DB 17; Length 64;
Best Local Similarity 55.6%; Pred. No. 31;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 1 QYSKIPWT 9
Db 51 HRYRRAPWT 59
```

```
RESULT 31
US-10-379-392-100
; Sequence 100, Application US/10379392
; Publication No. US20040110226A1
; GENERAL INFORMATION:
; APPLICANT: Lazar, Gregory Alan
; APPLICANT: Desjarlais, John Rudolf
; APPLICANT: Marshall, Shannon Alicia
; APPLICANT: Dahiyat, Basail I.
; TITLE OF INVENTION: ANTIBODY OPTIMIZATION
; FILE REFERENCE: A-71386-3 463077-236
; CURRENT APPLICATION NUMBER: US/10/379,392
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,843
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/384,197
; PRIOR FILING DATE: 2002-05-29
; NUMBER OF SEQ. ID NOS: 184
; SOFTWARE: PatentIn version 3.2
; SEQ. ID NO 100
; LENGTH: 103
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Humanized
US-10-379-392-100
```

```
Query Match 69.6%; Score 39; DB 16; Length 103;
Best Local Similarity 75.0%; Pred. No. 48;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 2 QYSKIPWT 9
Db 90 QYSTVPWT 97
```

```
RESULT 32
US-10-379-392-121
; Sequence 121, Application US/10379392
; Publication No. US20040110226A1
; GENERAL INFORMATION:
; APPLICANT: Lazar, Gregory Alan
; APPLICANT: Desjarlais, John Rudolf
; APPLICANT: Marshall, Shannon Alicia
```

```
; APPLICANT: Dahiyat, Basail I.
; TITLE OF INVENTION: ANTIBODY OPTIMIZATION
; FILE REFERENCE: A-71386-3 463077-236
; CURRENT APPLICATION NUMBER: US/10/379,392
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,843
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/384,197
; PRIOR FILING DATE: 2002-05-29
; NUMBER OF SEQ. ID NOS: 184
; SOFTWARE: PatentIn version 3.2
; SEQ. ID NO 121
; LENGTH: 103
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-379-392-121
```

```
Query Match 69.6%; Score 39; DB 16; Length 103;
Best Local Similarity 75.0%; Pred. No. 48;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 2 QYSKIPWT 9
Db 90 QYSTVPWT 97
```

```
RESULT 33
US-10-379-392-123
; Sequence 123, Application US/10379392
; Publication No. US20040110226A1
; GENERAL INFORMATION:
; APPLICANT: Lazar, Gregory Alan
; APPLICANT: Desjarlais, John Rudolf
; APPLICANT: Marshall, Shannon Alicia
; APPLICANT: Dahiyat, Basail I.
; TITLE OF INVENTION: ANTIBODY OPTIMIZATION
; FILE REFERENCE: A-71386-3 463077-236
; CURRENT APPLICATION NUMBER: US/10/379,392
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,843
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/384,197
; PRIOR FILING DATE: 2002-05-29
; NUMBER OF SEQ. ID NOS: 184
; SOFTWARE: PatentIn version 3.2
; SEQ. ID NO 123
; LENGTH: 103
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-379-392-123
```

```
Query Match 69.6%; Score 39; DB 16; Length 103;
Best Local Similarity 75.0%; Pred. No. 48;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 2 QYSKIPWT 9
Db 90 QYSTVPWT 97
```

```
RESULT 34
US-10-379-392-129
; Sequence 129, Application US/10379392
; Publication No. US20040110226A1
; GENERAL INFORMATION:
; APPLICANT: Lazar, Gregory Alan
; APPLICANT: Desjarlais, John Rudolf
; APPLICANT: Marshall, Shannon Alicia
; APPLICANT: Dahiyat, Basail I.
```


;; TITLE OF INVENTION: ANTIBODY OPTIMIZATION
;; FILE REFERENCE: A-71386-3 463077-236
;; CURRENT APPLICATION NUMBER: US/10/379,392
;; CURRENT FILING DATE: 2003-03-03
;; PRIOR APPLICATION NUMBER: US 60/360,843
;; PRIOR FILING DATE: 2002-03-01
;; PRIOR APPLICATION NUMBER: US 60/384,197
;; PRIOR FILING DATE: 2002-05-29
;; NUMBER OF SEQ ID NOS: 184
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 129
;; LENGTH: 103
;; TYPE: PRT
;; ORGANISM: Artificial sequence
;; FEATURE:
;; OTHER INFORMATION: Synthetic
;; NAME/KEY: MISC_FEATURE
;; LOCATION: (36)..(36)
;; OTHER INFORMATION: Xaa at position 36 can be Tyr, Phe, Met or Leu
;; NAME/KEY: MISC_FEATURE
;; LOCATION: (43)..(43)
;; OTHER INFORMATION: Xaa at position 43 can be Tyr, Phe, His, Asp, Thr, Ala, Asn or
;; OTHER INFORMATION: Ser
;; NAME/KEY: MISC_FEATURE
;; LOCATION: (87)..(87)
;; OTHER INFORMATION: Xaa at position 87 can be Phe, Tyr or Met
;; NAME/KEY: MISC_FEATURE
;; LOCATION: (89)..(89)
;; OTHER INFORMATION: Xaa at position 89 can be Met or Gln
;; NAME/KEY: MISC_FEATURE
;; LOCATION: (98)..(98)
;; OTHER INFORMATION: Xaa at position 98 can be Phe or Tyr
;; US-10-379-392-129
Query Match 69.6%; Score 39; DB 16; Length 103;
Best Local Similarity 75.0%; Pred. No. 48;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 2 QYSKLPMT 9
Db 90 QYSTVPMT 97
RESULT 35
US-10-379-392-131
;; Sequence 131, Application US/10379392
;; Publication No. US20040110226A1
;; GENERAL INFORMATION:
;; APPLICANT: Lazar, Gregory Alan
;; APPLICANT: Desjardins, John Rudolf
;; APPLICANT: Marshall, Shannon Alicia
;; APPLICANT: Dahiyat, Basail I.
;; TITLE OF INVENTION: ANTIBODY OPTIMIZATION
;; FILE REFERENCE: A-71386-3 463077-236
;; CURRENT APPLICATION NUMBER: US/10/379,392
;; CURRENT FILING DATE: 2003-03-03
;; PRIOR APPLICATION NUMBER: US 60/360,843
;; PRIOR FILING DATE: 2002-03-01
;; PRIOR APPLICATION NUMBER: US 60/384,197
;; PRIOR FILING DATE: 2002-05-29
;; NUMBER OF SEQ ID NOS: 184
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 131
;; LENGTH: 103
;; TYPE: PRT
;; ORGANISM: Artificial sequence
;; FEATURE:
;; OTHER INFORMATION: Synthetic

US-10-379-392-131
Query Match 69.6%; Score 39; DB 16; Length 103;
Best Local Similarity 75.0%; Pred. No. 48;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 2 QYSKLPMT 9
Db 90 QYSTVPMT 97
RESULT 36
US-09-056-160B-13
;; Sequence 13, Application US/09056160B
;; Patent No. US20020032315A1
;; GENERAL INFORMATION:
;; APPLICANT: Baca, Manuel
;; APPLICANT: Wells, James A.
;; APPLICANT: Presta, Leonard G.
;; APPLICANT: Lowman, Henry B.
;; APPLICANT: Chen, Yvonne M.
;; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
;; NUMBER OF SEQUENCES: 131
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Genentech, Inc.
;; STREET: 1 DNA Way
;; CITY: South San Francisco
;; STATE: California
;; COUNTRY: USA
;; ZIP: 94080
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Winpatin (Genentech)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/056,160B
;; FILING DATE: 06-Apr-1998
;; CLASSIFICATION: 424
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 60/054,856
;; FILING DATE: 06-AUG-1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Hasak, Janet E.
;; REGISTRATION NUMBER: 28,616
;; REFERENCE/DOCKET NUMBER: P1093R2
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 650/225-1896
;; TELEFAX: 650/952-9881
;; INFORMATION FOR SEQ ID NO: 13:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 107 amino acids
;; TYPE: Amino Acid
;; TOPOLOGY: Linear
;; US-09-056-160B-13
Query Match 69.6%; Score 39; DB 9; Length 107;
Best Local Similarity 75.0%; Pred. No. 50;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 2 QYSKLPMT 9
Db 90 QYSTVPMT 97
RESULT 37
US-09-056-160B-15
;; Sequence 15, Application US/09056160B
;; Patent No. US20020032315A1
;; GENERAL INFORMATION:
;; APPLICANT: Baca, Manuel
;; APPLICANT: Wells, James A.
;; APPLICANT: Presta, Leonard G.

APPLICANT: Lowman, Henry B.
APPLICANT: Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,160B
FILING DATE: 06-Apr-1998
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/054,856
FILING DATE: 06-Aug-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet B.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: P1093R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1896
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-056-160B-15

Query Match 69.6%; Score 39; DB 9; Length 107;
Best Local Similarity 75.0%; Pred. No. 50;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QVSKLPWT 9
Db 90 QVSTVPWT 97

RESULT 38
US-10-234-671-13
Sequence 13, Application US/10234671
Publication No. US20030190317A1
GENERAL INFORMATION:
APPLICANT: Baca, Manuel
Wells, James A.
Presta, Leonard G.
Lowman, Henry B.
Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/234,671
FILING DATE: 03-Sep-2002

CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/056160
FILING DATE: 06-Apr-1998
APPLICATION NUMBER: 60/126446
FILING DATE: 07-Apr-1997
APPLICATION NUMBER: 60/054856
FILING DATE: 06-Aug-1997
ATTORNEY/AGENT INFORMATION:
NAME: Cui, Steven X.
REGISTRATION NUMBER: 44,637
REFERENCE/DOCKET NUMBER: P1093R2C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-10-234-671-13

Query Match 69.6%; Score 39; DB 14; Length 107;
Best Local Similarity 75.0%; Pred. No. 50;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QVSKLPWT 9
Db 90 QVSTVPWT 97

RESULT 39
US-10-234-671-15
Sequence 15, Application US/10234671
Publication No. US20030190317A1
GENERAL INFORMATION:
APPLICANT: Baca, Manuel
Wells, James A.
Presta, Leonard G.
Lowman, Henry B.
Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/234,671
FILING DATE: 03-Sep-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/056160
FILING DATE: 06-Apr-1998
APPLICATION NUMBER: 60/126446
FILING DATE: 07-Apr-1997
APPLICATION NUMBER: 60/054856
FILING DATE: 06-Aug-1997
ATTORNEY/AGENT INFORMATION:
NAME: Cui, Steven X.
REGISTRATION NUMBER: 44,637
REFERENCE/DOCKET NUMBER: P1093R2C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674

TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-10-234-671-15

Query Match 69.6%; Score 39; DB 14; Length 107;
Best Local Similarity 75.0%; Pred. No. 50;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSKLPWT 9
|||:||||
DB 90 QYSTVPWT 97

RESULT 40
US-10-251-215-49
; Sequence 49, Application US/10251215
; Publication No. US20030219839A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Kretz-Rommel, Anke
; APPLICANT: Frederickson, Shana
; TITLE OF INVENTION: ANTI-PDGF ANTIBODIES AND METHODS FOR PRODUCING ENGINEERED
; TITLE OF INVENTION: ANTIBODIES
; FILE REFERENCE: 1087-36
; CURRENT APPLICATION NUMBER: US/10/251,215
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US 60/323,537
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: US 60/323,544
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: US 60/379,980
; PRIOR FILING DATE: 2002-05-13
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 49
; LENGTH: 107
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Humanized Light Chain
US-10-251-215-49

Query Match 69.6%; Score 39; DB 14; Length 107;
Best Local Similarity 87.5%; Pred. No. 50;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSKLPWT 9
|||:||||
DB 89 QYSKLPWT 96

Search completed: December 17, 2004, 18:38:02
Job time : 18.3933 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 17, 2004, 18:11:22 ; Search time 3.53933 Seconds
(without alignments)
244.665 Million cell updates/sec

Title: US-10-089-500-8
Perfect score: 56
Sequence: 1 HQSKLPWT 9

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	85.7	111	2	G38740 Ig kappa chain V r
2	48	85.7	111	2	E38740 Ig kappa chain V r
3	45	80.4	111	2	A38740 Ig kappa chain V r
4	45	80.4	111	2	C38740 Ig kappa chain V r
5	42	75.0	128	2	A47159 Ig lambda chain V
6	42	75.0	141	2	A49134 Ig kappa chain V-I
7	39	69.6	108	1	KIHUME Ig kappa chain V-I
8	39	69.6	258	2	AF2204 beta-carotene keto
9	38	67.9	288	2	T36237 probable phosphot
10	38	67.9	363	2	T39701 lipate-protein 11
11	38	67.9	581	2	C39768 cholinesterase (BC
12	38	67.9	602	1	ACHU cholinesterase (BC
13	38	67.9	603	2	S70849 cholinesterase (BC
14	38	67.9	1289	1	RMKRR3 mRNA guanylyltrans
15	37	66.1	108	1	KIHOUU Ig kappa chain V-I
16	37	66.1	134	1	A4HUI7 Ig kappa chain pre
17	37	66.1	136	2	C81739 Ig kappa chain pre
18	37	66.1	190	2	T31291 hypothetical prote
19	37	66.1	402	2	S47329 OXAI protein precu
20	37	66.1	585	2	T47364 hypothetical prote
21	37	66.1	821	2	H71475 probable cultr pho
22	37	66.1	823	2	C81739 conserved hypochet
23	37	66.1	1582	2	A56248 sulfonylurea recep
24	36	64.3	103	2	S18731 Ig kappa chain V-J
25	36	64.3	111	1	KVMS13 Ig kappa chain V r
26	36	64.3	518	2	D96681 protein F1822.2 [I
27	36	64.3	588	2	T26193 hypothetical prote
28	35	62.5	106	2	PL0262 Ig kappa chain V r
29	35	62.5	109	2	S26336 Ig light chain V r

30	35	62.5	125	2	S40333 Ig kappa chain V-J
31	35	62.5	140	2	H69405 hypothetical prote
32	35	62.5	296	2	B87293 hydrolase, probabl
33	35	62.5	312	2	T27004 hypothetical prote
34	35	62.5	318	2	B83527 hypothetical prote
35	35	62.5	376	2	T46096 hypothetical prote
36	35	62.5	413	2	T18945 hypothetical prote
37	35	62.5	431	2	A89761 hypothetical prote
38	35	62.5	440	2	T44138 chromosome condens
39	35	62.5	492	2	T18221 cytochrome-inducible
40	35	62.5	535	2	JC5762 probable acyl-CoA
41	35	62.5	549	2	B83149 complement C9 prec
42	35	62.5	574	2	B23677 gamma-glutamyltran
43	35	62.5	609	2	AE2062 DNA-directed DNA p
44	35	62.5	788	1	JDVJLH probable DNA-direc
45	35	62.5	1102	2	S28104

ALIGNMENTS

RESULT 1
G38740
Ig kappa chain V region (Py54) - mouse
C/Species: Mus musculus (house mouse)
C/Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 09-Jul-2004
C/Accession: G38740
R/Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
J. Biol. Chem. 266, 6607-6613, 1991
A/Title: Heavy and light chain variable region sequences and antibody properties of anti-
A/Reference number: A38740; MID:91177923; PMID:1706720
A/Accession: G38740
A/Status: preliminary; nucleic acid sequence not shown; not compared with conceptual trar
A/Molecule type: mRNA
A/Residues: 1-111 <RUF>
A/Cross-references: UNIPROT:Q91WS9
C/Suprafamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/19-93/Domain: immunoglobulin homology <IMW>

Query Match 85.7%; Score 48; DB 2; Length 111;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYSKLPWT 9
DB 93 QYSKLPWT 100

RESULT 2
E38740
Ig kappa chain V region (Py54) - mouse
C/Species: Mus musculus (house mouse)
C/Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 09-Jul-2004
C/Accession: E38740
R/Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
J. Biol. Chem. 266, 6607-6613, 1991
A/Title: Heavy and light chain variable region sequences and antibody properties of anti-
A/Reference number: A38740; MID:91177923; PMID:1706720
A/Accession: E38740
A/Status: preliminary; nucleic acid sequence not shown; not compared with conceptual trar
A/Molecule type: mRNA
A/Residues: 1-111 <RUF>
A/Cross-references: UNIPROT:Q91WS9
C/Suprafamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/19-93/Domain: immunoglobulin homology <IMW>

Query Match 85.7%; Score 48; DB 2; Length 111;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYSKLPWT 9

```
Db      93 QYSKLPWT 100
|||||
RESULT 3
A38740
Ig kappa chain V region (Py20) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 09-Jul-2004
C/Accession: A38740
R:Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
J. Biol. Chem. 266, 6607-6613, 1991
A>Title: Heavy and light chain variable region sequences and antibody properties of anti
A:Reference number: A38740; MUID:91177923; PMID:1706720
A:Accession: A38740
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A:Molecule type: mRNA
A:Residues: 1-111 <RUF>
A/Cross-references: UNIPROT:Q91WS9
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:19-93/Domain: immunoglobulin homology <IMM>

Query Match      80.4%; Score 45; DB 2; Length 111;
Best Local Similarity 87.5%; Pred. No. 0.44;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 QYSKLPWT 9
|||||
Db      93 QYSKVPWT 100

RESULT 4
C38740
Ig kappa chain V region (Py2) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 09-Jul-2004
C/Accession: C38740
R:Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
J. Biol. Chem. 266, 6607-6613, 1991
A>Title: Heavy and light chain variable region sequences and antibody properties of anti
A:Reference number: A38740; MUID:91177923; PMID:1706720
A:Accession: C38740
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A:Molecule type: mRNA
A:Residues: 1-111 <RUF>
A/Cross-references: UNIPROT:Q91WS9
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:19-93/Domain: immunoglobulin homology <IMM>

Query Match      80.4%; Score 45; DB 2; Length 111;
Best Local Similarity 87.5%; Pred. No. 0.44;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 QYSKLPWT 9
|||||
Db      93 QYSKVPWT 100

RESULT 5
A47159
Ig lambda chain V region (CEA-specific maid T84.66) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C/Accession: A47159
R:Gaida, F.U.; Pieper, D.; Roder, U.W.; Shively, J.E.; Wagener, C.; Neumater, M.
U. Biol. Chem. 268, 14138-14145, 1993
A>Title: Molecular characterization of a cloned idiotypic cascade containing a network a
A:Reference number: A47159; MUID:93300804; PMID:7686150
A:Accession: A47159
A:Status: preliminary
A:Molecule type: DNA; protein
```

```
A:Residues: 1-128 <GAT>
A:Experimental source: hybridoma 6G6.C4
A>Note: sequence extracted from NCBI backbone (NCBIN:134419, NCBIPI:134420)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:36-110/Domain: immunoglobulin homology <IMM>

Query Match      75.0%; Score 42; DB 2; Length 128;
Best Local Similarity 66.7%; Pred. No. 1.8;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 HOYSKLPWT 9
|||||
Db      109 HOYDNPWT 117

RESULT 6
A49134
Ig kappa chain V-I region (ISE) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C/Accession: A49134; S25115
R:Rocca, A.; Khamilchi, A.A.; Aucouturier, P.; Noel, L.H.; Denoroy, L.; Preud'homme, J.L.
Clin. Exp. Immunol. 91, 506-509, 1993
A>Title: Primary structure of a variable region of the V kappa I subgroup (ISE) in light
A:Reference number: A49134; MUID:93185310; PMID:7680298
A:Accession: A49134
A:Status: preliminary
A:Molecule type: mRNA; protein
A:Residues: 1-141 <ROC>
A/Cross-references: EMBL:X67322; NID:g33268; PIDN:CA47736.1; PID:g33269
A>Note: sequence extracted from NCBI backbone (NCBIP:127088)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:38-112/Domain: immunoglobulin homology <IMM>

Query Match      75.0%; Score 42; DB 2; Length 141;
Best Local Similarity 66.7%; Pred. No. 2;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 HOYSKLPWT 9
|||||
Db      111 HOYDSVPWT 119

RESULT 7
K1HWME
Ig kappa chain V-I region (WEA) - human
C:Species: Homo sapiens (man)
C>Date: 03-Aug-1984 #sequence_revision 03-Aug-1984 #text_change 09-Jul-2004
C/Accession: A01876
R:Goni, F.; Frangione, B.
Proc. Natl. Acad. Sci. U.S.A. 80, 4837-4841, 1983
A>Title: Amino acid sequence of the Fv region of a human monoclonal IgM (protein WEA) wit
A:Reference number: A93964; MUID:83273707; PMID:6410398
A:Accession: A01876
A:Molecule type: protein
A:Residues: 1-108 <GON>
A/Cross-references: UNIPROT:P01610
C:Comment: This chain was obtained from a monoclonal antibody against 3,4-pyruvylated ga)
C:Genetics:
A:Gene: GDB:IGKV1
A/Cross-references: GDB:136264
A/Map position: 2p12-2p12
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap)
hain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into 1a)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer
F:16-90/Domain: immunoglobulin homology <IMM>
F:23-88/Disulfide bonds: #status predicted

Query Match      69.6%; Score 39; DB 1; Length 108;
Best Local Similarity 75.0%; Pred. No. 5.1;
```

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 QYSKLPWT 9
|||
90 QYSSFPWT 97

RESULT 8
AF2204
beta-carotene ketolase [imported] - Nostoc sp. (strain PCC 7120)

C/Species: Nostoc sp. PCC 7120
A/Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C/Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C/Accession: AF2204
R/Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, Nakazaki, N.; Shimo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. 8, 205-213 2001
A/Title: Complete genomic sequence of the filamentous nitrogen-fixing Cyanobacterium Anabaena PCC 7120
A/Reference number: AB1807; MUID:21595285; PMID:11759840
A/Accession: AF2204
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-258 <KIR>
A/Cross-references: UNIPROT:Q9YSX0; GB:BA000019; PIDD:BAE74888.1; PID:G17132284; GSPDB:G17132284
A/Experimental source: strain PCC 7120
C/Genetics:
A/Gene: alr3189
C/Superfamily: beta-carotene ketolase

Query Match 69.6%; Score 39; DB 2; Length 258;
Best Local Similarity 62.5%; Pred. No. 13;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HOYSKLPW 8
||:||||
Db 240 HEYQDLPW 247

RESULT 9
T36237
Probable phosphotransferase - Streptomyces coelicolor
C/Species: Streptomyces coelicolor
C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C/Accession: T36237
R/Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, March 1999
A/Reference number: Z21577
A/Accession: T36237
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-288 <OLI>
A/Cross-references: UNIPROT:Q9X8F0; EMBL:AL049573; PIDD:CA840335.1; GSPDB:GN00070; SCOP:1.288
A/Experimental source: strain A3(2)
C/Genetics:
A/Gene: SCOPDB:SC39.27C

Query Match 67.9%; Score 38; DB 2; Length 288;
Best Local Similarity 75.0%; Pred. No. 22;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 HOYSKLPW 8
||:||||
Db 256 HVSQDLPW 263

RESULT 10
T39701
Lipase-protein lipase A - fission yeast (Schizosaccharomyces pombe)
C/Species: Schizosaccharomyces pombe
C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C/Accession: T39701
R/Mood, V.; Skelton, J.; Churcher, C.M.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, July 1999

A/Reference number: Z21870
A/Accession: T39701
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-363 <WOO>
A/Cross-references: UNIPROT:O13629; EMBL:AL109652; PIDD:CA851768.1; GSPDB:GN00067
A/Experimental source: strain 972h-; cosmid c17A3
C/Genetics:
A/Gene: p1038
A/Map position: 2

Query Match 67.9%; Score 38; DB 2; Length 363;
Best Local Similarity 55.6%; Pred. No. 28;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 HOYSKLPWT 9
||:||||
Db 322 HEDSIPWT 330

RESULT 11
C39768
Cholinesterase (EC 3.1.1.8) - rabbit
N/Alternate names: butyrylcholinesterase
C/Species: Oryctolagus cuniculus (domestic rabbit)
C/Date: 14-Feb-1992 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004
C/Accession: S10255; C39768
R/Idro, O.; Chatonnet, A.
Nucleic Acids Res. 18, 3990, 1990
A/Title: Complete sequence of rabbit butyrylcholinesterase.
A/Reference number: S10255; MUID:90326526; PMID:2374720
A/Accession: S10255
A/Status: translation not shown
A/Molecule type: DNA
A/Residues: 1-581 <RBI>
A/Cross-references: UNIPROT:P21927; EMBL:X52090; NID:G1476; PIDD:CA36308.1; PID:G137027;
R/Arpagaus, M.; Chatonnet, A.; Masson, P.; Newton, M.; Vaughan, T.A.; Bartels, C.F.; Negr
J. Biol. Chem. 266, 6966-6974, 1991
A/Title: Use of the polymerase chain reaction for homology probing of butyrylcholinester
A/Reference number: A39768; MUID:91201348; PMID:2016308
A/Accession: C39768
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 75-215 <ARP>
A/Cross-references: GB:M62779; NID:G164788; PIDD:AAA31169.1; PID:G164789
C/Genetics:

A/Intons: 485/2; 541/1
A/Status: preliminary
C/Superfamily: cholinesterase; cholinesterase homology
C/Keywords: carboxylic ester hydrolase; glycoprotein
F/35-535/Domain: cholinesterase homology <CHE>
Query Match 67.9%; Score 38; DB 2; Length 581;
Best Local Similarity 75.0%; Pred. No. 45;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HOYSKLPW 8
||:||||
Db 430 HRSSKLPW 437

RESULT 12
ACHU
Cholinesterase (EC 3.1.1.8) precursor [validated] - human
N/Alternate names: acetylcholine acetylhydrolase; butyrylcholinesterase; choline esterase II;
C/Species: Homo sapiens (man)
C/Date: 30-Jun-1987 #sequence_revision 23-Feb-1996 #text_change 09-Jul-2004
C/Accession: A33769; A26613; A33887; A34668; A00772
R/Arpagaus, M.; Kott, M.; Vacker, K.P.; Bartels, C.F.; La Du, B.N.; Lockridge, O.
Biochemistry 29, 124-131, 1990
A/Title: Structure of the gene for human butyrylcholinesterase. Evidence for a single co
A/Reference number: A33769; MUID:90212557; PMID:2322535
A/Accession: A33769
A/Molecule type: DNA

A:Residues: 'MSVQSNQAGAAAACSTSPRYWIFTPCKLCHLCRESEIN',1-602 <ARP>
A:Cross-references: UNIPROT:P06276; GB:M32391; GB:J02879
A>Note: two ATG codons found upstream of Met-1 do not lie in a favorable context for tra
R:Prodly, C.A.; Zevin-Sonkin, D.; Gnatt, A.; Goldberg, O.; Soreq, H.
Proc. Natl. Acad. Sci. U.S.A. 84, 3555-3559, 1987
A>Title: Isolation and characterization of full-length cDNA clones coding for cholinesterase
A:Reference number: A26613; MUID:87231856; PMID:30353536
A:Accession: A26613
A:Molecule type: mRNA
A:Residues: 1-133,'D',135-602 <PRO>
R:McTernan, C.; Adkins, S.; Chatonnet, A.; Vaughan, T.A.; Bartels, C.F.; Kott, M.; Rose
Proc. Natl. Acad. Sci. U.S.A. 84, 6682-6686, 1987
A>Title: Brain cDNA clone for human cholinesterase.
A:Reference number: A33887; MUID:88016155; PMID:3477799
A:Accession: A33887
A:Molecule type: mRNA
A:Residues: 'MSVQSNQAGAAAACSTSPRYWIFTPCKLCHLCRESEIN',1-602 <MCT>
A>Note: two ATG codons found upstream of Met-1 do not lie in a favorable context for tra
R:Moguelita, C.F.; McGuire, M.C.; Graesser, C.; Bartels, C.F.; Arpagaus, M.; Van der Spek,
Am. J. Hum. Genet. 46, 934-942, 1990
A>Title: Identification of a frameshift mutation responsible for the silent phenotype of
A:Reference number: A34668; MUID:90252779; PMID:2339692
A:Accession: A34668
A:Molecule type: DNA
A:Residues: 143-145,'VSNMNIIFPCL',<NOG>
A>Note: frameshift mutant in codon for residue 145 (Gly)
R:Lockridge, O.; Bartels, C.F.; Vaughan, T.A.; Wong, C.K.; Norton, S.E.; Johnson, L.L.
J. Biol. Chem. 262, 549-557, 1987
A>Title: Complete amino acid sequence of human serum cholinesterase.
A:Reference number: A00772; MUID:87109144; PMID:3542989
A:Accession: A00772
A:Molecule type: protein
A:Residues: 29-602 <LOC>
A:Experimental source: Plasma
C:Comment: Cholinesterase is present in most cells (except erythrocytes).
C:Genetics:
A:Gene: GDB:BCHR; CHE1
A:Cross-references: GDB:120558; OMIM:177400
A:Map position: 3q26.1-3q26.2
A:introns: 506/2; 562/1
C:Function:
A:Description: hydrolyses acylcholines to choline and a carboxylic acid
A>Note: this cholinesterase is highly reactive with organophosphate esters
C:Superfamily: cholinesterase; cholinesterase homology
C:Keywords: carboxylic ester hydrolase; glycoprotein; homotetramer
F:1-28/Domain: signal sequence #status predicted <SIG>
F:29-602/Product: cholinesterase #status experimental <MAT>
F:56-556/Domain: cholinesterase homology <CHE>
F:45,85,134,269,284,365,483,509,514/Binding site: carbohydrate (Asn) (covalent) #status
F:226/Active site: Ser #status experimental

Query Match 67.9%; Score 38; DB 1; Length 602;
Best Local Similarity 75.0%; Pred. No. 47;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HOYSKLPW 8
|:|||||
Db 451 HRSSKLPW 458

RESULT 13
S70849
cholinesterase (EC 3.1.1.8) - mouse
N:Alternate names: butyrylcholine esterase
C:Species: Mus musculus (house mouse)
C>Date: 28-Oct-1996 #sequence revision 08-Nov-1996 #text_change 09-Jul-2004
C:Accession: S70849; S15680; A39768
R:Taylor, P.
submitted to the EMBL Data Library, August 1992
A:Reference number: S70849
A:Accession: S70849
A:Molecule type: nucleic acid
A:Residues: 1-603 <TAY>

A:Cross-references: UNIPROT:Q03311; EMBL:M99492; NID:g191579; PID:AAA37328.1; PID:g19157
R:Rachinsky, T.L.; Camp, S.; Li, Y.; Ekstrom, T.J.; Newton, M.; Taylor, P.
Neuron 5, 317-327, 1990
A>Title: Molecular cloning of mouse acetylcholinesterase: tissue distribution of alternat
A:Reference number: JH0314; MUID:90380429; PMID:2400605
A:Accession: S15680
A:Status: nucleic acid sequence not shown
A:Molecule type: nucleic acid
A:Residues: 30-128,'P',130-603 <RAC>
A:Cross-references: EMBL:M99492
R:Arpagaus, M.; Chatonnet, A.; Masson, P.; Newton, M.; Vaughan, T.A.; Bartels, C.F.; McGr
J. Biol. Chem. 266, 6966-6974, 1991
A>Title: Use of the polymerase chain reaction for homology probing of butyrylcholinester
A:Reference number: A39768; MUID:91201348; PMID:2016308
A:Accession: A39768
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 97-128,'P',130-237 <ARP>
C:Superfamily: cholinesterase; cholinesterase homology
C:Keywords: carboxylic ester hydrolase; glycoprotein
F:57-557/Domain: cholinesterase homology <CHE>

Query Match 67.9%; Score 38; DB 2; Length 603;
Best Local Similarity 75.0%; Pred. No. 47;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HOYSKLPW 8
|:|||||
Db 452 HRSSKLPW 459

RESULT 14
RMRX3
mRNA guanylyltransferase (EC 2.7.7.50) - reovirus type 3
N:Alternate names: lambda 2 protein; mRNA capping enzyme
C:Species: reovirus type 3
A>Note: host Homo sapiens (man)
C>Date: 30-Sep-1989 #sequence revision 30-Sep-1989 #text_change 09-Jul-2004
C:Accession: A28471
R:Seiliger, L.S.; Zheng, K.; Shatkin, A.J.
J. Biol. Chem. 262, 16289-16293, 1987
A>Title: Complete nucleotide sequence of reovirus L2 gene and deduced amino acid sequence
A:Reference number: A28471; MUID:88058999; PMID:2824487
A:Accession: A28471
A:Molecule type: DNA
A:Residues: 1-1289 <SEL>
A:Cross-references: UNIPROT:P11079
C:Genetics:
A:Map position: segment L2
C:Superfamily: reovirus mRNA guanylyltransferase
C:Keywords: core protein; mRNA capping; nucleotidyltransferase; transcription

Query Match 67.9%; Score 38; DB 1; Length 1289;
Best Local Similarity 66.7%; Pred. No. 1e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 HOYSKLPW 9
|:|||||
Db 659 HQHSLTWT 667

RESULT 15
KIHUAV
Ig kappa chain V-I region (Au) - human
C:Species: Homo sapiens (man)
C>Date: 24-Apr-1984 #sequence revision 02-Jul-1998 #text_change 09-Jul-2004
C:Accession: A91653; A01862; S02573
R:Schlecht, H.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 353, 345-370, 1972
A>Title: Die Primärstruktur einer monoklonalen Immunglobulin-L-Kette vom kappa-Typ, Subg
A:Reference number: A91653; MUID:72189444; PMID:5028201
A:Accession: A91653
A:Molecule type: protein

A:Residues: 1-108 <SCH>
 A:Cross-references: UNIPROT:P01594
 A:Note: the C region of this chain has the Inv (3) marker
 R:Feilhammer, H.; Schiffer, M.; Epp, O.; Colman, P.M.; Lattman, E.E.; Schwager, P.; Strel
 Biophys. Struct. Mech. 1, 139-146, 1975
 A:Title: The structure determination of the variable portion of the Bence-Jones protein
 A:Reference number: A90729; PMID:77022433; PMID:1234024
 A:Contents: annotation; X-ray crystallography
 A:Note: the structure of the V region was determined by molecular replacement methods us
 R:Steiner, V.; Chang, J.Y.
 PDBS Lett. 222, 6-10, 1987
 A:Title: Chemical modification of the carboxyl groups of protein substrates enhances the
 A:Reference number: S05572; PMID:88005152; PMID:3115831
 A:Contents: annotation
 A:Comment: This is a Bence Jones protein.
 C:Genetics:
 A:Gene: GDB:1GKVI
 A:Cross-references: GDB:136264
 A:Map position: 2p12-2p12
 C:Complex: an immunoglobulin heterotrimer subunit consists of two identical light (kap
 hain disulfide bonds; in some cases, such as IGA and IGM, the subunits associate into la
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotrimer; immunoglobulin
 F:16-90/Domain: immunoglobulin homology <IMM>
 F:23-88/Disulfide bonds: #status predicted

Query Match 66.1%; Score 37; DB 1; Length 108;
 Best Local Similarity 75.0%; Pred. No. 12;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QYSKLPWT 9
 DB 90 QYDYLPT 97

RESULT 16

K4HU17
 Ig kappa chain precursor V-IV region (BI7) - human
 C:Species: Homo sapiens (man)
 C:Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #ext_change 21-Jan-2000
 C:Accession: A01905
 R:Marsh, P.; Mills, F.; Gould, H.
 Nucleic Acids Res. 13, 6531-6544, 1985
 A:Title: Detection of a unique human VkapapIV germ-line gene by a cloned cDNA probe.
 A:Reference number: A01905; PMID:86041854; PMID:2997713
 A:Accession: A01905
 A:Molecule type: mRNA
 A:Residues: 1-134 <MAR>
 A:Note: the sequence was determined from the differentiated gene
 A:Note: the authors translated the codon TGC for residue 76 as Trp
 C:Complex: An immunoglobulin heterotrimer subunit consists of two identical light (kap
 hain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into la
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotrimer; immunoglobulin
 F:21-30/Domain: signal sequence #status predicted <SIG>
 F:21-134/Product: Ig kappa chain V-IV region (BI7) #status predicted <MAR>
 F:21-43/Region: framework 1
 F:36-116/Domain: immunoglobulin homology <IMM>
 F:44-60/Region: complementarity-determining 1
 F:61-75/Region: framework 2
 F:76-82/Region: complementarity-determining 2
 F:83-114/Region: framework 3
 F:115-121/Region: complementarity-determining 3
 F:122-134/Region: framework 4
 F:43-114/Disulfide bonds: #status predicted

Query Match 66.1%; Score 37; DB 1; Length 134;
 Best Local Similarity 75.0%; Pred. No. 15;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QYSKLPWT 9
 DB 116 QYDYLPT 123

RESULT 17

A49137
 Ig kappa chain precursor V region - human
 C:Species: Homo sapiens (man)
 C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #ext_change 21-Jan-2000
 C:Accession: A49137; S24479
 R:Khamlich, A.A.; Aucuttier, P.; Silvain, C.; Bauwens, M.; Touchard, G.; Freund'homme,
 Clin. Exp. Immunol. 87, 122-126, 1992
 A:Title: Primary structure of a monoclonal kappa chain in myeloma with light chain depos
 A:Reference number: A49137; PMID:92127887; PMID:1733627
 A:Accession: A49137
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-136 <KHA>
 A:Cross-references: GB:X64135; GB:S79324; NID:G33059; PIDN:CAA45496.1; PID:G33060
 A:Note: sequence extracted from NCBI backbone (NCBIN:79324, NCBIP:79325)
 R:Cogne, M.C.C.
 submitted to the EMBL Data Library, January 1992
 A:Reference number: S24479
 A:Accession: S24479
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-136 <COG>
 A:Cross-references: EMBL:X64135; NID:G33059; PIDN:CAA45496.1; PID:G33060
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotrimer; immunoglobulin
 F:36-116/Domain: immunoglobulin homology <IMM>

Query Match 66.1%; Score 37; DB 2; Length 136;
 Best Local Similarity 75.0%; Pred. No. 15;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QYSKLPWT 9
 DB 116 QYDYLPT 123

RESULT 18

T31291
 hypothetical protein 1251 - Sphingomonas aromaticivorans plasmid pNL1
 C:Species: Sphingomonas aromaticivorans
 C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #ext_change 09-Jul-2004
 C:Accession: T31291
 R:Romine, M.F.; Stillwell, L.C.; Wong, K.K.; Thurston, S.J.; Slek, E.C.; Sensen, C.W.; Ge
 submitted to the EMBL Data Library, July 1998
 A:Description: Complete sequence of a 184 Kb catabolic plasmid from Sphingomonas aromatic
 A:Reference number: Z20992
 A:Accession: T31291
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-190 <ROM>
 A:Cross-references: UNIPROT:O85999; EMBL:AF079317; NID:G3378261; PID:G3378432; PIDN:ADDO
 C:Genetics:
 A:Genome: plasmid pNL1
 A:Note: orf1251

Query Match 66.1%; Score 37; DB 2; Length 190;
 Best Local Similarity 75.0%; Pred. No. 21;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 HOYSKLPW 8
 DB 114 HOYRKLW 121

RESULT 19

S47329
 OXAL protein precursor - Yeast (Saccharomyces cerevisiae)
 N:Alternate names: PBT1402 protein; protein YKR154W
 C:Species: Saccharomyces cerevisiae
 C:Date: 02-Dec-1994 #sequence_revision 02-Dec-1994 #ext_change 09-Jul-2004

C/Accession: S47329; S50657; S46384; A36328; S51575; S12291
R.Pratlje, E.
submitted to the EMBL Data Library, August 1993
A/Reference number: S47329
A/Accession: S47329
A/Molecule type: DNA
A/Residues: 1-402 <PRA>
A/Cross-references: UNIPROT:P39952; EMBL:X74456; NID:G521091; PID:G521092
R.Dietrich, F.S.
submitted to the EMBL Data Library, December 1994
A/Description: The sequence of S. cerevisiae cosmid 8229, 9115, 9132, 9981, and lambda
A/Reference number: S50657
A/Accession: S50657
A/Molecule type: DNA
A/Residues: 1-402 <DIE>
A/Cross-references: EMBL:U18917; NID:G603397; PID:G603394; MIPS:YER154W
R.Bonnefoy, N.; Chaiwet, F.; Hamel, P.; Slonimski, P.P.; Dujardin, G.
J. Mol. Biol. 239, 201-212, 1994
A/Title: OXA1, a Saccharomyces cerevisiae nuclear gene whose sequence is conserved from
A/Reference number: S46384; MUID:94254098; PMID:8196054
A/Accession: S46384
A/Molecule type: DNA
A/Residues: 1-107, 'R', 109-402 <BON>
A/Cross-references: EMBL:X77558
R.Ohmen, U.D.; Burke, K.A.; McEwen, J.E.
Mol. Cell. Biol. 10, 3027-3033, 1990
A/Title: Divergent overlapping transcripts at the PET122 locus in Saccharomyces cerevisiae
A/Reference number: A36328; MUID:90258894; PMID:2160592
A/Accession: A36328
A/Molecule type: DNA
A/Residues: 1-379 <OHM>
A/Cross-references: GB:X07558
R.Bauer, M.; Behrens, M.; Esser, K.; Michaelis, G.; Pratlje, E.
Mol. Gen. Genet. 245, 272-278, 1994
A/Title: PET1402, a nuclear gene required for proteolytic processing of cytochrome oxidase
A/Reference number: S51575; MUID:95115677; PMID:7816036
A/Accession: S51575
A/Molecule type: DNA
A/Residues: 1-402 <BAU>
A/Cross-references: EMBL:X74456; NID:G521091; PIDN:CAA52465.1; PID:G521092
A/Genetics: C/Genetics:
A/Genes: SGD:OXA1; PET1402
A/Cross-references: SGD:S0000956; MIPS:YER154W
A/Map position: 5R
A/Genome: nuclear
C/Function:
A/Description: required for a post-translational step in cytochrome oxidase biogenesis
A/Keywords: mitochondrion; transmembrane protein
F:108-316/Domain: stage III sporulation protein homology <SPOR>

Query Match 66.1%; Score 37; DB 2; Length 402;
Best Local Similarity 75.0%; Pred. No. 47;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 HOYSKLPW 8
DB 121 HVSGLPW 128

RESULT 20
T47364
Hypothetical protein F7M19.70 - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C/Accession: T47364
R.Nyakatura, G.; Fattmann, B.; Dauner, D.; Sterr, W.; Holland, R.; Welcheselgartner, M.;
Mayer, K.F.X.
submitted to the Protein Sequence Database, April 2000
A/Reference number: Z24458
A/Accession: T47364
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-585 <NYA>

A/Cross-references: UNIPROT:Q9M255; EMBL:AL136643
A/Experimental source: Cultivar Columbia; BAC clone F7M19
C/Genetics:
A/Map position: 3
A/Introns: 101/3; 233/2; 328/3; 361/2
A/Note: F7M19.70

Query Match 66.1%; Score 37; DB 2; Length 585;
Best Local Similarity 75.0%; Pred. No. 69;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QYKLPWT 9
DB 568 QYKLPWT 575

RESULT 21
H71475
probable chltr phosphoprotein - Chlamydia trachomatis (serotype D, strain UW3/Cx)
C/Species: Chlamydia trachomatis
C/Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 09-Jul-2004
C/Accession: H71475
R.Stephens, R.S.; Kaiman, S.; Lammell, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell,
Science 282, 754-759, 1998
A/Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia tract
A/Reference number: A71570; MUID:9900809; PMID:9784136
A/Accession: H71475
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-821 <ARN>
A/Cross-references: UNIPROT:O84749; GB:AE001346; GB:AE001273; NID:G3329203; PIDN:AAC6833;
A/Experimental source: serotype D, strain UW-3/Cx
C/Genetics:
A/Genes: CT744

Query Match 66.1%; Score 37; DB 2; Length 821;
Best Local Similarity 75.0%; Pred. No. 99;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 HOYSKLPW 8
DB 273 HALSKLPW 280

RESULT 22
C81739
conserved hypothetical protein TC0120 [imported] - Chlamydia muridarum (strain Nigg)
C/Species: Chlamydia muridarum, Chlamydia trachomatis Mopn
C/Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C/Accession: C81739
R.Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heideberg, J.F.; White, O.; Hickey, I.
C.; Dodson, R.; Gwin, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000
A/Title: Genome sequences of Chlamydia trachomatis Mopn and Chlamydia pneumoniae AR39.
A/Reference number: A81500; MUID:20150255; PMID:10684935
A/Accession: C81739
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-823 <RET>
A/Cross-references: UNIPROT:Q9PL10; GB:AE002279; GB:AE002160; NID:G7190148; PIDN:AAF3899E
A/Experimental source: strain Nigg (Mopn)
C/Genetics:
A/Genes: TC0120

Query Match 66.1%; Score 37; DB 2; Length 823;
Best Local Similarity 75.0%; Pred. No. 99;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 HOYSKLPW 8
DB 272 HALSKLPW 279

RESULT 23

A56248
sulfonilylurea receptor - golden hamster
C/Species: Mesocricetus auratus (golden hamster)
C/Date: 05-May-1995 #sequence_revision 05-May-1995 #text_change 02-Feb-2001
C/Accession: A56248
R/Aguiar-Bryan, L.; Nichols, C.G.; Wechsler, S.W.; Clement IV, J.P.; Boyd III, A.E.; Gd
Science 268, 423-426, 1995
A/Title: Cloning of the beta cell high-affinity sulfonilylurea receptor: a regulator of in
A/Reference number: A56248; MWID:95232552; PMID:7716547
A/Accession: A56248
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-1582 <AGU>
A/Cross-references: GB:L40623
C/Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology
C/Keywords: ATP; glycoprotein; nucleotide binding; P-loop
F/2-1582/Product: sulfonilylurea receptor #status experimental <MAT>
F/696-906/Domain: ATP-binding cassette homology <ABC1>
F/713-720/Region: nucleotide-binding motif A (P-loop)
F/1362-1555/Domain: ATP-binding cassette homology <ABC2>
F/1378-1386/Region: nucleotide-binding motif A (P-loop)
F/10/Binding site: carboxylate (Asn) (covalent) #status experimental

Query Match 66.1%; Score 37; DB 2; Length 1582;
Best Local Similarity 62.5%; Pred. No. 2e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HQYSLPMT 8
DB 991 HQRAKIPW 998

RESULT 24

S18731
Ig kappa chain V-J region (MSI-N17) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 19-Mar-1997 #sequence_revision 05-Dec-1998 #text_change 23-Jul-1999
C/Accession: S18731
R/Hiruma, T.; Takehita, S.; Yoshida, Y.; Yamagishi, H.
ImmunoL. Lett. 27, 19-24, 1991
A/Title: Structure of extrachromosomal circular DNAs generated by immunoglobulin light c
A/Reference number: S18731; MWID:91209891; PMID:1902191
A/Accession: S18731
A/Status: nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-103 <HIR>
A/Cross-references: EMBL:X54753; NID:G55294; PIDN:CA38555.1; PID:G55295
A/Experimental source: spleen, strain BALB/c-nu/nu
A/Note: The nucleotide sequence was submitted to the EMBL Data Library, October 1990
C/Complex: An immunoglobulin heterodimer subunit consists of two identical light (kappa) h
chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterodimer; immunoglobulin
F/11-85/Domain: immunoglobulin homology <IMM>
F/18-83/Disulfide bonds: #status predicted

Query Match 64.3%; Score 36; DB 2; Length 103;
Best Local Similarity 75.0%; Pred. No. 17;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 OYSLPMT 9
DB 85 QHSLPMT 92

RESULT 25

KWMS13
Ig kappa chain V region (PC2413) - mouse
C/Species: Mus musculus (house mouse)
C/Date: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change 09-Jul-2004
C/Accession: A01932
R/Weigert, M.; Galtman, L.; Loh, E.; Schilling, J.; Hood, L.

Nature 276, 785-790, 1978
A/Title: Rearrangement of genetic information may produce immunoglobulin diversity.
A/Reference number: A93204; MWID:79073152; PMID:103003
A/Accession: A01932
A/Molecule type: protein
A/Residues: 1-111 <WEI>

A/Cross-references: UNIPROT:P01657
C/Complex: An immunoglobulin heterodimer subunit consists of two identical light (kappa) h
chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterodimer
F/16-94/Domain: immunoglobulin homology <IMM>
F/23-92/Disulfide bonds: #status predicted

Query Match 64.3%; Score 36; DB 1; Length 111;
Best Local Similarity 55.6%; Pred. No. 18;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 HQYSLPMT 9
DB 93 HQYKVPMT 101

RESULT 26

D96681
Protein F1E22.2 [imported] - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C/Accession: D96681
R/Theologis, A.; Eckert, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Hulzar, L.
Nature 408, 816-820, 2000
A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.;
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luo, J.S.; Matt, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A/Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A/Reference number: A86141; MWID:21016719; PMID:11130712

A/Accession: D96681
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-518 <STO>
A/Cross-references: UNIPROT:Q9SH20; GB:AB005173; NID:G6686412; PIDN:AAF23846.1; GSPDB:GNK
C/Superfamily: Escherichia coli trypsin-like proteinase degS; GIGF domain homology; tryp
A/Map position: 1

Query Match 64.3%; Score 36; DB 2; Length 518;
Best Local Similarity 85.7%; Pred. No. 92;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HQYSLPMT 7
DB 387 HQYDKLP 393

RESULT 27

T26193
Hypothetical protein W05E10.4 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: T26193
R/Mortimore, B.
submitted to the EMBL Data Library, July 1996
A/Reference number: Z20168
A/Accession: T26193
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-588 <WIL>
A/Cross-references: UNIPROT:Q23176; EMBL:Z77670; PIDN:CAE01250.1; GSPDB:GN00023; CESP:W01

A:Experimental source: clone W05E10
C:Genetics:
A:Gene: CESP:W05E10.4
A:Map position: 5
A:Introns: 25/3; 37/2; 71/1; 103/2; 133/1; 299/3; 329/3; 426/3; 479/3; 504/3; 523/3
C:Superfamily: human alpha,alpha-trehalase

Query Match 64.3%; Score 36; DB 2; Length 588;
Best Local Similarity 71.4%; Pred. No. 1.1e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYSKLPWT 8
||:||||
Db 568 KYAKLPW 574

RESULT 28
PL0262
Ig kappa chain V region (anti-DNA, 60VK) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C:Accession: PL0262
R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Piletsky, D.; Marshak-Rothstein, A.
J. Exp. Med. 171, 265-297, 1990
A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic
A:Reference number: PL0231; PMID:90111618; PMID:2104919
A:Accession: PL0262
A:Molecule type: mRNA
A:Residues: 1-106 <SHL>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:1-23/Region: framework 1
F:16-90/Domain: immunoglobulin homology <IMM>
F:24-34/Region: complementarity-determining 1
F:35-49/Region: framework 2
F:50-56/Region: complementarity-determining 2
F:57-88/Region: framework 3
F:89-97/Region: complementarity-determining 3
F:98-106/Region: framework 4

Query Match 62.5%; Score 35; DB 2; Length 106;
Best Local Similarity 62.5%; Pred. No. 26;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 QYSKLPWT 9
||:||||
Db 90 QYASYPWT 97

RESULT 29
S26336
Ig light chain V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 21-Jan-2000
C:Accession: S26336
R:Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A:Title: Antibodies that are specific for a single amino acid interchange in a protein
A:Reference number: S26309; PMID:91341421; PMID:1908510
A:Accession: S26336
A:Molecule type: mRNA
A:Residues: 1-109 <STA>
A:Cross-references: EMBL:X59201
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:15-95/Domain: immunoglobulin homology <IMM>

Query Match 62.5%; Score 35; DB 2; Length 109;
Best Local Similarity 55.6%; Pred. No. 27;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 HOYSKLPWT 9
||:||||

Db 94 HQHSTPWT 102

RESULT 30
S40333
Ig kappa chain V-J region - human
C:Species: Homo sapiens (man)
C:Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40333
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin ch1 genes and their hypermutation.
A:Reference number: S40312; PMID:94080891; PMID:8258341
A:Accession: S40333
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-125 <RLB>
A:Cross-references: EMBL:X72443; NID:G441354; PIDN:CAA5111.1; PID:G441355
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:34-108/Domain: immunoglobulin homology <IMM>

Query Match 62.5%; Score 35; DB 2; Length 125;
Best Local Similarity 62.5%; Pred. No. 31;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 QYSKLPWT 9
||:||||
Db 108 QYNSYPWT 115

RESULT 31
H69405
hypothetical protein AF1249 - Archaeoglobus fulgidus
C:Species: Archaeoglobus fulgidus
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C:Accession: H69405
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, J.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kinkness, E.F.; Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A:Authors: Urtreback, T.; Cotton, M.D.; Spriggs, T.; Artlach, P.; Kaine, B.P.; Sykes, S.A.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo
A:Reference number: A69250; PMID:98049343; PMID:9389475
A:Accession: H69405
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-140 <RLB>
A:Cross-references: UNIPROT:Q29019; GB:AE001018; GB:AE000782; NID:G2689341; PIDN:AA9000;
C:Superfamily: Archaeoglobus fulgidus hypothetical protein AF1249

Query Match 62.5%; Score 35; DB 2; Length 140;
Best Local Similarity 66.7%; Pred. No. 35;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 HOYSKLPWT 9
||:||||
Db 36 HNGIKLPWT 44

RESULT 32
B87293
hydrolyase, probable [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 12-Jul-2004
C:Accession: B87293
R:Nierman, W.C.; Feldblum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.F.
B.; Laub, M.T.; Deboy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: AB7249; PMID:21173698; PMID:11259647

A/Accession: B87293
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-296 <STO>
A/Cross-references: UNIPROT:Q9AB76; GB:AE005673; NID:G13421508; PIDN:AAK2342.1; GSPDB:G
C/Genetics:
A/Gene: CC0355
C/Superfamily: tropinesterase

Query Match 62.5%; Score 35; DB 2; Length 296;
Best Local Similarity 71.4%; Pred. No. 78;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 YSKLPW 9
Db 144 YAKAPWT 150

RESULT 33

T27004

hypothetical protein Y48B6A.14 - *Caenorhabditis elegans*C/Species: *Caenorhabditis elegans*

C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C/Accession: T27004

A/Reference number: Z20297

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-312 <WIL>

A/Cross-references: UNIPROT:Q9U2A0; EMBL:AL110490; NID:el542263; PIDN:CAB54448.1; CESP:Y

A/Experimental source: clone Y48B6A

C/Genetics:

A/Gene: CESP:Y48B6A.14

A/Introns: 132/1; 210/1; 288/3

Query Match 62.5%; Score 35; DB 2; Length 312;
Best Local Similarity 83.3%; Pred. No. 82;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 YSKLPW 8
Db 19 YSKLPW 24

RESULT 34

B83527

hypothetical protein PA0955 [imported] - *Pseudomonas aeruginosa* (strain PA01)C/Species: *Pseudomonas aeruginosa*

C/Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004

C/Accession: B83527

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-318 <STO>

A/Cross-references: UNIPROT:Q91503; GB:AE004529; GB:AE004091; NID:G946851; PIDN:AA0434

A/Experimental source: strain PA01

C/Genetics:

A/Gene: PA0955

A/Introns: 132/1; 210/1; 288/3

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-318 <STO>

A/Cross-references: UNIPROT:Q91503; GB:AE004529; GB:AE004091; NID:G946851; PIDN:AA0434

A/Experimental source: strain PA01

C/Genetics:

A/Gene: PA0955

Query Match 62.5%; Score 35; DB 2; Length 318;
Best Local Similarity 71.4%; Pred. No. 84;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 YSKLPW 8
Db 19 YSKLPW 24

Db 166 EYSSLPW 172

RESULT 35

T46096

hypothetical protein T25B15.30 - *Arabidopsis thaliana*C/Species: *Arabidopsis thaliana* (mouse-ear cress)

C/Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004

C/Accession: T46096

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-376 <ALC>

A/Cross-references: UNIPROT:Q9FT56; EMBL:AL132972

A/Experimental source: cultivar Columbia; BAC clone T25B15

C/Genetics:

A/Map position: 3

A/Introns: 31/1; 51/2; 60/3; 76/2; 106/3; 163/1; 191/2; 226/3; 252/1; 274/3; 298/1; 326/1

Query Match 62.5%; Score 35; DB 2; Length 376;
Best Local Similarity 83.3%; Pred. No. 1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 YSKLPW 8
Db 83 YSKLPW 88

RESULT 36

T18945

hypothetical protein C05C10.4 - *Caenorhabditis elegans*C/Species: *Caenorhabditis elegans*

C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C/Accession: T18945

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-413 <WIL>

A/Cross-references: UNIPROT:Q09451; EMBL:Z48178; PIDN:CA88205.1; GSPDB:GN00020; CESP:CO

A/Experimental source: clone C05C10

C/Genetics:

A/Gene: CESP:C05C10.4

A/Map position: 2

A/Introns: 31/3; 96/3; 128/1; 155/3; 185/3; 255/1; 313/3; 360/3; 407/3

Query Match 62.5%; Score 35; DB 2; Length 413;
Best Local Similarity 83.3%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 YSKLPW 8
Db 225 YAKLPW 230

RESULT 37

A89761

hypothetical protein [imported] - *Staphylococcus aureus* (strain N315)C/Species: *Staphylococcus aureus*

C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004

C/Accession: A89761

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-413 <WIL>

A/Cross-references: UNIPROT:Q09451; EMBL:Z48178; PIDN:CA88205.1; GSPDB:GN00020; CESP:CO

A/Experimental source: clone C05C10

C/Genetics:

A/Gene: CESP:C05C10.4

A/Map position: 2

Query Match 62.5%; Score 35; DB 2; Length 413;
Best Local Similarity 83.3%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

A:Reference number: A89758; MUID:21311952; PMID:11418146
 A:Accession: A89761
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-431 <KUR>
 A:Cross-references: UNIPROT:Q9XB68; GB:BA000018; PID:G13699942; PIDN:BA841241.1; GSPDB:C
 A:Experimental source: strain N315
 C:Genetics:
 A:Gene: SA0024

Query Match 62.5%; Score 35; DB 2; Length 431;
 Best Local Similarity 83.3%; Pred. No. 1.2e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 YSKLPW 8
 |||:
 Db 77 YSKVPW 82

RESULT 38

T44138
 hypothetical protein [imported] - Staphylococcus aureus (fragment)

C:Species: Staphylococcus aureus

C>Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004

C:Accession: T44138

R:Itto, T.; Katayama, Y.; Hiramatsu, K.

Antimicrob. Agents Chemother. 43, 1449-1458, 1999

A:Title: Cloning and nucleotide sequence determination of the entire mec DNA of pre-meth

A:Reference number: Z22733; MUID:99278010; PMID:10348769

A:Accession: T44138

A:Status: preliminary; translated from GB/EMBL/DBD

A:Molecule type: DNA

A:Residues: 1-440 <ITO>

A:Cross-references: UNIPROT:Q9XB68; EMBL:D86934; PIDN:BA82240.1

A:Experimental source: strain N315

Query Match 62.5%; Score 35; DB 2; Length 440;
 Best Local Similarity 83.3%; Pred. No. 1.2e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 YSKLPW 8
 |||:
 Db 86 YSKVPW 91

RESULT 39

T18221

chromosome condensation regulator protein - yeast (Candida albicans)

C:Species: Candida albicans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T18221

R:Barrell, B.G.; Rajandream, M.A.

submitted to the EMBL Data Library, November 1998

A:Reference number: Z18831

A:Accession: T18221

A:Status: preliminary; translated from GB/EMBL/DBD

A:Molecule type: DNA

A:Residues: 1-492 <BAR>

A:Cross-references: UNIPROT:O94013; EMBL:AL033396; PIDN:CAA21948.1

C:Genetics:

A:Note: Rc1-like

C:Superfamily: pheromone response pathway component SRM1

Query Match 62.5%; Score 35; DB 2; Length 492;
 Best Local Similarity 85.7%; Pred. No. 1.3e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYSKLP 7
 |||:
 Db 31 HSYSKLP 37

RESULT 40

JC5762
 cytokine-inducible SH2 protein 4 - human

C:Species: Homo sapiens (man)

C>Date: 24-Jan-1998 #sequence_revision 13-Mar-1998 #text_change 09-Jul-2004

C:Accession: JC5762

R:Masuhara, M.; Sakamoto, H.; Matsunoto, A.; Suzuki, R.; Yasukawa, H.; Mitsu, K.; Wakio

Biochem. Biophys. Res. Commun. 239, 439-446, 1997

A:Title: Cloning and characterization of novel CIS family genes.

A:Reference number: JC5760; MUID:98008857; PMID:9344848

A:Accession: JC5762

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-535 <MAS>

A:Cross-references: UNIPROT:O14544; DDBJ:AB006968; MTD:G2463524; PIDN:BA822538.1; PID:dl

C:Comment: This protein plays a role in the negative regulation of cytokine signaling by

F384-461/Domain: SH2 homology <SH2>

Query Match 62.5%; Score 35; DB 2; Length 535;
 Best Local Similarity 62.5%; Pred. No. 1.4e+02;
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 HOYSKLP 8
 |||:
 Db 130 HHSKLP 137

Search completed: December 17, 2004, 18:30:16
 Job time : 3.53933 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 17, 2004, 18:29:23 ; Search time 26.8969 Seconds
(Without alignments)
192.513 Million cell updates/sec

Title: US-10-089-500-8
Perfect score: 56
Sequence: 1 HQYSKLPT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues
Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02:*
1: uniProt_sprot:*
2: uniProt_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	78.6	107	Q9JL84	Q9JL84 mus musculu
2	43	76.8	770	Q9TOY1	Q9TOY1 lactobacill
3	41	73.2	107	AAR11015	AAR11015 mus muscu
4	41	73.2	572	Q6BN22	Q6BN22 debaryomyce
5	40	71.4	623	Q8XVB0	Q8XVB0 ralsctonia s
6	39	69.6	108	KVIR_HUMAN	P01610 homo sapien
7	39	69.6	258	Q8YSA0	Q8YSA0 anabaena sp
8	39	69.6	351	Q9VST8	Q9VST8 dirosophila
9	38	67.9	288	Q9XEP0	Q9XEP0 streptomyce
10	38	67.9	336	Q7NAA3	Q7NAA3 photorhabdu
11	38	67.9	349	Q9GKJ6	Q9GKJ6 sus scrofa
12	38	67.9	353	Q13629	Q13629 schizosach
13	38	67.9	386	Q6FOG0	Q6FOG0 candida gla
14	38	67.9	389	Q89UG7	Q89UG7 bradyrhizob
15	38	67.9	434	Q7SB85	Q7SB85 ashbya goss
16	38	67.9	434	AAS51605	AAS51605 ashbya goss
17	38	67.9	581	CHLE_RABIT	P11927 oryctolagus
18	38	67.9	597	Q9JKC1	Q9JKC1 rattus norv
19	38	67.9	602	CHLE_HUMAN	P06276 homo sapien
20	38	67.9	603	CHLE_MOUSE	Q03311 mus musculu
21	38	67.9	603	Q90ZK8	Q90ZK8 gallus gall
22	38	67.9	603	BAC34196	BAC34196 mus muscu
23	38	67.9	657	Q6MT24	Q6MT24 bdellovibri
24	38	67.9	657	CAE78158	CAE78158 bdellovibri
25	38	67.9	658	Q8MY38	Q8MY38 papilio xuc
26	38	67.9	1036	Q6CJY8	Q6CJY8 kluyveromyc
27	38	67.9	1289	MCE_REOVD	P11079 reovirus ty
28	38	67.9	1289	Q91RA1	Q91RA1 reovirus ty
29	37	66.1	95	AAR11062	AAR11062 mus muscu
30	37	66.1	99	AAR11071	AAR11071 mus muscu
31	37	66.1	108	KVIB_HUMAN	P01594 homo sapien

32	37	66.1	108	Q9CTV5	Q9CTV5 mus musculu
33	37	66.1	134	KV4C_HUMAN	P06314 homo sapien
34	37	66.1	134	Q8VDD0	Q8VDD0 mus musculu
35	37	66.1	190	Q85999	Q85999 sphingomona
36	37	66.1	242	Q9PU09	Q9PU09 latimeria c
37	37	66.1	245	Q8UTP6	Q8UTP6 brachydanio
38	37	66.1	330	Q6MOC7	Q6MOC7 bdellovibri
39	37	66.1	330	CAE78520	CAE78520 bdellovibri
40	37	66.1	388	Q9PLA1	Q9PLA1 arabidopsis
41	37	66.1	402	OXAI_YEAST	P39952 saccharomyc
42	37	66.1	402	Q46434	Q46434 chlamydia t
43	37	66.1	444	Q56955	Q56955 human papil
44	37	66.1	566	Q7QFL1	Q7QFL1 anopheles g
45	37	66.1	585	Q9M255	Q9M255 arabidopsis

ALIGNMENTS

RESULT 1					
ID	Q9JL84	PRELIMINARY;	PRT;	107 AA.	
AC	Q9JL84;				
DT	01-OCT-2000 (TREMBlrel. 15, Created)				
DT	01-OCT-2000 (TREMBlrel. 15, Last sequence update)				
DT	01-OCT-2003 (TREMBlrel. 25, Last annotation update)				
DE	Anti-myosin immunoglobulin light chain variable region (Fragment).				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=BLB/C;				
RX	MEDLINE=20448942; PubMed=10992488;				
RA	Maikael S., Liao L., Cunningham M.W., Diamond B.;				
RT	"T-Cell-dependent antibody response to the dominant epitope of streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive with cardiac myosin."				
RI	Infect. Immun. 68:5803-5808(2000).				
DR	EMBL; AF206022; AAF69320.1; -.				
DR	HSSP; P01594; 1UV5.				
DR	InterPro; IPR007110; IG_1like.				
DR	InterPro; IPR003596; IG_V.				
DR	Pfam; PF00047; IG_1.				
DR	SMART; SM00406; IG_1.				
DR	PROSITE; PS50835; IG_LIKE; 1.				
FT	NON_TER 1				
FT	NON_TER 107				
FT	SEQUENCE 107 AA; 11648 MW; ACF9B1253ACA1B5D CRC64;				
Query Match					
Best Local Similarity		78.6%;	Score 44;	DB 2;	Length 107;
Matches 7;		Conservative	Pred. No. 3.6;	Mismatches 1;	Indels 0;
Gaps 0;					
Qy	2 QYSKLPT 9				
Db	90 QYSKLPT 97				
RESULT 2					
ID	Q9TOY1	PRELIMINARY;	PRT;	770 AA.	
AC	Q9TOY1;				
DT	01-MAY-2000 (TREMBlrel. 13, Created)				
DT	01-MAY-2000 (TREMBlrel. 13, Last sequence update)				
DT	01-MAY-2004 (TREMBlrel. 26, Last annotation update)				
DE	Putative primase.				
OS	Lactobacillus casei bacteriophage A2.				
OC	Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.				
OX	NCBI_TaxID=51369;				
RN	[1]				

RP SEQUENCE FROM N.A.
RX MEDLINE=97197195; PubMed=9044284;
RA Garcia P., Alonso J.C., Suarez J.E.;
RT "Molecular Analysis of the cos Region of the Lactobacillus casei
RT Bacteriophage A2. Gene product 3, gp3, specifically binds to its
RT downstream cos region."; Mol. Microbiol. 23:505-514 (1997).
RN (12)
RP SEQUENCE FROM N.A.
RX MEDLINE=98317291; PubMed=9642205;
RA Ladero V., Garcia P., Bascaran V., Herrero M., Alvarez M.,
RA Suarez J.E.;
RT "Identification of the repressor-encoding gene of the Lactobacillus
RT Bacteriophage A2."; J. Bacteriol. 180:3474-3476 (1998).
RN (3)
RP SEQUENCE FROM N.A.
RX MEDLINE=98445458; PubMed=9770432;
RA Alvarez M.A., Herrero M., Suarez J.E.;
RT "The Site-Specific Recombination system of the Lactobacillus spp
RT Bacteriophage A2 integrates in Gram Positive and Gram Negative
RT Bacteria."; J. Bacteriol. 180:193-193 (1998).
RN (4)
RP SEQUENCE FROM N.A.
RX MEDLINE=20351728; PubMed=10891412;
RA Moscoso M., Suarez J.E.;
RT "Characterization of the DNA replication module of bacteriophage A2
RT and use of its origin of replication as a defence against infection
RT during milk fermentation by Lactobacillus casei."; J. Bacteriol. 180:111-111 (2000).
RN (5)
RP SEQUENCE FROM N.A.
RX MEDLINE=99214330; PubMed=10196287;
RA Garcia P., Ladero V., Alonso J.C., Suarez J.E.;
RT "Cooperative interaction of CI protein regulates lysogeny of
RT Lactobacillus casei by bacteriophage A2."; J. Virol. 73:3920-3929 (1999).
RN (6)
RP SEQUENCE FROM N.A.
RA Ladero V., Garcia P., Alonso J.C., Suarez J.E.;
RT "A2 Cro, the lysogenic cycle repressor, specifically binds to the
RT genetic switch region of Lactobacillus casei bacteriophage A2."; J. Bacteriol. 184:6026-6036 (2002).
RN (8)
RP SEQUENCE FROM N.A.
RA Garcia P., Ladero V., Suarez J.E.;
RT Submitted (May-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ251789; CAB63672.1; -
DR InterPro; IPR004968; Pox D5.
DR InterPro; IPR006500; Primase_C.
DR Pfam; PF03288; Pox D5; 1.
DR TIGRfam; TIGR01613; primase_Cterm; 1.
SQ SEQUENCE 770 AA; 88233 MW; 382B4F853010DCB CRC64;

Query Match 76.8%; Score 43; DB 2; Length 770;
Best Local Similarity 55.6%; Pred. No. 40;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HOYSKLPWT 9
|:|:|:|:
Db 27 HKYTKIPWS 35

RESULT 3

AAR1015
ID AAR1015 PRELIMINARY; PRT; 107 AA.
AC AAR1015;
DT 02-MAR-2004 (TREMBLrel. 27, Created)
DT 02-MAR-2004 (TREMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TREMBLrel. 27, Last annotation update)
DE ANA Immunoglobulin kappa light chain (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=B6.S1el; TISSUE=Spleen;
RA Liang Z., Xie C., Chen C., Kreska D., Hsu K., Zhou J.X., Mohan C.;
RT "Antinuclear autoantibodies from B6.S1el mice."
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY436855; AAR1015.1; -
FT NON_TER 1 107
FT NON_TER 1 107
SQ SEQUENCE 107 AA; 11408 MW; 0AAFB831B786EAFD CRC64;

Query Match 73.2%; Score 41; DB 2; Length 107;
Best Local Similarity 66.7%; Pred. No. 13;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 HOYSKLPWT 9
|:|:|:|:
Db 82 HQMSYPTWT 90

RESULT 4
ID 06BN22 PRELIMINARY; PRT; 572 AA.
AC 06BN22;
DT 01-OCT-2004 (TREMBLrel. 28, Created)
DT 01-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT 01-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE Similarities with sp||P47168 Saccharomyces cerevisiae YXR136C.
GN ORFNames=DEHAOP01045g;
OS Debaryomyces hansenii (Yeast) (Torulaopora hansenii).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Debaryomyces.
OX NCBI_TaxID=4959;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=CBS767;
RG GENOLEVURES;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA LaFontaine I., de Montigny J., Marcq C., Neuveglise C., Talla E.,
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Baray S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
RA Boismare A., Boyer J., Cattolico L., Confantolero F., de Darvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Gropi A.,
RA Hantaye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Kozul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Pottier S., Richard G.F., Straub M.L., Suleau A.,
RA Swenene D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Galliardin C., Weisenbach J.,
RA Wincker P., Souciet J.L.;
RT "Genome evolution in yeasts."
RL Nature 430:35-44 (2004).
RN (2)
RP SEQUENCE FROM N.A.
RC STRAIN=CBS767;
RG Genoscope;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR382138; CAG88702.1; -
SQ SEQUENCE 572 AA; 65217 MW; 73D939503DEB2E8D CRC64;

Query Match 73.2%; Score 41; DB 2; Length 572;

Best Local Similarity 66.7%; Pred. No. 69;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 HOYSKLPMT 9
Db 155 HNHKLPMT 163

RESULT 5
O8XVB0 PRELIMINARY; PRT; 623 AA.

AC O8XVB0
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE PROBABLE GAMMA-GLUTAMYLTRANSPETIDASE PROTEIN (EC 2.3.2.2).
GN Name=gg2; Synonyms=RS00172; OrderedLocustName=RS0221;
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Ralstonia.
OX NCBI_TaxID=305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GM11000;
RX MEDLINE=21681879; PubMed=11823852;
RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
RA Arlat M., Billault A., Broctier P., Camus J.C., Catolico L.,
RA Chandler M., Choine N., Claudel-Renard C., Cunac S., Demange N.,
RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schlex T.,
RA Sigler P., Theault P., Whalen M., Wincker P., Levy M.,
RA Weissenbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum";
RL Nature 415:497-502(2002).
DR EMBL; AL646072; CAD16628.1; -.
DR MEROPS; T03.001; -.
DR GO; GO:0008415; F:acyltransferase activity; IEA.
DR GO; GO:0008440; F:gamma-glutamyltransferase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR InterPro; IPR000101; GGT peptidase.
DR Pfam; PF01019; G-Glu transferase; 1.
DR PRINTS; PR01210; GGTTRANSFERASE.
DR Acyltransferase; Complete proteome; Transferase.
KW ACyltransferase; Complete proteome; Transferase.
SQ SEQUENCE 623 AA; 65009 MW; 2201015F85FEA576 CRC64;

Query Match 71.4%; Score 40; DB 2; Length 623;
Best Local Similarity 75.0%; Pred. No. 1,1e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 OYSKLPMT 9
Db 181 RYKLPMT 188

RESULT 6
KXIR HUMAN STANDARD; PRT; 108 AA.
AC P01610;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE IG kappa chain V-I region WEA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=83273707; PubMed=6410398;
RA Goni F., Frangione B.;
RT "Amino acid sequence of the Fv region of a human monoclonal IgM
(protein WEA) with antibody activity against 3',4'-pyruvylated galactose
in Klebsiella polysaccharides K30 and K33.";
Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).

CC -1- MISCELLANEOUS: This chain was obtained from a monoclonal antibody
CC against 3',4'-pyruvylated galactose and isolated from a patient with
CC Waldenstrom's macroglobulinemia.
DR PIR; A01876; K1HWE.
DR HSP; P80362; 1WTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region;
KW Monoclonal antibody.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 34 Complementarity-determining-1.
FT DOMAIN 35 49 Framework-2.
FT DOMAIN 50 56 Complementarity-determining-2.
FT DOMAIN 57 88 Framework-3.
FT DOMAIN 89 97 Complementarity-determining-3.
FT DOMAIN 98 107 Framework-4.
FT DISULFID 23 88 By similarity.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11840 MW; 9249B61F0945618C CRC64;

Query Match 69.6%; Score 39; DB 1; Length 108;
Best Local Similarity 75.0%; Pred. No. 30;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 OYSKLPMT 9
Db 90 QYSSFPMT 97

RESULT 7
O8YSAO PRELIMINARY; PRT; 258 AA.
AC O8YSAO;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Beta-carotene ketolase.
GN OrderedLocustName=alx13189;
OS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxID=103690;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21595285; PubMed=11759840;
RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
RA Matanabe A., Iriyuchi M., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakazaki N., Shimo S., Sugimoto M., Takazawa M., Yamada M.,
RA Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
cyanobacterium Anabaena sp. strain PCC 7120.";
RL DNA Res. 8:205-213(2001).
DR EMBL; AF003592; BAB74888.1; -.
DR PIR; AF2204; AF2204.
DR GO; GO:0016701; F:oxidoreductase activity; acting on single d. . .; IEA.
DR GO; GO:0016119; P:carotene metabolism; IEA.
DR InterPro; IPR011393; Carotene_ketolas.
DR InterPro; IPR005804; FA_decat.
DR InterPro; IPR010257; FA_decat_sub.
DR Pfam; PF00487; FA_decatase; 1.
DR PIRSF; PIRSF027840; Carotene_ketolas; 1.
DR ProDom; PD001081; FA_decat_sub; 1.
KW Complete proteome.
SQ SEQUENCE 258 AA; 30313 MW; 8F8C8BAFC8F8F61B CRC64;

Query Match 69.6%; Score 39; DB 2; Length 258;
Best Local Similarity 62.5%; Pred. No. 71;

Qy	Matches	5;	Conservative	2;	Mismatches	1;	Indels	0;	Gaps
Db	1	HQSKLFP 8							
	240	HEYPOLFP 247							
RESULT 8									
Q9VST8	AC	PRELIMINARY;							
Q9VST8	Q9VST8	PRT;					351	AA.	
DT	01-MAY-2000	(TREMBLrel. 13, Created)							
DT	01-MAY-2000	(TREMBLrel. 13, Last sequence update)							
DT	05-JUL-2004	(TREMBLrel. 27, Last annotation update)							
DE	CG4942-PA	(LDJ38503p).							
OS	ORFNames=CG4942;								
OS	Drosophila melanogaster (fruit fly).								
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;								
OC	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;								
OC	Ephydroidea; Drosophilidae; Drosophila.								
CX	NCBI_Taxid=7227;								
RE	[1]								
RP	SEQUENCE FROM N.A.								
RX	MEDLINE=20196006; PubMed=10731132;								
RA	Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,								
RA	Amaratunga P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,								
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,								
RA	Sutton G.C., Wortman J.R., Blandell M.D., Zhang Q., Chen L.X.,								
RA	Brandon R.C., Rogers Y.H., Blaziel R.G., Chang M., Pfeiffer B.D.,								
RA	Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,								
RA	Abtill J.F., Agbayanl A., An H.J., Andrews-Pfannkuch C., Baldwin D.,								
RA	Ballew R.M., Baau A.B., Baxendale U., Bayraktaroglu L., Beasley E.M.,								
RA	Besson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,								
RA	Bockova D., Botchan M.R., Bouck J., Brokstein P., Bottler P.,								
RA	Buttis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,								
RA	Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,								
RA	de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,								
RA	Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,								
RA	Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Flischmann W.,								
RA	Fosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glaser K.,								
RA	Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,								
RA	Harris N.D., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,								
RA	Hostin D., Houston K.A., Howland T.J., Wei M.H., Ileguam C.,								
RA	Jatall W., Kalush F., Kapten G.H., Ke Z., Kennison J.A., Ketchum K.A.,								
RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulip D., Lai Z.,								
RA	Laake P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,								
RA	Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,								
RA	Meikulov G., Mishina N.V., Mobarry C., Morris J., Mosheret A.,								
RA	Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,								
RA	Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,								
RA	Palazolo M., Piltman G.S., Pan S., Pollard J., Puti V., Reese M.G.,								
RA	Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,								
RA	Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,								
RA	Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,								
RA	Svirskas R., Tector C., Turner R., Venner E., Wang A.H., Wang X.,								
RA	Wang Z.Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,								
RA	Williams S.M., Woodgett, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,								
RA	Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,								
RA	Zhang X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,								
RA	Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;								
RT	"The genome sequence of Drosophila melanogaster.";								
RL	Science 287:2185-2195(2000).								
RP	SEQUENCE FROM N.A.								
RX	MEDLINE=22426065; PubMed=12537568;								
RA	Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W.,								

Query Match	Best Local Similarity	Score 39;	DB 2;	Length 351;
Matches 6;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
OY	1 HQYSLPWP 8			
DB	79 HDYSLPWP 86			
RESULT 9				
Q9X8F0	PRELIMINARY;	PRT;	288 AA.	
AC	Q9X8F0;			
DT	01-NOV-1999 (TREMBLrel. 12, Created)			
DT	01-NOV-1999 (TREMBLrel. 12, Last sequence update)			
DE	01-JUN-2003 (TREMBLrel. 24, Last annotation update)			
GN	OrderedLocustNames=SCO3277; ORNNames=SCB39.27c;			
OC	Striptomyces coelicolor.			
OC	Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;			

OC Streptomycineae; Streptomycetaceae; Streptomycetes.
 OX NCBI_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2) / M145;
 RX MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;
 RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
 RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieiser H.,
 RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
 RA Croft A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
 RA Huang C.-H., Kieiser T., Larke L., Murphy L.D., Oliver K., O'Neill S.,
 RA Rabinovitch E., Rajandream M.A., Rutherford K.M., Rutter S.,
 RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
 RA Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,
 RA Hopwood D.A.;
 RT "Complete genome sequence of the model actinomycete Streptomyces
 coelicolor A3(2)";
 RL Nature 417:141-147(2002).
 DR EMBL; AL93915; CAB4035.1; -.
 DR PIR; T36237; T36237.
 DR GO; GO:0016740; P:transferase activity; IEA.
 DR InterPro; IPR002575; APH trans.
 DR InterPro; IPR011009; Kinase-like.
 DR Pfam; PF01636; APH; 1.
 KW Complete proteome; Transferase.
 SQ SEQUENCE 288 AA; 31415 MW; 40B5BCE48A42B5C CRC64;

Query Match 67.9%; Score 38; DB 2; Length 288;
 Best Local Similarity 75.0%; Pred. No. 1.2e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 HOYSKLPW 8
 Db 256 HYSKLPW 263

RESULT 10
 ID Q7NAA3 PRELIMINARY; PRT; 336 AA.
 AC Q7NAA3;
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Complete genome; segment 1/17.
 GN OrderedLocustNames=plu0031;
 OS Photorhabdus luminescens (subsp. laumondii).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Photorhabdus.
 OX NCBI_TaxID=141679;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TT01;
 RX MEDLINE=22957627; PubMed=14528314;
 RA Duchaud E., Ruenick C., Frangeul L., Buchrieser C., Givaudan A.,
 RA Taouart S., Bocs S., Bouraux-Bude C., Chandelier M., Chariot J.-F.,
 RA Dasse E., Derose R., Deruelle S., Freysinet G., Gaudreau S.,
 RA Zouine M., Lancia A., Powell K., Sigler P., Vincent R., Wingate V.,
 RA "The genome sequence of the entomopathogenic bacterium Photorhabdus
 luminescens";
 RT Nat. Biotechnol. 21:1307-1313(2003).
 RL EMBL; BX571859; CAE12326.1; -.
 DR Photoclat; plu0031; -.
 DR InterPro; IPR000276; GPCR Rhodosp.
 DR PROSITE; PS00237; G_PROTEIN_RECPT_P1_1; UNKNOWN_1.
 KW Complete proteome.
 SQ SEQUENCE 336 AA; 38412 MW; 7EB8746696E2B8B6 CRC64;

Query Match 67.9%; Score 38; DB 2; Length 336;
 Best Local Similarity 75.0%; Pred. No. 1.4e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 2 QYSKLPWT 9

Db 104 QYHNPWT 111

RESULT 11
 ID Q9GKJ6 PRELIMINARY; PRT; 349 AA.
 AC Q9GKJ6;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Butyrylcholinesterase (Fragment).
 GN Name=BCH;
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21419000; PubMed=11528129;
 RA Van Poucke M., Verle M., Tuggle C., Plumi F., Genet C.,
 RA Van Zeveren A., Peelman L.J.;
 RT "Integration of porcine chromosome 13 maps";
 RL Cytogenet. Cell Genet. 93:297-303(2001).
 CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
 DR EMBL; AF222914; AAC41127.1; -.
 DR GO; GO:0003824; F:catalytic activity; IEA.
 DR GO; GO:0004104; F:cholinesterase activity; IEA.
 DR InterPro; IPR002018; Carboxylesterase.
 DR InterPro; IPR000997; Cholinesterase.
 DR InterPro; IPR000379; Ser_ester.
 DR Pfam; PF00135; Coesterase; 1.
 DR PRINTS; PR00878; CHOLINESTRASE.
 DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
 FT NON_TER 1 1
 FT NON_TER 349 349
 SQ SEQUENCE 349 AA; 39061 MW; D6354B14725B58 CRC64;

Query Match 67.9%; Score 38; DB 2; Length 349;
 Best Local Similarity 75.0%; Pred. No. 1.5e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HOYSKLPW 8
 Db 311 HRSKLPW 318

RESULT 12
 ID O13629 PRELIMINARY; PRT; 363 AA.
 AC O13629;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE LIPOTE-PROTEIN LIGASE A (SPBC17A3.09c protein) (P1037 protein).
 GN Name=PL037; Synonym=SPBC17A3.09c;
 OS Schizosaccharomyces pombe (fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetaceae; Schizosaccharomycetaceae;
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972 h-;
 RX MEDLINE=20089027; PubMed=10620777;
 RA Machida M., Yamazaki S., Kunihito S., Tanaka T., Kuehida N., Jinno K.,
 RA Haikawa Y., Yamazaki J., Yamamoto S., Sekine M., Oguchi A., Nagai Y.,
 RA Sakai M., Aoki K., Ogura K., Kudoh Y., Kikuchi H., Zhang M.Q.,
 RA Yanagida M.;
 RT "A 38 kb segment containing the cdc2 gene from the left arm of fission
 yeast chromosome II: sequence analysis and characterization of the
 genomic DNA and cDNAs encoded on the segment.";
 RL Yeast 16:71-80(2000).

```

RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=972 h-;
RA Director-General of Biotechnology Center, Kuehida N., Machida M.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=972h-;
RA MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.,
RA Collins M., Connor R., Cronin A., Davis P., Felwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagsels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S., Warren T., Whitehead S.,
RA Woodward J., Volkart G., Aert R., Robben J., Grymoprez B.,
RA Wellens I., Vanstreels E., Rieger M., Schaefer M., Muller-Auer S.,
RA Gabel C., Fuchs M., Dusterhoft A., Fritzc C., Holzer E., Moestl D.,
RA Hilbert H., Borzym K., Langer I., Beck A., Lehnach H., Reinhardt R.,
RA Fohl T.M., Eger P., Zimmermann W., Wedler H., Wambut R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreyan S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucan M., Rochet M., Gallardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsberg S.L.,
RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RA "The genome sequence of Schizosaccharomyces pombe.";
RT Nature 415:871-880(2002).
RL EMBL; AB004537; BAA21417.1; -;
DR EMBL; AL109652; CAB51768.1; -;
DR PIR; T39701; T39701.
DR GenedB; SPombe; SPBC17A3.09c; -;
DR GO; GO:0016874; P:lipase activity; IEA.
DR GO; GO:0006464; P:protein modification; IEA.
DR InterPro; IPR004143; BPL_L1PA_L1PB.
DR InterPro; IPR004562; Lipolytrans.
DR Pfam; PF03099; BPL_L1PA_L1PB.1.
DR TIGRfam; TIGR00545; Lipolytrans; 1.
DR LIGASE.
KW SEQUENCE 363 AA; 40651 MW; A6BF82EB7CB8EB13 CRC64;
SQ
Query Match 67.9%; Score 38; DB 2; Length 363;
Best Local Similarity 55.6%; Pred. No. 1.5e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 HOYSKLPWT 9
DB 322 HELUSIPWT 330

```

```

RG GENOLEVURES.
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talla E.,
RA Goffard N., Fiangoul L., Aigle M., Anthonard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
RA Boissrame A., Boyer J., Cattolico L., Contandoleri F., de Darvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dunazet H., Groppi A.,
RA Hantraye F., Hennequin C., Jannaux N., Joyet P., Kachouri R.,
RA Kerrest A., Kozul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Micaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
RA Pellens S., Potier S., Richard G.F., Straub M.L., Suleau A.,
RA Swenne D., Tekla F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gallardin C., Weissendach J.,
RA Wincker P., Souciet J.L.;
RT "Genome evolution in yeasts.";
RL Nature 430:35-44(2004).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to the OXA1/OXA family.
DR EMBL; CR380955; CAG60471.1; -;
DR InterPro; IPR01708; 60kDa_innermem.
DR Pfam; PF02096; 60KD_IMP; 1.
KW Transmembrane.
SQ SEQUENCE 386 AA; 43188 MW; 55DBD0BC41423962 CRC64;
Query Match 67.9%; Score 38; DB 2; Length 386;
Best Local Similarity 75.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 HOYSKLPW 8
DB 110 HAYSGLPW 117

```

```

RESULT 13
Q6FOGO PRELIMINARY; PRT; 386 AA.
ID Q6FOGO
AC Q6FOGO;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Strain CBS138 chromosome 1 complete sequence.
GN ORFNames=CAGL01065349;
OS Candida glabrata (Yeast) (Torulopsis glabrata).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_Taxid=5478;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CBS138;

```

```

RESULT 14
Q89UG7 PRELIMINARY; PRT; 389 AA.
ID Q89UG7
AC Q89UG7;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE ABC transporter permease protein.
GN OrderedlocusNames=blt1450;
OS Bradyrhizobium japonicum.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Bradyrhizobium.
OX NCBI_Taxid=375;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=USDA110;
RX MEDLINE=22484998; PubMed=12597275;
RA Kaneko T., Nakamura Y., Sato S., Minamitsawa K., Uchiyumi T.,
RA Sasamoto S., Watanabe A., Idesawa K., Iriyuchi M., Kawashima K.,
RA Kohara M., Matsumoto M., Shimo S., Tsuruoka H., Wada T., Yamada M.,
RA Tabata S.;
RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
RT Bradyrhizobium japonicum USDA110.";
RL DNA Res. 9:189-197(2002).
DR EMBL; AP005940; BAC46715.1; -;
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:000610; P:transport; IEA.
DR InterPro; IPR01851; Bac_innermem_transp.
DR Pfam; PF02653; BPD_transp_2; 1.
KW Complete proteome.
SQ SEQUENCE 389 AA; 42197 MW; 2C7D90C36B8E1B26 CRC64;
Query Match 67.9%; Score 38; DB 2; Length 389;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 YSKLPW 8

```

```

DB      117 YSKLPW 122

RESULT 15
075885      PRELIMINARY;      PRT;      434 AA.
ID 075885;
AC 075885;
DT 05-JUL-2004 (TEMBLrel. 27, Created)
DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TEMBLrel. 27, Last annotation update)
DE ADL315CP.
DE Name=ADL315C;
OS Ashbya gossypii (Yeast) (Eremothecium gossypii).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Eremothecium.
OX NCBI_TaxID=33169;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 10895;
RX PubMed=15001715;
RA Voegel S.E., Brachat S., Dietrich F.S., Lerch A., Gaffney T.,
RA Mohr C., Pohlmann R., Luedi P., Choi S., Wing R.A., Flavler A.,
RA Gaffney T.D., Philippen P.;
RT "The Ashbya gossypii genome as a tool for mapping the ancient
RT Saccharomyces cerevisiae genome.";
RL Science 304:304-307(2004).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 10895;
RA Voegel S.E., Brachat S., Dietrich F.S., Lerch A., Gaffney T.,
RA Philippen P.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE016889; AAS51605.1; -.
DR AGD: ADL315C; -.
DR InterPro: IPR010109; Kinase_like.
DR InterPro: IPR000719; Prot_Kinase.
DR InterPro: IPR002290; Ser_thr_kinase.
DR InterPro: IPR008271; Ser_thr_kin_AS.
DR InterPro: IPR001245; Tyr_kinase.
DR Pfam: PF00069; Pkinase; 1.
DR ProDom: PD000001; Prot_Kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TYKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; UNKNOWN_1.
KM ATP-binding; Kinase; Transferase.
SQ SEQUENCE 434 AA; 49672 MW; E3F62F511479CF1B CRC64;

Query Match      67.9%; Score 38; DB 2; Length 434;
Best Local Similarity 71.4%; Pred. No. 1.8e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      2 QYSKLPW 8
DB      326 QYAKIPW 332

```

```

RC STRAIN=ATCC 10895;
RX PubMed=15001715;
RA Dietrich F.S., Voegel S., Brachat S., Lerch A., Gates K., Steiner S.,
RA Mohr C., Pohlmann R., Luedi P., Choi S., Wing R.A., Flavler A.,
RA Gaffney T.D., Philippen P.;
RT "The Ashbya gossypii genome as a tool for mapping the ancient
RT Saccharomyces cerevisiae genome.";
RL Science 304:304-307(2004).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 10895;
RA Voegel S.E., Brachat S., Dietrich F.S., Lerch A., Gaffney T.,
RA Philippen P.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE016889; AAS51605.1; -.
SQ SEQUENCE 434 AA; 49672 MW; E3F62F511479CF1B CRC64;

Query Match      67.9%; Score 38; DB 2; Length 434;
Best Local Similarity 71.4%; Pred. No. 1.8e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      2 QYSKLPW 8
DB      326 QYAKIPW 332

RESULT 17
CHLE_RABIT
ID CHLE_RABIT      STANDARD;      PRT;      581 AA.
AC P21937;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Cholinesterase precursor (EC 3.1.1.8) (Acylcholine acylhydrolase)
DE (Choline esterase II) (Butyrylcholine esterase)
DE (Pseudocholinesterase).
GN Name=BCH;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=New Zealand;
RX MEDLINE=90326526; PubMed=2374720;
RA Ubblo O., Roudani S., Chatonnet A.;
RT "Complete sequence of rabbit butyrylcholinesterase.";
RL Nucleic Acids Res. 18:3990-3990(1990).
RN [2]
RP SEQUENCE OF 75-215 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=91201348; PubMed=2016308;
RA Arpaug M., Chatonnet A., Masson P., Newton M., Vaughan T.A.,
RA Barthele C.F., Nogueira C.P., la Du B.N., Lockridge O.;
RT "Use of the polymerase chain reaction for homology probing of
RT butyrylcholinesterase from several vertebrates.";
RL J. Biol. Chem. 266:6966-6974(1991).
CC -1- CATALYTIC ACTIVITY: An acylcholine + H(2O) = choline + a
CC carboxylic acid anion.
CC -1- SUBUNIT: Homotetramer. The tetramer is composed of two dimers. The
CC two subunits in a dimer are linked by a disulfide bond.
CC -1- TISSUE SPECIFICITY: Present in most cells except erythrocytes.
CC -1- MISCELLANEOUS: Cholinesterase is highly reactive with
CC organophosphate esters.
CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).

```

CC -----
DR EMBL; X52090; CAA36308.1; -
DR EMBL; X52091; CAA36308.1; JOINED.
DR EMBL; X52092; CAA36308.1; JOINED.
DR EMBL; M62779; AAA31169.1; -
DR PIR; S10255; C39768.
DR HSSP; P22303; 1F8U.
DR InterPro; IPR002018; CarbesteraeB.
DR InterPro; IPR000997; Cholinesterase.
DR InterPro; IPR000379; Ser_estr.
DR Pfam; PF00135; Coesterase; 1.
DR PRINTS; PR00878; CHOLINESTRASE.
DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
DR Glycoprotein; Hydrolyase; Serine esterase; Signal.
FT CHAIN 1 581
FT SIGNAL 1 8
FT ACT_SITE 205 205
FT ACT_SITE 332 332
FT ACT_SITE 445 445
FT DISULFID 72 99
FT DISULFID 259 270
FT DISULFID 407 526
FT DISULFID 578 578
FT CARBOHYD 64 64
FT CARBOHYD 113 113
FT CARBOHYD 248 248
FT CARBOHYD 263 263
FT CARBOHYD 348 348
FT CARBOHYD 462 462
FT CARBOHYD 488 488
FT CARBOHYD 492 492
FT CARBOHYD 493 493
SQ SEQUENCE 581 AA; 66156 MW; FE8B199E7B32EB0A CRC64;
Query Match 67.9%; Score 38; DB 1; Length 581;
Best Local Similarity 75.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 HOYSKLPW 8
Db 430 HRSSKLPW 437
RESULT 18
Q9JKC1 PRELIMINARY; PRT; 597 AA.
ID 09JKC1
AC 09JKC1
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Butyrylcholinesterase.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RA Li B., Stribley J., Tieu A., Xie W., Schopfer L.M., Hammond P.,
RA Brimjoin S., Hintich S.H., Lockridge O.,
RN Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RA Tieu A.M., Lockridge O., Bartels C.F.,
RN Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
DR EMBL; AF244349; AAF44713.1; -
DR HSSP; P22303; 1F8U.
DR GO; GO:0003824; F: catalytic activity; IEA.
DR GO; GO:0004104; F: cholinesterase activity; IEA.
DR InterPro; IPR002018; CarbesteraeB.

DR InterPro; IPR000997; Cholinesterase.
DR InterPro; IPR000379; Ser_estr.
DR Pfam; PF00135; Coesterase; 1.
DR PRINTS; PR00878; CHOLINESTRASE.
DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
DR Hydrolyase.
SQ SEQUENCE 597 AA; 67776 MW; 771204D166C7EBAC CRC64;
Query Match 67.9%; Score 38; DB 2; Length 597;
Best Local Similarity 75.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 HOYSKLPW 8
Db 446 HRSSKLPW 453
RESULT 19
CHLE_HUMAN STANDARD; PRT; 602 AA.
ID CHLE_HUMAN
AC P06276;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Cholinesterase precursor (EC 3.1.1.8) (Acylcholine acylhydrolyase)
DE (Pseudochoinesterase)
GN Name=BChE; Synonyms=CHE1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90212557; PubMed=2322535;
RA Arpaus M., Kott M., Vatsis K.P., Bartels C.F., la Du B.N.,
RA Lockridge O.,
RT "Structure of the gene for human butyrylcholinesterase. Evidence for a
RT single copy.";
RL Biochemistry 29:124-131(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal;
RX MEDLINE=87231856; PubMed=3035536;
RA Prody C.A., Zevin-Sonkin D., Gnatt A., Goldberg O., Soreg H.,
RT Isolation and characterization of full-length cDNA clones coding for
RT cholinesterase from fetal human tissues.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:3555-3559(1987).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=88016155; PubMed=3477799;
RA McTernan C., Atkins S., Chaconet A., Vaughan T.A., Bartels C.F.,
RA Kott M., Roseberry T.L., la Du B.N., Lockridge O.,
RT "Brain cDNA clone for human cholinesterase.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:6682-6686(1987).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Frange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abrahams R.D., Mullan S.J.,
RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman W., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzyzinski M.T., Skalska U., Smailus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences".
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RP SEQUENCE OF 29-602.
RC TISSUE=Plasma;
RX MEDLINE=87109144; PubMed=3542989;
RA Lockridge O., Bartels C.F., Vaughan T.A., Wong C.K., Norton S.E.,
RA Johnson L.L.,
RT "Complete amino acid sequence of human serum cholinesterase.";
RL J. Biol. Chem. 262:549-557(1987).
RN [6]
RP DISULFIDE BONDS.
RX MEDLINE=88007487; PubMed=3115973;
RA Lockridge O., Adkins S., la Du B.N.,
RT "Location of disulfide bonds within the sequence of human serum
RT cholinesterase.";
RL J. Biol. Chem. 262:12945-12952(1987).
RN [7]
RP REVIEW.
RX MEDLINE=89149758; PubMed=3067729;
RA Lockridge O.,
RT "Structure of human serum cholinesterase.";
RL Bioessays 9:125-128(1988).
RN [8]
RP VARIANT ATYPICAL GLY-98.
RX MEDLINE=89128896; PubMed=2915589;
RA McGuire M.C., Nogueira C.P., Bartels C.F., Lightstone H., Hajra A.,
RA van der Spek A.F.J., Lockridge O., la Du B.N.,
RT "Identification of the structural mutation responsible for the
RT dibucaine-resistant (atypical) variant form of human serum
RT cholinesterase.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:953-957(1989).
RN [9]
RP VARIANT ILE-358.
RX MEDLINE=96287386; PubMed=8680411;
RA Iida S., Kinoshita M., Fujii H., Moriyama Y., Nakamura Y., Yura N.,
RA Moriwa K.,
RT "Mutations of human butyrylcholinesterase gene in a family with
RT hypocholinesterasemia.";
RL Hum. Mutat. 6:349-351(1995).
CC -1- CATALYTIC ACTIVITY: An acylcholine + H(2)O = choline + a
CC carboxylic acid anion.
CC -1- SUBUNIT: Homotetramer. The tetramer is composed of two dimers. The
CC two subunits in a dimer are linked by a disulfide bond.
CC -1- TISSUE SPECIFICITY: Present in most cells except erythrocytes.
CC -1- DISEASE: Mutant alleles of CHB1 are responsible for
CC hypocholinesterasemia resulting in succinylcholine sensitivity.
CC Homozygous persons sustain prolonged apnea after administration of
CC the muscle relaxant succinylcholine in connection with surgical
CC anaesthesia.
CC -1- MISCELLANEOUS: Cholinesterase is highly reactive with
CC organophosphate esters.
CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see <http://www.isb-sdb.ch/announce/>
CC or send an email to license@isb-sdb.ch).
CC -----
DR EMBL: M32391; AAA99296.1; -;
DR EMBL: M32389; AAA99296.1; JOINED.
DR EMBL: M32390; AAA99296.1; JOINED.
DR EMBL: M16541; AAA98113.1; -;
DR EMBL: M16541; AAA52015.1; -;

[illegible]

DE (Choline esterase II) (Butyrylcholine esterase)
 DE (Pseudocholesterase).
 OS Name=Bche;
 OC Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90380429; PubMed=2400605;
 RA Rachinsky T.L., Camp S., Li Y., Ekstrom T.J., Newton M., Taylor P.;
 RT "Molecular cloning of mouse acetylcholinesterase: tissue distribution
 of alternatively spliced mRNA species.";
 RL Neuron 5:317-327(1990).
 RN [2]
 RP SEQUENCE OF 97-237 FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=91201348; PubMed=2016308;
 RA Arpaugh M., Chatonnet A., Masson P., Newton M., Vaughan T.A.,
 RA Bartels C.F., Nogueira C.P., La Du B.N., Lockridge O.;
 RT "Use of the polymerase chain reaction for homology probing of
 butyrylcholinesterase from several vertebrates.";
 RL J. Biol. Chem. 266:6966-6974(1991).
 CC -1- CATALYTIC ACTIVITY: An acylcholine + H(2)O = choline + a
 CC carboxylic acid anion.
 CC -1- SUBUNIT: Homotetramer. The tetramer is composed of two dimers. The
 CC two subunits in a dimer are linked by a disulfide bond.
 CC -1- TISSUE SPECIFICITY: Present in most cells except erythrocytes.
 CC -1- MISCELLANEOUS: Cholinesterase is highly reactive with
 CC organophosphate esters.
 CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: M69492; AAA37328.1; -.
 DR PIR, S70849; S70849.
 DR HSSP, P22303; IP8U.
 DR MGD; MGI:894278; Bche.
 DR InterPro; IPR002018; Carboxylesterase.
 DR InterPro; IPR000997; Cholinesterase.
 DR InterPro; IPR000379; Ser. esters.
 DR Pfam; PF00135; COESTERASE_1.
 DR PRINTS; PR00878; CHOLNESTRASE.
 DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
 DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
 KW Glycoprotein; Hydrolase; Serine esterase; Signal.
 FT SIGNAL 1 29
 FT CHAIN 30 603 Cholinesterase.
 FT ACT_SITE 227 227 Acyl-ester intermediate (By similarity).
 FT ACT_SITE 354 354 Charge relay system (By similarity).
 FT ACT_SITE 467 467 Charge relay system (By similarity).
 FT DISULFID 94 121 By similarity.
 FT DISULFID 281 292 By similarity.
 FT DISULFID 429 548 By similarity.
 FT DISULFID 600 600 Interchain (By similarity).
 FT CARBOHYD 86 86 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 135 135 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 270 270 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 370 370 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 484 484 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 510 510 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 515 515 N-linked (GlcNAc...) (Potential).
 FT CONFLICT 129 129 R -> P (in Ref. 2).
 SQ SEQUENCE 603 AA; 68521 MW; 719B1B220D1E5367 CRC64;

Query Match Score 38; DB 1; Length 603;
 Best Local Similarity 75.0%; Pred. No. 2.5e+02;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 HOYSKLPW 8
 Db 452 HRSSKLPW 459
 RESULT 21
 ID Q90ZK8 PRELIMINARY; PRT; 603 AA.
 AC Q90ZK8;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Butyrylcholinesterase precursor (EC 3.1.1.8).
 GN Name=Bche;
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OC NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Geisler K., Chatonnet A., Layer P.G.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
 CC EMBL; AJ306928; CAC37792.1; -.
 DR HSSP; P21836; INSM.
 DR GO; GO:0004104; F:cholinesterase activity; IEA.
 DR GO; GO:0016787; F:hydrolase activity; IEA.
 DR InterPro; IPR002018; Carboxylesterase.
 DR InterPro; IPR000997; Cholinesterase.
 DR Pfam; PF00135; COESTERASE_1.
 DR PRINTS; PR00878; CHOLNESTRASE.
 DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
 DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
 KW Hydrolase; Signal.
 FT SIGNAL 1 29 Potential.
 FT CHAIN 30 603 butyrylcholinesterase.
 SQ SEQUENCE 603 AA; 68480 MW; A350FDDF68574ADF CRC64;
 Query Match Score 38; DB 2; Length 603;
 Best Local Similarity 75.0%; Pred. No. 2.5e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 HOYSKLPW 8
 Db 451 HRSSKLPW 458
 RESULT 22
 ID BAC34196 PRELIMINARY; PRT; 603 AA.
 AC BAC34196;
 DT 14-APR-2004 (TrEMBLrel. 27, Created)
 DT 14-APR-2004 (TrEMBLrel. 27, Last sequence update)
 DT 14-APR-2004 (TrEMBLrel. 27, Last annotation update)
 DE Adult male liver tumor cDNA, RIKEN full-length enriched library,
 DE clone: C730038G20 product: butyrylcholinesterase.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Liver;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium;
 RA The RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT Nature 420:563-573 (2002)."
 RL


```

RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=liver;
RX MEDLINE=21085660; Pubmed=11217851;
RA RIKEN PANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=liver;
RX MEDLINE=99279253; Pubmed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=liver;
RX MEDLINE=20499374; Pubmed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
  Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
  prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=liver;
RX MEDLINE=20530913; Pubmed=11076861;
RA Shibata K., Itoh M., Aizawa K., Kikuno S., Sasaki N., Carninci P.,
  Kono H., Akiyama J., Nishi K., Kikuno T., Tahtiro H., Itoh M.,
  Suni N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
  Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
  Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe M.,
  Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsunaga S., Kawai J.,
  Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
  sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=liver;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
  Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
  Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozawa T.,
  Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
  Katoh H., Kawai T., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
  Kuribara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
  Nishi K., Nomura K., Numazaki R., Ohno M., Ohseco N., Okazaki Y.,
  Saito K., Saitoh K., Sakai C., Sakai K., Sakazume N., Sano H.,
  Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
  Tagawa A., Takehashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
  Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RT Submitted (Jul-2001) to the EMBL/GenBank/DBJ database.
RL EMBL: AK050337; BAC34196.1; -;
SQ SEQUENCE 603 AA; 68462 MW; 2CB79C46797B3713 CRC64;

Query Match 67.9%; Score 38; DB 2; Length 603;
Best Local Similarity 75.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 HQSKLPW 8
DB 452 HRSSKLPW 459

RESULT 23
Q6M124 PRELIMINARY; PRT; 657 AA.
ID Q6M124;
AC Q6M124;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein precursor (EC 3.6.3.14).
GN OrderedLocusName=Bd3355;

```

```

OS Bdellovibrio bacteriovorus.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Bdellovibrionales;
OC Bdellovibrionaceae; Bdellovibrio.
OX NCBI_TaxID=959;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HD100 / DSM 50701 / ATCC 15356 / NCIB 9529;
RX Pubmed=14752164;
RA Rendall S., Jagtap P., Rosinus A., Eppinger M., Baar C., Lanz C.,
  Keller H., Lambert C., Evans K.J., Goessmann A., Meyer F.,
  Sockett R.E., Schuster S.C.;
RT "A predator unmasked: life cycle of Bdellovibrio bacteriovorus from a
  genomic perspective.";
RL Science 303:689-692(2004).
DR EMBL: BX842655; CAE78158.1; -;
DR GO: GO:0016787; R:hydrolase activity; IEA.
KW Complete proteome; Hydrolase; Hypothetical protein; Signal.
FT SIGNAL 1
SQ SEQUENCE 657 AA; 74124 MW; B3C8FA18D745419C CRC64;

Query Match 67.9%; Score 38; DB 2; Length 657;
Best Local Similarity 71.4%; Pred. No. 2.8e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 2 QYSKLPW 8
DB 455 EYSKLPW 461

RESULT 24
CAE78158 PRELIMINARY; PRT; 657 AA.
ID CAE78158;
AC CAE78158;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein precursor (EC 3.6.3.14).
GN BD3355.
OS Bdellovibrio bacteriovorus.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Bdellovibrionales;
OC Bdellovibrionaceae; Bdellovibrio.
OX NCBI_TaxID=959;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HD100 / DSM 50701 / ATCC 15356 / NCIB 9529;
RX Pubmed=14752164;
RA Rendall S., Jagtap P., Rosinus A., Eppinger M., Baar C., Lanz C.,
  Keller H., Lambert C., Evans K.J., Goessmann A., Meyer F.,
  Sockett R.E., Schuster S.C.;
RT "A predator unmasked: life cycle of Bdellovibrio bacteriovorus from a
  genomic perspective.";
RL Science 303:689-692(2004).
DR EMBL: BX842655; CAE78158.1; -;
KW Hydrolase; Hypothetical protein; Signal.
FT SIGNAL 1
SQ SEQUENCE 657 AA; 74124 MW; B3C8FA18D745419C CRC64;

Query Match 67.9%; Score 38; DB 2; Length 657;
Best Local Similarity 71.4%; Pred. No. 2.8e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 2 QYSKLPW 8
DB 455 EYSKLPW 461

RESULT 25
Q8MY38 PRELIMINARY; PRT; 698 AA.
ID Q8MY38;
AC Q8MY38;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

```

DE Gag-like protein.
 GN Name=ORF1;
 OS Papilio xuthus.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
 OC Papilionoidea; Papilionidae; Papilioninae; Papilio.
 NCBI_TaxId=66420;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22511580; PubMed=12644555;
 RA Kojima K.K., Fujiwara H.;
 RT "Evolution of target specificity in R1 clade non-LTR
 retrotransposons."
 RL Mol. Biol. Evol. 20:351-361 (2003).
 DR EMBL; AB078928; BAC06449.1;
 DR GO; GO:0003676; F:nucleic acid binding; IEA.
 DR InterPro; IPR001878; Znf.CCHC.
 DR Pfam; PF00098; Zf-CCHC; 2.
 DR PRINTS; PR00939; C2HCZNFINGER.
 DR SMART; SM00343; Znf_C2HC; 2.
 DR PROSITE; PS50158; ZF_CCHC; 2.
 SQ SEQUENCE 698 AA; 75954 MW; E10A654A5A6F90A5 CRC64;

Query Match 67.9%; Score 38; DB 2; Length 698;
 Best Local Similarity 66.7%; Pred. No. 2.9e+02;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 HOXSCLPWT 9
 ||:||||
 Db 375 HQKELPWT 383

RESULT 26

Q6CY8 PRELIMINARY; PRT; 1036 AA.
 AC Q6CY8;
 DT 01-OCT-2004 (TrEMBLrel. 28, Created)
 DT 01-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Strain NRRL Y-1140 chromosome F of strain NRRL Y-1140 of Kluyveromyces
 DE lactis.
 GN ORFNames=K1LA0F149279;
 OS Kluyveromyces lactis (Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
 NCBI_TaxId=28985;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NRRL Y-1140;
 RG GENOLEVURES;
 RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
 RA Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
 RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
 RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
 RA Boistrame A., Boyer J., Catolico L., Confaniollet F., de Daruvar A.,
 RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Gropi A.,
 RA Hantaye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
 RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
 RA Nicaud J.M., Nikoleki M., Ozias S., Ozier-Kalogeropoulos O.,
 RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
 RA Sweeney D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
 RA Zenilou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
 RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissbach J.,
 RA Wincker P., Souciet J.L.;
 RT "Genome evolution in yeasts."
 RT Nature 430:35-44 (2004).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NRRL Y-1140;
 RA Genoscope;
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; CR382126; CAG98459.1;
 SQ SEQUENCE 1036 AA; 118499 MW; 22DF98B5DBF3705C CRC64;

Query Match 67.9%; Score 38; DB 2; Length 1036;
 Best Local Similarity 55.6%; Pred. No. 4.4e+02;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HOXSCLPWT 9
 ||:||||
 Db 571 HFYKVPWS 579

RESULT 27

MCE.REOVD STANDARD; PRT; 1289 AA.
 ID MCE.REOVD
 AC P11079;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-JUL-1989 (Rel. 11, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE mRNA capping enzyme (mRNA guanylyltransferase) (EC 2.7.7.50) (GTP--RNA
 DE guanylyltransferase).
 GN Name=L2;
 OS Reovirus type 3 (strain Dearing) (T3D).
 OS Viruses; dsRNA viruses; Reoviridae; Orthoreovirus.
 NCBI_TaxId=10886;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88058999; PubMed=2824487;
 RA Seltzer L.S., Zheng K., Shatkin A.J.;
 RT "Complete nucleotide sequence of reovirus L2 gene and deduced amino
 RT acid sequence of viral mRNA guanylyltransferase."
 RL J. Biol. Chem. 262:16289-16293 (1987).
 CC -1- FUNCTION: mRNA capping.
 CC -1- CATALYTIC ACTIVITY: GTP + (5')pp-pur-mRNA = diphosphate +
 CC G(5')pp-pur-mRNA.
 CC CC

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----

DR EMBL; J03488; AAA47253.1; --
 DR PIR; A28471; RMXR3.
 DR InterPro; IPR010311; Reovirus_L2.
 DR Pfam; PF06016; Reovirus_L2; 1.
 KM mRNA capping; mRNA processing; Nucleosideyltransferase; Transferase.
 FT DOMAIN 941 968
 FT DOMAIN 941 968
 SQ SEQUENCE 1289 AA; 14406 MW; 8C497F0B6937018B CRC64;

Query Match 67.9%; Score 38; DB 1; Length 1289;
 Best Local Similarity 66.7%; Pred. No. 5.4e+02;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 HOXSCLPWT 9
 ||:||||
 Db 659 HQHSLTWT 667

RESULT 28

Q91RA1 PRELIMINARY; PRT; 1289 AA.
 ID Q91RA1
 AC Q91RA1;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Core-spike protein lambda-2.
 DE Reovirus type 3 (strain Dearing) (T3D).
 OS Viruses; dsRNA viruses; Reoviridae; Orthoreovirus;
 OC Mammalian orthoreoviruses.
 NCBI_TaxId=10886;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=Hall;
 RX MEDLINE=21425393; PubMed=11531411;
 RA Bren L.A., Broering T.J., McCutcheon A.M., Harrison S.J.,
 RA Luongo C.L., Nibert W.L.;
 RT "Mammalian reovirus L2 gene and lambda2 core spike protein sequences
 RT and whole-genome comparisons of reoviruses type 1 Lang, type 2 Jones,
 RT and type 3 Dearing.";
 RL Virology 287:333-348 (2001).
 DR EMBL; AF378010; AAK57514.1; -;
 DR InterPro: IPR010311; Reovirus_L2.
 DR Pfam: PF06016; Reovirus_L2; 1.
 SQ SEQUENCE 1289 AA; 143843 MW; E41D982522E2B8F4 CRC64;

Query Match
 Best Local Similarity 66.7%; Score 38; DB 2; Length 1289;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 HOYSKLPMT 9
 DB 659 HOHSSLTWT 667

RESULT 29

AA11062 PRELIMINARY; PRT; 95 AA.
 AC AAR11062;
 DT 02-MAR-2004 (T-EMBLrel. 27, Created)
 DT 02-MAR-2004 (T-EMBLrel. 27, Last sequence update)
 DE 02-MAR-2004 (T-EMBLrel. 27, Last annotation update)
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=B6.S1el; TISSUE=Spleen;
 RA Liang Z., Xie C., Chen C., Kreska D., Hsu K., Zhou J.X., Mohan C.;
 RT "Antinuclear autoantibodies from B6.S1el mice."
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY436902; AAR11062.1; -;
 FT NON_TER 1
 FT NON_TER 95
 SQ SEQUENCE 95 AA; 10220 MW; 680C89BE1C872248 CRC64;

Query Match
 Best Local Similarity 66.1%; Score 37; DB 2; Length 95;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 HOYSKLPMT 9
 DB 84 HOHSSCPMT 92

RESULT 30

AA11071 PRELIMINARY; PRT; 99 AA.
 AC AAR11071;
 DT 02-MAR-2004 (T-EMBLrel. 27, Created)
 DT 02-MAR-2004 (T-EMBLrel. 27, Last sequence update)
 DE 02-MAR-2004 (T-EMBLrel. 27, Last annotation update)
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=B6.S1el; TISSUE=Spleen;
 RA Liang Z., Xie C., Chen C., Kreska D., Hsu K., Zhou J.X., Mohan C.;
 RT "Antinuclear autoantibodies from B6.S1el mice."
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY436911; AAR11071.1; -;

FT NON_TER 1 1
 FT NON_TER 99 99
 SQ SEQUENCE 99 AA; 10529 MW; BBC09D5304E08F98 CRC64;

Query Match
 Best Local Similarity 66.1%; Score 37; DB 2; Length 99;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 OYSKLPMT 9
 DB 88 QYQFPMT 95

RESULT 31

KV1B_HUMAN
 ID KV1B_HUMAN STANDARD; PRT; 108 AA.
 AC P01554;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 01-OCT-2004 (Rel. 45, Last annotation update)
 DE Ig kappa chain V-1 region AU.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.

RX MEDLINE=72189444; PubMed=5028201;
 RA Schiechl H., Hilschmann N.;
 RT "Rule of antibody structure. The primary structure of a monoclonal
 RT immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones
 RT protein Au)."
 RL Hoppe-Seyler's Z. Physiol. Chem. 353:345-370 (1972).
 RN [2]

RP X-RAY CRYSTALLOGRAPHY
 RX MEDLINE=77022433; PubMed=1234024;
 RA Fehlmayer H., Schiffer M., Epp O., Colman P.M., Lattman E.E.,
 RA Schwager P., Steigemann W., Schramm H.J.;
 RT "The structure determination of the variable portion of the Bence-
 RT Jones protein Au".
 RL Biophys. Struct. Mech. 1:139-146 (1975).

CC -1- MISCELLANEOUS: The structure of the V region was determined by
 CC molecular replacement methods using the known structure of the V
 CC region of the kappa chain REI.
 CC -1- MISCELLANEOUS: The C region of this chain has the INV (3) marker.

DR PIR; A91653; KIHUMU.
 DR PDB; 1JVS; X-ray; A=1-107,
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; P:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig_1.
 DR SMART; SM00406; IgV_1.
 DR PROSITE; PS00835; IG_Like; 1.
 KM 3D-structure; Bence-Jones protein; Direct protein sequencing;
 KW Immunoglobulin V region.

FT DOMAIN 1 23 Framework-1.
 FT DOMAIN 24 34 Complementarity-determining-1.
 FT DOMAIN 35 49 Framework-2.
 FT DOMAIN 50 56 Complementarity-determining-2.
 FT DOMAIN 57 88 Framework-3.
 FT DOMAIN 89 97 Complementarity-determining-3.
 FT DOMAIN 98 107 Framework-4.
 FT DISULFID 23 88 By similarity.

FT STRAND 4 5
 FT STRAND 10 13
 FT TURN 15 16
 FT STRAND 19 25
 FT TURN 30 31
 FT STRAND 33 38
 FT TURN 40 41

```

FT STRAND 44 49
FT TURN 50 52
FT STRAND 53 54
FT TURN 56 57
FT TURN 60 61
FT STRAND 62 63
FT TURN 68 69
FT STRAND 70 75
FT HELIX 80 85
FT STRAND 85 90
FT STRAND 97 98
FT STRAND 102 106
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11939 MW; E8011187BE6FB9 CRC64;

Query Match 66.1%; Score 37; DB 1; Length 108;
Best Local Similarity 75.0%; Pred. No. 68;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QISKLPT 9
Db 90 QYDPLPT 97

RESULT 32
Q9CTV5 PRELIMINARY; PRT; 108 AA.
ID Q9CTV5;
AC Q9CTV5;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE Mus musculus 6 days neonate head cDNA, RIKEN full-length enriched
DE library, clone:543043C04 product:hypothetical protein, full insert
DE sequence. (Fragment).
GN Name=543043C04Rik;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=99279253; PubMed=10349636;
RA Carninci P.; Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RA The FANTOM Consortium;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=20499374; PubMed=11042159;
RA Kono H., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and substructure of cap-trapper-selected cDNAs to
RT Prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;

```

```

RX MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Kono H., Akiyama J., Nishi K., Kitsuai T., Taahito H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RL sequencing pipeline with 384 multicapillary sequencer.";
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Furumishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hirooka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Kono H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Nunazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (Aug-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK019949; BAB31930.1;
DR MGD; MGI:1925346; 543043C04Rik.
KW Hypothetical protein.
FT NON_TER 1 108
SQ SEQUENCE 108 AA; 11561 MW; 8B2DBF61623608F CRC64;

Query Match 66.1%; Score 37; DB 2; Length 108;
Best Local Similarity 75.0%; Pred. No. 68;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QISKLPT 9
Db 17 QISRLPT 24

RESULT 33
KVAC_HUMAN STANDARD; PRT; 134 AA.
ID KVAC_HUMAN;
AC P06314;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-IV region B17 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86041854; PubMed=2997713;
RA Marsh P., Mills F., Gould H.;
RT "Detection of a unique human V kappa IV germline gene by a cloned cDNA
RT probe.";
RL Nucleic Acids Res. 13:6531-6544(1985).
RN [2]
RP REVISION TO 76.
RA Marsh P.;
RL Submitted (OCT-1986) to the EMBL/GenBank/DBJ databases.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).

```

```

CC -----
DR EMBL; X02990; CAA26733.1; -.
DR HSSP; P01625; ILVE.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KM Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 134 Ig kappa chain V-IV region B17.
FT DOMAIN 21 43 Framework-1.
FT DOMAIN 44 60 Complementarity-determining-1.
FT DOMAIN 61 75 Framework-2.
FT DOMAIN 76 82 Complementarity-determining-2.
FT DOMAIN 83 114 Complementarity-3.
FT DOMAIN 115 121 Complementarity-determining-3.
FT DOMAIN 122 133 Framework-4.
FT DISULFID 43 114 By similarity.
FT NON_TER 134 134
SQ SEQUENCE 134 AA; 14966 MW; 6413A22F0738832 CRC64;

Query Match
Best Local Similarity 66.1%; Score 37; DB 1; Length 134;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 QYSKLPWT 9
Db 116 QYVNLPT 123

RESULT 34
Q8VDD0 PRELIMINARY; PRT; 134 AA.
ID Q8VDD0;
AC Q8VDD0;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Anti-MOG Z12 variable light chain (Fragment).
GN Name=anti-MOG kappa;
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murine; Mus.
OX NCBI_TaxID=10090;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RA Semi P.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN (2)
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RA Cheraiovsky Y.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; A416331; CAC94866.1; -.
DR PIR; G27887; G27887.
DR HSSP; P01834; IMIM.
DR InterPro; IPR007110; Ig-1like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 134 134
SQ SEQUENCE 134 AA; 14525 MW; CFDF8E223682D0CF CRC64;

Query Match
Best Local Similarity 66.1%; Score 37; DB 2; Length 134;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 HOYSKLPWT 9

```

```

Db 110 HOSSYPWT 118

RESULT 35
ID 085999 PRELIMINARY; PRT; 190 AA.
AC 085999;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein orf1251 precursor.
GN Name=orf1251;
OS Spingomonas aromaticivorans.
OC Plasmid pNL1.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Spingomonadales;
OC Spingomonadaceae; Novosphingobium.
OX NCBI_TaxID=48935;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=F199;
RX MEDLINE=99175459; Pubmed=10049392;
RA Romine M.F., Stillwell L.C., Wong K.-K., Thurston S.J., Sisk E.C.,
RA Sensen C., Gaasterland T., Fredrickson J.K., Saffer J.D.,
RT "Complete sequence of a 184-kilobase catabolic plasmid from
RT Spingomonas aromaticivorans F199."
RL J. Bacteriol. 181:1585-1602(1999).
DR EMBL; AF079317; AB04015.1; -.
DR PIR; T31291; T31291.
DR InterPro; IPR007110; Ig-1like.
DR InterPro; IPR006311; Tat.
DR TIGRPFAMs; TIGR01409; Tat_signal_seg. 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KM Hypothetical protein; Plasmid; Signal.
FT SIGNAL 1 31 Potential.
SQ SEQUENCE 190 AA; 20392 MW; 2FA2F9B979F9822 CRC64;

Query Match
Best Local Similarity 66.1%; Score 37; DB 2; Length 190;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 HOYSKLPW 8
Db 114 HOYRKLRW 121

RESULT 36
Q9PU09 PRELIMINARY; PRT; 242 AA.
ID Q9PU09;
AC Q9PU09;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Dm20 (Fragment).
GN Name=Dm20;
OS Latimeria chalumnae (Latimeria) (Coelacanth).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Coelacanthiformes; Coelacanthidae; Latimeria.
OX NCBI_TaxID=7897;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=99310421; Pubmed=10403627;
RA Tohyama Y., Kasama-Yoshida H., Sakuma M., Kobayashi Y., Cao Y.,
RA Hasegawa M., Kojima H., Tamai Y., Tanokura M., Kurihara T.;
RT "Gene structure and amino acid sequence of Latimeria chalumnae
RT (Coelacanth) myelin Dm20: phylogenetic relation of the fish."
RL Neurochem. Res. 24:867-873(1999).
DR EMBL; AB025938; BAA84207.1; -.
DR EMBL; AB025933; BAA84207.1; JOINED.
DR EMBL; AB025934; BAA84207.1; JOINED.
DR EMBL; AB025935; BAA84207.1; JOINED.
DR EMBL; AB025936; BAA84207.1; JOINED.
DR EMBL; AB025937; BAA84207.1; JOINED.

```

DR InterPro; IPR001614; Myelin_PLP.
 DR Pfam; PF01275; Myelin_PLP; 1.
 DR PRINTS; PR00214; MYELINPLP.
 DR SMART; SM00002; PLP; 1.
 FT NON TER 1 1
 SQ SEQUENCE 242 AA; 26991 MW; 9BB3556B38F5DE2 CRC64;

Query Match 66.1%; Score 37; DB 2; Length 242;
 Best Local Similarity 75.0%; Pred. No. 1.5e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QYSKLPWT 9
 DB 168 QYGLPWT 175

RESULT 37

Q8UT6 PRELIMINARY; PRT; 245 AA.
 AC Q8UT6;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Dmalphal.
 GN Name=Dlpia;
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OC NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Werner H., Schweitzer J., Schachner M., Nave K.-A.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY070259; AAL59885.1; -.
 DR ZFIN; ZDB-GENE-001202-1; dlpia.
 DR InterPro; IPR001614; Myelin_PLP.
 DR Pfam; PF01275; Myelin_PLP; 1.
 DR PRINTS; PR00214; MYELINPLP.
 DR SMART; SM00002; PLP; 1.
 DR PROSITE; PS01004; MYELIN_PLP_2; 1.
 SQ SEQUENCE 245 AA; 27510 MW; 764B19BF8B949C9A CRC64;

Query Match 66.1%; Score 37; DB 2; Length 245;
 Best Local Similarity 75.0%; Pred. No. 1.6e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QYSKLPWT 9
 DB 171 QYGLPWT 178

RESULT 38

O6MOC7 PRELIMINARY; PRT; 330 AA.
 AC O6MOC7;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 GN OrderedlocusNames=Bd0547;
 OS Bdellovibrio bacteriovorus.
 OC Bacteria; Proteobacteria; Deltaproteobacteria; Bdellovibrionales;
 OC Bdellovibrionaceae; Bdellovibrio.
 OC NCBI_TaxID=959;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=HD100 / DSM 50701 / ATCC 15356 / NCIB 9529;
 RX PubMed=14752164;
 RA Rendulic S., Jagtap P., Rosinus A., Eppinger M., Baar C., Lanz C.,
 RA Keller H., Lambert C., Evans K.J., Goessmann A., Meyer F.,
 RA Sockett R.E., Schuster S.C.;
 RT "A predator unmasked: life cycle of Bdellovibrio bacteriovorus from a

RT genomic perspective."; Science 303:689-692(2004).
 RL EMBL; BX842647; CAE78520.1; -.
 DR EMBL; BX842647; CAE78520.1; -.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 330 AA; 37401 MW; E67D64135E164929 CRC64;

Query Match 66.1%; Score 37; DB 2; Length 330;
 Best Local Similarity 62.5%; Pred. No. 2.1e+02;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYSKLPW 8
 DB 207 NOTDKVFW 214

RESULT 39

CAE78520 PRELIMINARY; PRT; 330 AA.
 AC CAE78520;
 DT 02-MAR-2004 (TrEMBLrel. 27, Created)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 GN BD0547.
 OS Bdellovibrio bacteriovorus.
 OC Bacteria; Proteobacteria; Deltaproteobacteria; Bdellovibrionales;
 OC Bdellovibrionaceae; Bdellovibrio.
 OC NCBI_TaxID=959;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=HD100 / DSM 50701 / ATCC 15356 / NCIB 9529;
 RX PubMed=14752164;
 RA Rendulic S., Jagtap P., Rosinus A., Eppinger M., Baar C., Lanz C.,
 RA Keller H., Lambert C., Evans K.J., Goessmann A., Meyer F.,
 RA Sockett R.E., Schuster S.C.;
 RT "A predator unmasked: life cycle of Bdellovibrio bacteriovorus from a
 RT genomic perspective."; Science 303:689-692(2004).
 RL EMBL; BX842647; CAE78520.1; -.
 DR EMBL; BX842647; CAE78520.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 330 AA; 37401 MW; E67D64135E164929 CRC64;

Query Match 66.1%; Score 37; DB 2; Length 330;
 Best Local Similarity 62.5%; Pred. No. 2.1e+02;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYSKLPW 8
 DB 207 NOTDKVFW 214

RESULT 40

O9FLA1 PRELIMINARY; PRT; 388 AA.
 AC O9FLA1;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Similarity to heat shock transcription factor.
 OS Arabidopsis thaliana (Mouse-ear cress).
 GN Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OC NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=98344145; PubMed=9679202;
 RX Kaneke T., Kotani H., Nakamura Y., Sato S., Asamizu E., Miyajima N.,
 RA Tabata S.;

RT "Structural analysis of Arabidopsis thaliana chromosome 5. V. Sequence
 RT features of the regions of 1,381,565 bp covered by twenty one
 RT physically assigned PI and TAC clones."; DNA Res. 5:131-145(1998).

DR EMBL; AB010693; BAB10879.1; -.
 DR GO; GO:0003773; F:heat shock protein activity; IEA.
 DR InterPro; IPR001810; F-box.
 DR InterPro; IPR006566; FBD.
 DR InterPro; IPR008945; Skp1_Skp2.
 DR Pfam; PF00646; F-box; 1.
 DR SMART; SM00579; FBD; 1.
 DR PROSITE; PS50181; FBOX; 1.
 KW Heat shock.
 SQ SEQUENCE 388 AA; 45144 MW; 3117852CD27D24F5 CRC64;

Query Match 66.1%; Score 37; DB 2; Length 388;
 Best Local Similarity 75.0%; Pred. No. 2.5e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 HOYSKLPW 8
 DB 256 HSYSKLGW 263

Search completed: December 17, 2004, 19:14:44
 Job time : 28.8989 secs

this Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 17, 2004, 18:10:02 ; Search time 361.68 Seconds
(without alignments)
118,029 Million cell updates/sec

Title: US-10-089-500-9

Perfect score: 624
Sequence: 1 EVOLVESGQDFVQPGSLRV.....KLGYTFDSWQGTLLTVSS 119

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	624	100.0	119 4 AAB81985	Aab81985 Gangliosid
2	624	100.0	119 6 ABU11010	Abu11010 Modified
3	624	100.0	582 4 AAB81987	Aab81987 Gangliosid
4	579	92.8	119 4 AAB81989	Aab81989 Gangliosid
5	579	92.8	119 6 ABU11012	Abu11012 Modified
6	579	92.8	130 2 AAR33256	Aar33256 Rat Immun
7	579	92.8	130 2 AAR33341	Aar33341 KM641 L C
8	579	92.8	130 3 AAY28369	Aay28369 pKM641 HA
9	579	92.8	130 3 AAB81627	Aab81627 Murine im
10	579	92.8	138 4 AAB81977	Aab81977 Gangliosid
11	579	92.8	138 6 ABU11002	Abu11002 Modified
12	579	92.8	582 4 AAB81991	Aab81991 Gangliosid
13	502	80.4	274 8 ADO25153	Ado25153 Melanoma
14	499	80.0	119 5 AAE28151	Aae28151 Human con
15	498	79.8	119 4 AAB62088	Aab62088 Human Vh
16	498	79.8	119 4 AAB60401	Aab60401 Consensus
17	498	79.8	119 4 AAB61586	Aab61586 Human var
18	498	79.8	119 5 AAU74541	Aau74541 Human sub
19	498	79.8	119 8 ADE71455	Ade71455 Human ant
20	498	79.8	119 8 ADJ88009	Adj88009 Human var
21	498	79.8	119 8 ADN12055	Adn12055 Variable
22	498	79.8	119 8 ADP43329	Adp43329 Human mon
23	493.5	79.1	224 6 ABR01511	Abri01511 Human ant
24	492.5	78.9	126 6 ADA89891	Ada89891 MS-Roche
25	492	78.8	119 8 ADO36357	Ado36357 Intracell

26	492	78.8	119 8 ADQ75230	Adq75230 Immunoglo
27	492	78.8	121 7 ADL91330	Adl91330 VH chain
28	492	78.8	131 4 AAU43320	Aau43320 Human nov
29	491.5	78.8	251 8 ADI58099	Adi58099 Reg IV-sp
30	490.5	78.6	118 7 ADJ95639	Adj95639 Insulin-1
31	489.5	78.4	126 6 ADA89974	Ada89974 Anti-Abet
32	489	78.4	119 2 AAR95216	Aar95216 Human fce
33	489	78.4	143 6 ADA43059	Ada43059 Human ant
34	489	78.4	240 3 AAY15125	Aay15125 Anti-huma
35	489	78.4	240 3 AAY15125	Aay15125 Anti-mur
36	489	78.4	228 8 ADI58058	Adi58058 Reg IV-sp
37	488.5	78.3	220 6 ABR01519	Abri01519 Human ant
38	488.5	78.3	248 8 ADG34309	Adg34309 Neurokin
39	487.5	78.1	443 2 AAM13564	Aam13564 Humanised
40	487	78.0	121 5 ABB57571	Abb57571 HLA-DR-sp
41	487	78.0	123 6 ABR55827	Abri55827 Heavy cha
42	487	78.0	245 4 AAB67620	Aab67620 Human leu
43	487	78.0	247 5 ABP45942	Abp45942 Human Bly
44	487	78.0	247 7 ADG96769	Adg96769 Single ch
45	486.5	78.0	136 5 ADI45736	Adi45736 Single ch

ALIGNMENTS

RESULT 1
AAB81985
ID AAB81985 standard; protein; 119 AA.

AC AAB81985;
DT 03-JUL-2001 (first entry)
DE Ganglioside GD3 specific antibody related protein SEQ ID NO: 9.
XX Ganglioside; GD3; complementarity determining region; CDR; antibody;
XX cancer.
OS Synthetic.
XX WO200123432-A1.
XX 05-APR-2001.
XX 29-SEP-2000; 2000WC-JP006774.
XX PF 30-SEP-1999; 99JP-00278291.
XX PR 06-APR-2000; 2000JP-00105088.
XX (KYOW) KYOWA HAKKO KOGYO KK.
XX PA Hanai N, Shitara K, Nakamura K, Niwa R;
XX PI WPI; 2001-266143/27.
XX DR New human type complementation-determining region-transplanted antibody
XX PT and derivatives against ganglioside GD3; useful in diagnosis and therapy
XX of e.g. tumors with low antigenicity; little side effects but potent
XX activity in cancer.
XX Claim 20; Page 142-143; 183pp; Japanese.
XX PS The present invention describes a monoclonal antibody which can react
XX CC specifically with ganglioside GD3. The antibody and its derivatives are
XX CC useful in the diagnosis and therapy of tumors, particularly cancer
XX CC diagnosis. The present sequence is a protein used in the exemplification
XX of the invention
XX Sequence 119 AA;
SQ Query Match 100.0%; Score 624; DB 4; Length 119;
Best Local Similarity 100.0%; Pred.No. 8.2e-50;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVGLVESGGDFVQPGGSLRVSCAASGFAFSHYAMSWVRQAPGKLEWVAYISSGGSGTTY 60
 |||
 DB 1 EVGLVESGGDFVQPGGSLRVSCAASGFAFSHYAMSWVRQAPGKLEWVAYISSGGSGTTY 60
 |||
 QY 61 SDSVKGRFTISRDNASKNTLYLQWRSLRAEDSAVYFCTRVKLGTYYPDSWQGTLLTVSS 119
 |||
 DB 61 SDSVKGRFTISRDNASKNTLYLQWRSLRAEDSAVYFCTRVKLGTYYPDSWQGTLLTVSS 119
 |||

RESULT 2 ABU1010

ID ABU1010 standard; protein; 119 AA.

XX ABU1010;

XX 04-FEB-2003 (first entry)

XX Modified ganglioside GD3 antibody associated protein #3.

XX Ganglioside GD3; anti-ganglioside GD3 antibody; tumour; melanoma.

XX Synthetic.

OS WO200278739-A1.

XX 10-OCT-2002.

PF 29-MAR-2002; 2002WO-JP003170.

XX 29-MAR-2001; 2001JP-00097483.

XX (KYOW) KYOWA HAKKO KOGYO KK.

XX Shitara K, Niwa R, Kanazawa J, Asada M;

XX WPI; 2003-067410/06.

XX Drugs containing genetically-modified antibody against ganglioside GD3,
 PT its fragment, immunocompetent cell activators or/and antitumor agents in
 PT combination, applicable in treating malignant tumor like melanoma.

PS Claim 8; Page 99; 121pp; Japanese.

XX The invention describes drugs contain a genetically-modified antibody
 CC against ganglioside GD3 or its fragment and at least 1 of a substance
 CC capable of activating immunocompetent cells and a substance having an
 CC anticancer activity in combination. The drugs can be used to treat tumour
 CC like melanoma and can provide a treatment with enhanced therapeutic
 CC effect and little side-reactions, particularly to relieve problems of
 CC side-effects during the conventional single administration. This sequence
 CC represents a protein associated with the anti- ganglioside GD3 antibody
 CC

XX Sequence 119 AA;

Query Match 100.0%; Score 624; DB 6; Length 119;

Best Local Similarity 100.0%; Pred. No. 8.2e-50;
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVGLVESGGDFVQPGGSLRVSCAASGFAFSHYAMSWVRQAPGKLEWVAYISSGGSGTTY 60
 |||
 DB 1 EVGLVESGGDFVQPGGSLRVSCAASGFAFSHYAMSWVRQAPGKLEWVAYISSGGSGTTY 60
 |||
 QY 61 SDSVKGRFTISRDNASKNTLYLQWRSLRAEDSAVYFCTRVKLGTYYPDSWQGTLLTVSS 119
 |||
 DB 61 SDSVKGRFTISRDNASKNTLYLQWRSLRAEDSAVYFCTRVKLGTYYPDSWQGTLLTVSS 119
 |||

RESULT 3 AAB81987

ID AAB81987 standard; protein; 582 AA.

XX AAB81987;

XX 03-JUL-2001 (first entry)

XX Ganglioside GD3 specific antibody related protein SEQ ID NO: 53.

DE Ganglioside; GD3; complementarity determining region; CDR; antibody;

XX cancer.

XX Synthetic.

OS WO200123432-A1.

XX 05-APR-2001.

XX 29-SEP-2000; 2000WO-JP006774.

XX 30-SEP-1999; 99JP-00278291.

XX 06-APR-2000; 2000JP-00105088.

XX (KYOW) KYOWA HAKKO KOGYO KK.

XX Hanai N, Shitara K, Nakamura K, Niwa R;

XX WPI; 2001-266143/27.

XX New human type complementation-determining region-transplanted antibody
 PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
 PT of e.g. tumors, with low antigenicity, little side effects but potent
 PT activity in cancer.

XX Claim 41; Page 168-172; 183pp; Japanese.

XX The present invention describes a monoclonal antibody which can react
 CC specifically with ganglioside GD3. The antibody and its derivatives are
 CC useful in the diagnosis and therapy of tumours, particularly cancer
 CC diagnosis. The present sequence is a protein used in the exemplification
 CC of the invention
 CC

XX Sequence 582 AA;

Query Match 100.0%; Score 624; DB 4; Length 582;

Best Local Similarity 100.0%; Pred. No. 4.3e-49;
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVGLVESGGDFVQPGGSLRVSCAASGFAFSHYAMSWVRQAPGKLEWVAYISSGGSGTTY 60
 |||
 DB 1 EVGLVESGGDFVQPGGSLRVSCAASGFAFSHYAMSWVRQAPGKLEWVAYISSGGSGTTY 60
 |||
 QY 61 SDSVKGRFTISRDNASKNTLYLQWRSLRAEDSAVYFCTRVKLGTYYPDSWQGTLLTVSS 119
 |||
 DB 61 SDSVKGRFTISRDNASKNTLYLQWRSLRAEDSAVYFCTRVKLGTYYPDSWQGTLLTVSS 119
 |||

RESULT 4 AAB81989

ID AAB81989 standard; protein; 119 AA.

XX AAB81989;

XX 03-JUL-2001 (first entry)

XX Ganglioside GD3 specific antibody related protein SEQ ID NO: 55.

DE Ganglioside; GD3; complementarity determining region; CDR; antibody;

XX cancer.

XX Mus musculus.

XX WO200123432-A1.

XX 05-APR-2001.

XX 29-SEP-2000; 2000WO-JP006774.

XX 30-SEP-1999; 99JP-00278291.
 PR 06-APR-2000; 2000JP-00105088.
 XX (KYOW) KYOWA HAKKO KOGYO KK.
 PA Hanai N, Shitara K, Nakamura K, Niwa R;
 PI WPI; 2001-266143/27.
 DR
 XX
 PT New human type complementation-determining region-transplanted antibody
 PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
 PT of e.g. tumors, with low antigenicity, little side effects but potent
 PT activity in cancer.
 XX
 PS Claim 10; Page 173-174; 183pp; Japanese.
 CC The present invention describes a monoclonal antibody which can react
 CC specifically with ganglioside GD3. The antibody and its derivatives are
 CC useful in the diagnosis and therapy of tumors, particularly cancer
 CC diagnosis. The present sequence is a protein used in the exemplification
 CC of the invention
 CC
 XX Sequence 119 AA;
 SQ
 Query Match 92.8%; Score 579; DB 4; Length 119;
 Best Local Similarity 91.6%; Pred. No. 1.1e-45;
 Matches 109; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
 Oy 1 EVQLVESGDDPVQPGGSLRVSCAAGFAFSPHYAMSWVRQAPGKLEWVAIYSSGSGTTY 60
 Db 1 EYTLVESGDDPVQPGGSLRVSCAAGFAFSPHYAMSWVRQAPKRLWVAIYSSGSGTTY 60
 Oy 61 SDSVKGRFTISRDNKNTLYLQWRSLRAEDSAVYFCTRYVLTGYYPDSWGQGTLLTVSS 119
 Db 61 SDSVKGRFTISRDNKNTLYLQWRSLRSEDSDAMVFCTRYVLTGYYPDSWGQGTLLTVSS 119
 RESULT 5
 ABU11012
 ID ABU11012 standard; protein; 119 AA.
 AC ABU11012;
 XX
 DT 04-FEB-2003 (first entry)
 XX
 DE Modified ganglioside GD3 antibody associated protein #5.
 XX
 KW Ganglioside GD3; anti-ganglioside GD3 antibody; tumour; melanoma.
 XX
 OS Mus musculus.
 XX
 PN WO200278739-A1.
 XX
 PD 10-OCT-2002.
 XX
 PF 29-MAR-2002; 2002WO-JP003170.
 XX
 PR 29-MAR-2001; 2001JP-00097483.
 XX
 PA (KYOW) KYOWA HAKKO KOGYO KK.
 XX
 PI Shitara K, Niwa R, Kanazawa J, Asada M;
 XX
 DR WPI; 2003-067410/06.
 XX
 PT Drugs containing genetically-modified antibody against ganglioside GD3,
 PT its fragment, immunocompetent cell activators or/and anticancer agents in
 PT combination, applicable in treating malignant tumor like melanoma.
 XX
 PS Claim 7; Page 112-113; 121pp; Japanese.
 CC The invention describes drugs contain a genetically-modified antibody

CC against ganglioside GD3 or its fragment and at least 1 of a substance
 CC capable of activating immunocompetent cells and a substance having an
 CC anticancer activity in combination. The drugs can be used to treat tumour
 CC like melanoma and can provide a treatment with enhanced therapeutic
 CC effect and little side-reactions, particularly to relieve problems of
 CC side-effects during the conventional single administration. This sequence
 CC represents a protein associated with the anti- ganglioside GD3 antibody
 CC
 XX Sequence 119 AA;
 SQ
 Query Match 92.8%; Score 579; DB 6; Length 119;
 Best Local Similarity 91.6%; Pred. No. 1.1e-45;
 Matches 109; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
 Oy 1 EVQLVESGDDPVQPGGSLRVSCAAGFAFSPHYAMSWVRQAPGKLEWVAIYSSGSGTTY 60
 Db 1 EYTLVESGDDPVQPGGSLRVSCAAGFAFSPHYAMSWVRQAPKRLWVAIYSSGSGTTY 60
 Oy 61 SDSVKGRFTISRDNKNTLYLQWRSLRAEDSAVYFCTRYVLTGYYPDSWGQGTLLTVSS 119
 Db 61 SDSVKGRFTISRDNKNTLYLQWRSLRSEDSDAMVFCTRYVLTGYYPDSWGQGTLLTVSS 119
 RESULT 6
 AAR33256
 ID AAR33256 standard; protein; 130 AA.
 AC AAR33256;
 XX
 DT 25-MAR-2003 (revised)
 DT 12-JUL-1993 (first entry)
 XX
 DE Rat immunoglobulin H chain variable region of pK4641HA3.
 XX
 KW Promoter; variable; region; rat; immunoglobulin; heavy; H; chain;
 KW humanised; chimeric; antibody; expression vector.
 XX
 OS Rattus rattus.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..10 "Signal peptide"
 FT Protein 11..130
 FT /note= "Mature protein"
 XX
 PN EP533199-A2.
 XX
 PD 24-MAR-1993.
 XX
 PF 18-SEP-1992; 92EP-00116026.
 XX
 PR 18-SEP-1991; 91JP-00238375.
 XX
 PA (KYOW) KYOWA HAKKO KOGYO CO LTD.
 XX
 PI Shitara K, Hanai N, Hasegawa M, Miyaji H, Kuwana Y;
 XX
 DR WPI; 1993-095510/12.
 DR N-PSDB; AA033257.
 XX
 PT Humanised chimeric antibody prodn. against ganglioside GD3 - for treating
 PT cancers, such as melanoma, neuroblastoma, etc.
 XX
 PS Claim 6; Page 29-30; 63pp; English.
 XX
 CC The sequences given in AAR33256-57 represent rat heavy and light chain
 CC variable regions respectively. The DNA sequences encoding these proteins
 CC were used in the construction of humanised chimeric antibody expression
 CC vectors. In these humanised antibodies none of the amino acids of the non
 CC -human animal Ab variable region have been changed. (Updated on 25-MAR-
 CC 2003 to correct FN field.)
 CC
 XX Sequence 130 AA;
 SQ

```

Query Match          92.8%; Score 579; DB 2; Length 130;
Best Local Similarity 91.6%; Pred. No. 1.2e-45;
Matches 109; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 EVOLVESGDFVQPGGSLRVSCAASGFAFSHYMSWVROAPGKLEWVAYISSGSGTTY 60
DB 11 EVTLVSGGDFVQPGGSLRVSCAASGFAFSHYMSWVROTPAKRLWVAYISSGSGTTY 70

QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRYKLTGYYPDSWGQGTLLTVSS 119
DB 71 SDSVKGRFTISRDNKNTLYLQMRSLRSEDSAVYFCTRYKLTGYYPDSWGQGTLLTVSS 129

RESULT 7
AAR53341
ID AAR53341 standard; protein; 130 AA.
XX
AC AAR53341;
XX
DT 18-NOV-1994 (first entry)
XX
DE KM641 L chain variable region.
XX
KM Monoclonal antibody; Ab; ganglioside GM2; chimera; chimeric antibody;
KM expression vector; heavy; light; chain; hypervariable region; CDR;
KM constant region; hybridoma; Ig; immunoglobulin; promoter; enhancer.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT Peptide 1..10
FT /label= sig_peptide
XX
PN AU9346181-A.
XX
PD 17-MAR-1994.
XX
PF 07-SEP-1993; 93AU-00046181.
XX
PR 07-SEP-1992; 92JP-00238452.
XX
PA (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI Nakamura K, Koike M, Shitara K, Hanai N, Kuwana Y, Hasegawa M;
DR WPI; 1994-126857/16.
DR N-PSDB; AAQ45439.
XX
PT Humanised antibody specific for ganglioside GM2 - used for producing a
PT cytotoxic effect on cancers such as melanoma, neuroblastoma and glioma.
XX
PS Example 2; Page 116-117; 191pp; English.
XX
CC Example 2 describes the construction of the vector pCh1641HA1 for
CC chimeric human antibody H chain expression. mRNA from mouse anti-CD3
CC monoclonal Ab KM641-producing cells was isolated and KM641 H and L chain
CC cDNAs isolated. The base sequences of the Ig variable regions in KM641 H
CC chain cDNA (pKM641HA3) and KM641 L chain cDNA (pKM641LA2) are given in
CC AAQ45438-39. A KM641-derived chimeric human Ab H chain expression vector
CC was constructed by joining the H chain variable region gene from
CC pKM641HA1 to a vector for chimeric human Ab H chain expression using the
CC synthetic DNAs given in AAQ63439 and AAQ63440
XX
SQ Sequence 130 AA;

Query Match          92.8%; Score 579; DB 2; Length 130;
Best Local Similarity 91.6%; Pred. No. 1.2e-45;
Matches 109; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 EVOLVESGDFVQPGGSLRVSCAASGFAFSHYMSWVROAPGKLEWVAYISSGSGTTY 60
DB 11 EVTLVSGGDFVQPGGSLRVSCAASGFAFSHYMSWVROTPAKRLWVAYISSGSGTTY 70

```

```

QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRYKLTGYYPDSWGQGTLLTVSS 119
DB 71 SDSVKGRFTISRDNKNTLYLQMRSLRSEDSAVYFCTRYKLTGYYPDSWGQGTLLTVSS 129

RESULT 8
AAI28369
ID AAI28369 standard; protein; 130 AA.
XX
AC AAI28369;
XX
DT 04-NOV-1999 (first entry)
XX
DE pKM641 HA3 immunoglobulin heavy chain.
XX
KM antibody; nucleotide; genomic; hypervariable region; chimeric;
KM light chain; amino acid.
XX
OS Mus sp.
XX
PN US939532-A.
XX
PD 17-AUG-1999.
XX
PF 07-JUN-1995; 95US-00483528.
XX
PR 07-SEP-1993; 93US-00116778.
XX
PA (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI Nakamura K, Hanai N, Kuwana Y, Hasegawa M, Koike M, Shitara K;
DR WPI; 1999-468416/39.
DR N-PSDB; AAX99482.
XX
PT Chimeric human antibody expression vectors.
XX
PS Example 1; Col 99-101; 188pp; English.
XX
CC This immunoglobulin region was isolated from pKM641HA3. This sequence has
CC no methionine initiation codon and the leader sequence was partly
CC lacking. The chimeric human antibodies are useful in the treatment of
CC cancer, especially that which is of neural ectodermal origin. In contrast
CC to prior art constructs based on mouse monoclonal antibodies, the
CC chimeric human antibodies do not cause anti-mouse immunoglobulin
CC production. The chimeric human antibodies have a prolonged half-life and
CC a reduced frequency of adverse effects when compared to mouse monoclonal
CC antibodies
XX
SQ Sequence 130 AA;

Query Match          92.8%; Score 579; DB 2; Length 130;
Best Local Similarity 91.6%; Pred. No. 1.2e-45;
Matches 109; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 EVOLVESGDFVQPGGSLRVSCAASGFAFSHYMSWVROAPGKLEWVAYISSGSGTTY 60
DB 11 EVTLVSGGDFVQPGGSLRVSCAASGFAFSHYMSWVROTPAKRLWVAYISSGSGTTY 70

QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRYKLTGYYPDSWGQGTLLTVSS 119
DB 71 SDSVKGRFTISRDNKNTLYLQMRSLRSEDSAVYFCTRYKLTGYYPDSWGQGTLLTVSS 129

RESULT 9
AAB01627
ID AAB01627 standard; protein; 130 AA.
XX
AC AAB01627;
XX
DT 07-DEC-2000 (first entry)
XX

```

```

DE  Murine immunoglobulin heavy chain variable region.
XX
XX  Mouse; immunoglobulin; H chain; heavy chain; variable region; cancer;
XX  humanised antibody.
OS  Mus sp.
XX
XX  Key Location/Qualifiers
FH Peptide 1..10
FT Peptide /label= signal_peptide
FT Protein 11..130
FT /label= mature_immunoglobulin_heavy_chain_variable_region
FN EPI013761-A2.
PD
PD 28-JUN-2000.
XX
XX 18-SEP-1992; 99EP-00124345.
XX
XX 18-SEP-1991; 91JP-00238375.
XX 18-SEP-1992; 92EP-00116026.
XX
XX (KYOW ) KYOWA HAKKO KOGYO KK.
PA
XX
PI Shitara K, Hanai N, Hasegawa M, Miyaji H, Kuwana Y;
XX
XX WPI; 2000-402204/35.
DR N-PSDB; AAA51003.
XX
XX New humanized chimera antibody KM-871 useful for treating cancer,
PT comprises variable region of mouse monoclonal antibody, reactive with
PT ganglioside and human antibody constant region.
XX
XX Claim 14; Page 27-28; 655p; English.
XX
XX The present sequence is a murine immunoglobulin heavy chain variable
XX region from plasmid KM-641. The coding sequence was used in the creation
XX of an expression vector, along with the sequence for a human antibody, to
XX produce humanised chimaeric antibodies, which can be used to treat
XX cancer. Humanised chimaeric antibodies are more effective than mouse
XX antibodies as they do not provoke a reaction in the human and side
XX effects, such as the formation of anti-mouse immunoglobulin antibody and
XX the rapid half-life of the immunoglobulins, do not occur
XX
XX Sequence 130 AA;
SQ
Query Match 92.8%; Score 579; DB 3; Length 130;
Best Local Similarity 91.6%; Pred. No. 1.2e-45;
Matches 109; Conservative 5; Mismatches 5; Indels 0; Gaps 0
OY 1 EVQLVESGDDFVPGSGSLRVSCAAGFPAFASHYAMSVMRQAPGKGLHWVAIYSSGGSGITY 60
DB 11 EYTLVESGDDFVPGSGSLRVSCAAGFPAFASHYAMSVMRQTPAKRIEHWVAIYSSGGSGITY 70
OY 61 SDSVKGRTTISDNSKNTLYLQMRSLRAEDSAVYCTRYKLTGYTFDSWGQTLITVSS 119
DB 71 SDSVKGRTTISDNSKNTLYLQMRSLREDSAMVCTRYKLTGYTFDSWGQTLITVSS 129
RESULT 10
AAB81977
ID AAB81977 standard; protein; 138 AA.
XX
XX AAB81977;
AC
XX 03-JUL-2001 (first entry)
XX
XX Ganglioside GD3 specific antibody related protein SEQ ID NO: 1.
DE
XX Ganglioside; GD3; complementarity determining region; CDR; antibody;
KW cancer.
XX
XX Mus musculus.
OS

```

```

XX  WO200123432-A1.
XX
XX
XX  05-APR-2001.
XX
XX  29-SEP-2000; 2000WO-JP006774.
XX
XX  30-SEP-1999; 99JP-00278291.
XX  06-APR-2000; 2000JP-00105086.
XX
XX  (KYOW ) KYOWA HAKKO KOGYO KK.
XX
XX  Hanai N, Shitara K, Nakamura K, Niwa R;
XX  WPI; 2001-266143/27.
XX
XX  New human type complementation-determining region-transplanted antibody
XX  PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
XX  of e.g. tumors, with low antigenicity, little side effects but potent
XX  PT activity in cancer.
XX
XX  Example 1; Page 138-139; 183pp; Japanese.
XX
XX  The present invention describes a monoclonal antibody which can react
XX  CC specifically with ganglioside GD3. The antibody and its derivatives are
XX  CC useful in the diagnosis and therapy of tumors, particularly cancer
XX  CC diagnosis. The present sequence is a protein used in the exemplification
XX  CC of the invention
XX
XX  Sequence 138 AA;
XX
XX  Query Match 92.8%; Score 579; DB 4; Length 138;
XX  Best Local Similarity 91.6%; Pred. No. 1.3e-45;
XX  Matches 109; Conservative 5; Mismatches 5; Indels 0; Gaps 0.
XX
QY 1 EVLVESGDDVPQPGSGRVSQASGAFSHYAMSWVQAPGKLEWYAYISSGGSGITY 60
DB 20 EYLVESGDDVPKPGSGLRVSCASGAFSHYAMSWVQAPKRLWYAYISSGGSGITY 79
QY 61 SDSVVGRTTISRDNKNTLYLQMSLRRAEDSAVYFCTREVKLGITYYFDSWGQGTLLTVSS 119
DB 80 SDSVVGRTTISRDNKNTLYLQMSLRRAEDSAVYFCTREVKLGITYYFDSWGQGTLLTVSS 138
XX
XX  RESULT 11
XX  ABU11002
XX  ID ABU11002 standard; protein; 138 AA.
XX
XX  AC ABU11002;
XX
XX  04-FEB-2003 (first entry)
XX
XX  Modified ganglioside GD3 antibody associated protein #1.
XX  DE
XX  Ganglioside GD3; anti-ganglioside GD3 antibody; tumour; melanoma.
XX  KW
XX  Mus musculus.
XX  OS
XX  WO200278739-A1.
XX  PN
XX  10-OCT-2002.
XX  PD
XX  29-MAR-2002; 2002WO-JP003170.
XX  PF
XX  29-MAR-2001; 2001JP-00097483.
XX  PR
XX  (KYOW ) KYOWA HAKKO KOGYO KK.
XX  PA
XX  Shitara K, Niwa R, Kanazawa J, Asada M;
XX  PI
XX  WPI; 2003-067410/06.
XX  DR
XX
XX  Drugs containing genetically-modified antibody against ganglioside GD3.

```

PT its fragment, immunocompetent cell activators or/and antitumor agents in
PT combination, applicable in treating malignant tumor like melanoma.
XX
PS Example 3; Page 97; 121pp; Japanese.
XX
CC The invention describes drugs contain a genetically-modified antibody
CC against ganglioside GD3 or its fragment and at least 1 of a substance
CC capable of activating immunocompetent cells and a substance having an
CC antitumor activity in combination. The drugs can be used to treat tumour
CC like melanoma and can provide a treatment with enhanced therapeutic
CC effect and little side-reactions, particularly to relieve problems of
CC side-effects during the conventional single administration. This sequence
CC represents a protein associated with the anti- ganglioside GD3 antibody
CC
SQ Sequence 138 AA;

Query Match 92.8%; Score 579; DB 6; Length 138;
Best Local Similarity 91.6%; Pred. No. 1.3e-45;
Matches 109; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 1 EVLVSSGDFVQPGSLRVSCAASGFAFSHYAMSWVRQAPGKGLWVAYISSGSGTTY 60
DB 20 EVLVSSGDFVQPGSLRVSCAASGFAFSHYAMSWVRQAPARLEWVAYISSGSGTTY 79
Qy 61 SDSVKGRFTISRDNKNTLYLQWRSIRAEBSAVYFCTRVKLGTYYPDSWGQTTLVSS 119
DB 80 SDSVKGRFTISRDNKNTLYLQWRSIRAEBSAVYFCTRVKLGTYYPDSWGQTTLVSS 138

RESULT 12
AAB81991
ID AAB81991 standard; protein; 582 AA.
XX
AC AAB81991;
XX
DT 03-JUL-2001 (first entry)
XX
DE Ganglioside GD3 specific antibody related protein SEQ ID NO: 57.
XX
KM Ganglioside; GD3; complementarity determining region; CDR; antibody;
KM cancer.
XX
OS Synthetic.
XX
PN WO200123432-A1.
XX
PD 05-APR-2001.
XX
PF 29-SEP-2000; 2000MO-JP006774.
XX
PR 30-SEP-1999; 99JP-00278291.
XX
PR 06-APR-2000; 2000JP-00105088.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Hanai N, Shitara K, Nakamura K, Niwa R;
XX
DR WPI; 2001-266143/27.
XX
PT New human type complementation-determining region-transplanted antibody
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
PT of e.g. tumors, with low antigenicity, little side effects but potent
PT activity in cancer.
XX
PS Claim 39; Page 175-179; 183pp; Japanese.
XX
CC The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumours, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention
XX
SQ Sequence 582 AA;

Query Match 92.8%; Score 579; DB 4; Length 582;
Best Local Similarity 91.6%; Pred. No. 6e-45;
Matches 109; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 1 EVLVSSGDFVQPGSLRVSCAASGFAFSHYAMSWVRQAPGKGLWVAYISSGSGTTY 60
DB 1 EVLVSSGDFVQPGSLRVSCAASGFAFSHYAMSWVRQAPARLEWVAYISSGSGTTY 60
Qy 61 SDSVKGRFTISRDNKNTLYLQWRSIRAEBSAVYFCTRVKLGTYYPDSWGQTTLVSS 119
DB 61 SDSVKGRFTISRDNKNTLYLQWRSIRAEBSAVYFCTRVKLGTYYPDSWGQTTLVSS 119

RESULT 13
AD025153
ID AD025153 standard; protein; 274 AA.
XX
AC AD025153;
XX
DT 01-JUL-2004 (first entry)
XX
DE Melanoma cell adhesion molecule binding protein, scFv5.
XX
KM melanoma cell adhesion molecule; MCAM; invasion; metastasis; cancer;
KM metastatic; sarcoma; cytostatic; anti-idiotypic.
XX
OS Unidentified.
XX
PN EP1382615-A1.
XX
PD 21-JAN-2004.
XX
PF 15-JUL-2002; 2002EP-00015591.
XX
PR 15-JUL-2002; 2002EP-00015591.
XX
PA (XERI-) XERION PHARM AG.
XX
PI Unger CM, Zehetmeier C;
XX
DR WPI; 2004-101663/11.
XX
DR N-PSDB; AD025162.
XX
PT Novel polypeptide useful for detecting melanoma cell adhesion molecules,
PT for treating or preventing metastasis in patient.
XX
PS Claim 1; SEQ ID NO 5; 63pp; English.
XX
CC The invention relates to a novel polypeptide e.g. an antibody fragment,
CC that binds to melanoma cell adhesion molecules (MCAM), comprising a
CC sequence chosen from fully defined sequences of 276, 277, 278, 274, 275,
CC 281 and 273 amino acids as given in the specification. The invention
CC further comprises: a bioconjugate comprising the melanoma cell adhesion
CC molecule binding protein; a diagnostic kit comprising the protein and/or
CC the bioconjugate and a container; a pharmaceutical composition comprising
CC the protein and/or bioconjugate and a carrier; an isolated nucleic acid
CC molecule encoding the protein; a vector comprising the nucleic acid; a
CC host cell comprising the nucleic acid and vector; use of a molecule
CC inhibiting MCAM function in the manufacture of a medicament for the
CC treatment or prevention of invasion and/or metastasis of naturally
CC occurring cancer cells, where invasiveness and/or metastatic potential of
CC the cancer cells depends on melanoma cell adhesion molecule (MCAM)
CC function; and a method for identifying a protein which binds specifically
CC to the extracellular region of MCAM, where the protein is capable of
CC inhibiting invasiveness of sarcoma cells. The novel protein and
CC compositions have cytostatic activity. The MCAM binding protein and
CC bioconjugate are useful for the detection of MCAM, or for identifying a
CC MCAM inhibiting molecule that specifically binds to human MCAM. The MCAM
CC binding protein and bioconjugate are useful for treating or preventing
CC metastasis in a patient, involves administering the MCAM binding protein
CC and bioconjugate to inhibit MCAM mediated invasiveness and/or metastatic
CC potential. The MCAM inhibiting molecule is useful for inhibiting MCAM

CC function in the manufacture of a medicament for treating or preventing
CC invasion and/or metastasis of naturally occurring cancer cells. The MCM
CC inhibiting molecule inhibits gene expression of MCM, where the molecule
CC is an antisense oligonucleotide, an siRNA or siRNA-like hairpin RNA, or a
CC vector leading to the cellular presence of an siRNA or siRNA-like hairpin
CC RNA. The MCM inhibiting molecule inhibits gene expression of MCM, where
CC the molecule binds to the extracellular region of MCM, more particularly
CC the molecule is chosen from a small chemical compound, an antibody, an
CC antibody fragment, an anti-idiotypic antibody, the MCM binding protein
CC or its biocoupling agent. This sequence represents an MCM binding protein of
CC the invention.

XX SQ Sequence 274 AA;

Query Match 80.4%; Score 502; DB 8; Length 274;

Best Local Similarity 79.0%; Pred. No. 3,4e-38; Mismatches 16; Indels 0; Gaps 0;

Matches 94; Conservative 9; Mismatches 16; Indels 0; Gaps 0;

QY 1 EVOLVESGDPVPGGSLRVSCAAGFAFSGHYAMSWVRQAPGKLEWNAVYISGGSGTYY 60
DB 1 EVOLVESGGGLVPGGSLRLSCAASGFTFSYAMSWVRQAPGKLEWNAVYISGGSGTYY 60
QY 61 SDVKGKRFITSRDNSKNTLYLQWRSLRAEDSAVYFCTRVLTGTYRPSMGQTLTLYSS 119
DB 61 ADSVKGRFITSRDNSKNTLYLQWNSLRAEDTAVYYCAKSVLAKYFDFYWGQGLVTVSS 119

RESULT 14

AAE28151 AAE28151 standard; protein; 119 AA.

XX AA28151;

DT 27-DEC-2002 (first entry)

DE Human consensus heavy chain variable domain subgroup III (huIII).

XX Human; interferon alpha; IFNalpha; insulin-dependent diabetes mellitus;

KM autoimmune disease; systemic lupus erythematosus; autoimmune thyroiditis;

KM antibody therapy; immunosuppressive; antiinflammatory; dermatological;

XX 9F3 monoclonal antibody; heavy chain variable domain.

XX Homo sapiens.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Region 26..35 /note="Complementarity determining region 1 (CDR1)"

FT Region 50..66 /note="Complementarity determining region 2 (CDR2)"

FT Region 99..106 /note="Complementarity determining region 3 (CDR3)"

FT Region 106 /note="Complementarity determining region 3 (CDR3)"

XX Region 106

XX WO200266649-A2.

XX 29-AUG-2002.

XX 29-JAN-2002; 2002WO-US002709.

XX 22-FEB-2001; 2001US-0270775P.

XX 09-JAN-2002; 2002US-00044896.

XX (GETH) GENENTECH INC.

XX Chuntarapat A, Kim JK, Presta LG, Stewart T;

XX WPI; 2002-682767/73.

XX New anti-interferon alpha monoclonal antibody, 9F3, useful for treating

XX autoimmune diseases e.g. insulin-dependent diabetes mellitus, systemic

XX lupus erythematosus and autoimmune thyroiditis.

XX Disclosure; Page 98; 100pp; English.

XX The present invention relates to novel anti-interferon alpha (IFNalpha)
CC monoclonal antibody, 9F3 which binds to and neutralises a biological
CC activity of IFN-alpha subtypes. The anti-IFNalpha monoclonal antibodies
CC of the invention are useful for treating autoimmune diseases such as
CC insulin-dependent diabetes mellitus, systemic lupus erythematosus and
CC autoimmune thyroiditis. They are useful as reagents in diagnostic assays
CC for IFN-alpha expression, for the affinity purification of various IFN-
CC alpha subtypes from recombinant cell culture or natural resources and for
CC the detection of IFN-alpha in diagnostic assay methods. Sequences of the
CC invention are also useful in antibody therapy. The present sequence is
CC human consensus heavy chain variable domain subgroup III (huIII)

XX SQ Sequence 119 AA;

Query Match 80.0%; Score 499; DB 5; Length 119;

Best Local Similarity 80.7%; Pred. No. 2,6e-38; Mismatches 13; Indels 2; Gaps 1;

Matches 96; Conservative 8; Mismatches 13; Indels 2; Gaps 1;

QY 1 EVOLVESGDPVPGGSLRVSCAAGFAFSGHYAMSWVRQAPGKLEWNAVYISGGSGTYY 60
DB 1 EVOLVESGGGLVPGGSLRLSCAASGFTFSYAMSWVRQAPGKLEWNAVYISGGSGTYY 60
QY 61 SDVKGKRFITSRDNSKNTLYLQWRSLRAEDSAVYFCTRVLTGTYRPSMGQTLTLYSS 119
DB 61 ADSVKGRFITSRDNSKNTLYLQWNSLRAEDTAVYYCARGVG--YYDWGQGLVTVSS 117

RESULT 15

AAE2088 AAE2088 standard; protein; 119 AA.

XX AA2088;

DT 29-MAY-2001 (first entry)

DE Human Vh consensus framework humIII.

XX ErbB2 receptor; anti-ErbB2 antibody; tumour; cancer; breast cancer;

KM leukemia; cytostatic; carcinoma.

XX Homo sapiens.

XX WO200115730-A1.

XX 08-MAR-2001.

XX 25-AUG-2000; 2000WO-US023391.

XX 27-AUG-1999; 99US-0151018P.

XX 23-JUN-2000; 2000US-0213822P.

XX (GETH) GENENTECH INC.

XX Baughman SA, Shak S;

XX WPI; 2001-235058/24.

XX Treating a human patient with a disorder characterized by overexpression

XX of ErbB2 receptor such as a tumor or cancer (e.g. metastatic breast

XX carcinoma) comprises administering several dosages of an anti-ErbB2

XX antibody.

XX Disclosure; Fig 5B; 71pp; English.

XX The invention relates to treating cancer in a human susceptible to or

XX diagnosed with a disorder characterized by overexpression of ErbB2

XX receptor. The method comprises administering an initial dose of at least

XX approx.5 mg/kg of the anti-ErbB2 antibody, and administering subsequent

XX doses of the antibody in approximately the same amount or less than the

XX initial dose. The method is useful for treating a disorder characterized

XX by overexpression of ErbB2 receptor, particularly a benign or malignant

XX tumour, or a cancer. The cancer is selected from breast cancer

CC (particularly metastatic breast carcinoma), leukemia, squamous cell
CC cancer, small-cell lung cancer, non-small cell lung cancer, pancreatic
CC cancer, gastrointestinal cancer, glioblastoma, cervical cancer, ovarian
CC cancer, liver cancer, bladder cancer, hepatoma, colon cancer, colorectal
CC cancer, endometrial carcinoma, salivary gland carcinoma, kidney cancer,
CC liver cancer, prostate cancer, vulval cancer, thyroid cancer, hepatic
CC carcinoma and various types of head and neck cancer. The present sequence
CC represents the human variable heavy chain consensus framework humIII
CC (heavy subgroup III)
CC
CC
SQ Sequence 119 AA:

Query Match 79.8%; Score 498; DB 4; Length 119;
Best Local Similarity 79.8%; Pred. No. 3.3e-38;
Matches 95; Conservative 8; Mismatches 16; Indels 0; Gaps 0;

QY 1 EVOLVSGGDFVQPGSLRVSCAAGFARSHVMSWRQAPGKGLVAVIISGGSGTTY 60
Db 1 EVOLVSGGGLVQPGSLRLSCAAGFTFSYMSWRQAPGKGLVAVISDGGSTTY 60

QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLGTYYPDSWGQTLTVSS 119
Db 61 ADSVKRFTISRDNKNTLYLQWNSLRAEDTAVYYCARGRVGYSLVDYWGQTLTVSS 119

RESULT 16
AAB60401 ID AAB60401 standard; protein; 119 AA.
XX
XX AAB60401;
XX
DT 24-APR-2001 (first entry)
XX
DE Consensus human heavy chain subgroup III framework, SEQ ID NO:6.
XX
XX
KM Anti-ErbB2 monoclonal antibody 2C4; HER2; humanised. VH;
KM heavy chain variable region; cancer; cytostatic; EGFR-expressing cancer;
KM epidermal growth factor receptor; colon cancer; tumour;
KM colorectal cancer; non-small cell lung cancer; metastatic breast cancer;
KM affinity purification; subgroup III framework.
XX
XX Homo sapiens.
OS Synthetic.
OS
XX WO200100245-A2.
PN 04-JAN-2001.
XX
PD 23-JUN-2000; 2000MO-US017366.
XX
PF 25-JUN-1999; 99US-0141316P.
XX
PR (GETH) GENENTECH INC.
XX
PA Adams CW, Preesta LG, Sliwkowsky M;
PI WPI; 2001-080862/09.
XX
DR WPI; 2001-080862/09.
XX
XX Treating cancer in a human, where the cancer expresses epidermal growth
PT factor receptor (EGFR), comprises administering an antibody which binds
PT ErbB2.
XX
XX Example 3; Fig 7B; 89pp; English.
XX
XX The invention relates to a method for treating cancer in a human patient,
CC wherein the cancer expresses epidermal growth factor receptor (EGFR)
CC comprising administering an antibody which binds ErbB2 (HER2; AAB60408).
CC In particular, the anti-ErbB2 antibody is the murine monoclonal antibody
CC 2C4 (AAB60396, AAB60397) or a humanised version of 2C4 (AAB60398,
CC AAB60399). The invention also encompasses an isolated nucleic acid
CC encoding a humanised ErbB2-binding antibody; vectors and host cells
CC comprising such nucleic acids; the recombinant production of a humanised
CC ErbB2-binding antibody; and an immunconjugate comprising a humanised

CC ErbB2-binding antibody and a cytotoxic drug. The ErbB2-binding antibodies
CC act by antagonising ErbB receptors, and as inhibitors of transforming
CC growth factor alpha (TGF-alpha)-activated mitogen activated protein
CC kinase (MAPK). The method of the invention is used for treating cancer,
CC especially colon cancer, rectal cancer, colorectal cancer, lung cancer
CC (especially non-small cell lung cancer), or breast cancer (especially
CC metastatic breast cancer). The antibodies may also have non-therapeutic
CC uses e.g., as affinity purification agents. Using an antibody which binds
CC to ErbB2 to treat cancer is preferable to the use of EGFR-targeted
CC drugs, as EGFR is also highly expressed in other tissues such as the
CC liver and skin, where the active drug will also bind, with skin toxicity
CC having been observed for EGFR-targeted drugs. Antibodies which bind
CC ErbB2 are anticipated to have a better safety profile than such drugs.
CC The present sequence represents the consensus human heavy chain subgroup
CC III framework used to humanise the anti-ErbB2 antibody 2C4
CC
CC
SQ Sequence 119 AA:

Query Match 79.8%; Score 498; DB 4; Length 119;
Best Local Similarity 79.8%; Pred. No. 3.3e-38;
Matches 95; Conservative 8; Mismatches 16; Indels 0; Gaps 0;

QY 1 EVOLVSGGDFVQPGSLRVSCAAGFARSHVMSWRQAPGKGLVAVIISGGSGTTY 60
Db 1 EVOLVSGGGLVQPGSLRLSCAAGFTFSYMSWRQAPGKGLVAVISDGGSTTY 60

QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLGTYYPDSWGQTLTVSS 119
Db 61 ADSVKRFTISRDNKNTLYLQWNSLRAEDTAVYYCARGRVGYSLVDYWGQTLTVSS 119

RESULT 17
AAB61586 ID AAB61586 standard; protein; 119 AA.
XX
XX AAB61586;
XX
DT 04-APR-2001 (first entry)
XX
DE Human variable heavy chain consensus sequence.
XX
XX ErbB2; cytostatic; prostate cancer; receptor tyrosine kinase; human;
KM antibody; ErbB receptor; monoclonal antibody 2C4; variable heavy chain.
XX
XX Homo sapiens.
OS Synthetic.
OS
XX WO200100238-A1.
PN 04-JAN-2001.
XX
PD 23-JUN-2000; 2000MO-US017423.
XX
PF 25-JUN-1999; 99US-0141315P.
XX
PR (GETH) GENENTECH INC.
XX
PA (SLOK) SLOAN KETTERING INST CANCER RES.
XX
PI Agus DB, Scher HI, Sliwkowski MX;
XX
DR WPI; 2001-159131/16.
XX
XX Treating prostate cancer in a human comprises administering an antibody
PT which binds ErbB2 and blocks ligand activation of an ErbB receptor.
XX
XX Example 3; Fig 7; 93pp; English.
XX
XX The ErbB family of receptor tyrosine kinases are important mediators of
CC cell growth, differentiation and survival. The receptor family includes
CC four distinct members including Epidermal Growth Factor Receptor (EGFR or
CC ErbB1), HER2 (ErbB2 or p185^{neu}), HER3 (ErbB3) and Her4 (ErbB4 or tyro2).
CC The present invention relates to a method for treating prostate cancer.
CC The method comprises administering an antibody which binds ErbB2 and
CC blocks ligand activation of an ErbB receptor. Preferably, the antibody

CC blocks binding of monoclonal antibody 2C4 to ErbB2 and/or blocks TGF-
CC alpha activation of mitogen-activated protein kinase (MAPK). The present
CC sequence is the consensus framework for the human variable heavy chain.
CC This sequence was used in a sequence alignment homology with the variable
CC heavy chain of antibody 2C4 (see AAB61582)

XX Sequence 119 AA;

Query Match 79.8%; Score 498; DB 4; Length 119;
Best Local Similarity 79.8%; Pred. No. 3.3e-18;
Matches 95; Conservative 8; Mismatches 16; Indels 0; Gaps 0;

QY 1 EVOLVESGDFVQPGSLRVSCAASGFAFSHYAMSWVRQAPGKLEWNAVYSSGGSGTTY 60
DB 1 EVOLVESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKLEWNAVYSSDGGSTTY 60
QY 61 SDSVKGRFTISRNSKNTLYLQWRSIAPEDSAVYFCRTVKLTGYTPDSKQGTLLTVSS 119
DB 61 ADSVKGRFTISRNSKNTLYLQWNSIAPEDTAVYCARGRVGYSLVDYWGQGTLLTVSS 119

RESULT 18

AAU74541
ID AAU74541 standard; protein; 119 AA.

XX AAU74541;

DT 23-APR-2002 (first entry)

XX Human subgroup V_H III heavy chain variable region.

XX Human; subgroup V_H III; ErbB; epidermal growth factor receptor;
XX anti-ErbB antibody-maytansinoid conjugate; cancer; tumour; breast; ovary;
XX stomach; endometrium; salivary gland; lung; kidney; colon; colorectum;
XX thyroid; pancreas; prostate; bladder; ErbB2; neuronal disorder;
XX glioma; glioblastoma; astrocytic disorder; hypochalamic disorder; antibody;
XX glandular disorder; macrophage disorder; epithelial disorder;
XX stromal disorder; blastocoele disorder; inflammatory disorder;
XX angioendothelial disorder; immunological disorder; heavy chain variable region.

XX Homo sapiens.

XX US2002001587-A1.

XX 03-JAN-2002.

XX 16-MAR-2001; 2001US-00811123.

XX 16-MAR-2000; 2000US-0189844P.

XX 05-OCT-2000; 2000US-0238327P.

XX (ERIC/) ERICKSON S.

XX (SCHW/) SCHWALL R.

XX (SLIW/) SLIWKOWSKI M.

XX Erickson S, Schwall R, Sliwkowski M;

XX MPI; 2002-163686/21.

XX Claim 26; Fig 1; 93pp; English.

XX The invention relates to treating a tumour in a mammal, where the tumour
XX is characterized by the overexpression of an epidermal growth factor
XX receptor (ErbB) and does not respond or responds poorly, to treatment
XX with an anti-ErbB antibody, comprising administering to the mammal an
XX anti-ErbB antibody-maytansinoid conjugate. The method is useful for
XX treating cancer or tumours of the breast, stomach, endometrium,
XX salivary gland, lung, kidney, colon, colorectum, thyroid, pancreas,
XX prostate and bladder, preferably breast cancer. The breast cancer is a

CC metastatic breast cancer or an aggressive form of metastatic breast
CC cancer which overexpresses ErbB2. The method is also useful for treating
CC neuronal, glial, astrocytic, hypochalamic, glandular, macrophage,
CC epithelial, stromal, blastocoele, inflammatory, angiogenic and
CC immunological disorders. This sequence represents the human subgroup V_H
CC III heavy chain variable region used in the method of the invention

XX Sequence 119 AA;

Query Match 79.8%; Score 498; DB 5; Length 119;
Best Local Similarity 79.8%; Pred. No. 3.3e-18;
Matches 95; Conservative 8; Mismatches 16; Indels 0; Gaps 0;

QY 1 EVOLVESGDFVQPGSLRVSCAASGFAFSHYAMSWVRQAPGKLEWNAVYSSGGSGTTY 60
DB 1 EVOLVESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKLEWNAVYSSDGGSTTY 60
QY 61 SDSVKGRFTISRNSKNTLYLQWRSIAPEDSAVYFCRTVKLTGYTPDSKQGTLLTVSS 119
DB 61 ADSVKGRFTISRNSKNTLYLQWNSIAPEDTAVYCARGRVGYSLVDYWGQGTLLTVSS 119

RESULT 19

ADE71455
ID ADE71455 standard; protein; 119 AA.

XX ADE71455;

DT 29-JAN-2004 (first entry)

XX Human antibody variable heavy chain framework.

XX cytochrome; ErbB2 antagonist; tyrosine kinase inhibitor; cancer; ErbB2;
XX ErbB2 antibody; carcinoma; lymphoma; blastoma; sarcoma; liposarcoma;
XX neuroendocrine tumour; mesothelioma; schwannoma; meningioma;
XX adenocarcinoma; melanoma; leukaemia; lymphoid malignancy;
XX squamous cell cancer; epithelial squamous cell cancer; lung cancer;
XX small-cell lung cancer; non-small cell lung cancer;
XX adenocarcinoma of the lung; squamous carcinoma of the lung;
XX cancer of the peritoneum; hepatocellular cancer; gastric cancer;
XX stomach cancer; gastrointestinal cancer; pancreatic cancer; glioblastoma;
XX cervical cancer; ovarian cancer; liver cancer; bladder cancer; hepatoma;
XX breast cancer; colon cancer; rectal cancer; colorectal cancer;
XX endometrial carcinoma; uterine carcinoma; salivary gland carcinoma;
XX kidney cancer; renal cancer; prostate cancer; vulval cancer;
XX thyroid cancer; hepatic carcinoma; anal carcinoma; penile carcinoma;
XX testicular cancer; oesophageal cancer; tumour of the biliary tract;
XX head and neck cancer; human antibody; variable heavy chain framework.

XX Homo sapiens.

XX US2003086924-A1.

XX 08-MAY-2003.

XX 10-OCT-2002; 2002US-00268501.

XX 25-JUN-1999; 99US-0141316P.

XX 23-JUN-2000; 2000US-00602812.

XX (GETH) GENENTECH INC.

XX Sliwkowski MX;

XX MPI; 2004-020226/02.

XX Treating cancer (e.g. carcinoma, lymphoma or sarcoma) that expresses
XX ErbB2 by administering to a patient an anti-ErbB2 antibody, and
XX optionally an epidermal growth factor receptor-targeted drug or a
XX tyrosine kinase inhibitor.

XX Example 3; SEQ ID NO 6; 56pp; English.

CC The invention describes a method of treating cancer that expresses ErbB2
CC comprising administering to a patient an antibody that binds ErbB2.
CC Specifically claimed are antibodies that bind ErbB2, particularly
CC monoclonal antibody 2C4 or humanised 2C4, or monoclonal antibody 4D5 or
CC humanised 4D5. The methods are useful for treating cancer in a patient,
CC particularly a human. The cancer includes carcinoma, lymphoma, blastoma,
CC sarcoma, liposarcoma, neuroendocrine tumour, mesothelioma, schwannoma,
CC meningioma, adenocarcinoma, melanoma, leukaemia, lymphoid malignancy,
CC squamous cell cancer, epithelial squamous cell cancer, lung cancer, small
CC -cell lung cancer, non-small cell lung cancer, adenocarcinoma of the
CC lung, squamous carcinoma of the lung, cancer of the peritoneum,
CC hepatocellular cancer, gastric or stomach cancer, gastrointestinal
CC cancer, pancreatic cancer, glioblastoma, cervical cancer, ovarian cancer,
CC liver cancer, bladder cancer, hepatoma, breast cancer, colon cancer,
CC rectal cancer, colorectal cancer, endometrial or uterine carcinoma,
CC salivary gland carcinoma, kidney or renal cancer, prostate cancer, vulval
CC carcinoma, thyroid cancer, hepatic carcinoma, anal carcinoma, penile
CC carcinoma, testicular cancer, esophageal cancer, a tumour of the biliary
CC tract, or head and neck cancer. This is the amino acid sequence of human
CC antibody variable heavy chain framework that was used to produce a
CC humanised antibody.

XX SQ Sequence 119 AA;

XX Query Match 79.8%; Score 498; DB 8; Length 119;

XX Best Local Similarity 79.8%; Pred. No. 3.3e-38; Mismatches 16; Indels 0; Gaps 0;

XX Matches 95; Conservative 8; Mismatches 16; Indels 0; Gaps 0;

Qy 1 EVQLVSGGDFVQPGSLRVSCAAGFAFSGHYAMSWVRQAPGKLEWVAIISGGSGTYY 60

Db 1 EVQLVSGGGLVPGSLRLSCAAGFTFSYAMSWVRQAPGKLEWVAIISGDSGTYY 60

Qy 61 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVLTGTYYPDSWGQGLTVTSS 119

Db 61 ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARGRVGYSLVDYWGQGLTVTSS 119

RESULT 20

ADJ88009 standard; protein; 119 AA.

AC ADJ88009;

DT 06-MAY-2004 (first entry)

DE Human variable heavy chain consensus peptide.

DE Cancer; ErbB2; gene therapy; human.

OS Homo sapiens.

OS unidentified.

PN US2004013667-A1.

PN 22-JAN-2004.

PF 27-JUN-2003; 2003US-00608626.

PR 25-JUN-1999; 99US-0141316P.

PR 23-JUN-2000; 2000US-00602812.

PR 10-OCT-2002; 2002US-00268501.

PA (GETH) GENENTECH INC.

PI Kelsey SM, Sliwkowski MX;

DR WPI; 2004-121529/12.

PT Treating cancer that expresses ErbB2 e.g., breast, colon, rectal or
PT colorectal cancer comprises administering an antibody that binds to ErbB2
PT to a patient.

PS Example 3; SEQ ID NO 6; 56pp; English.

XX The present invention relates to methods for treating cancer such as
CC carcinoma, lymphoma, blastoma, medulloblastoma, retinoblastoma, sarcoma,
CC liposarcoma, synovial cell sarcoma, neuroendocrine tumour, carcinoid
CC tumour, gastrinoma, islet cell cancer, mesothelioma, schwannoma, acoustic
CC neuroma, meningioma, adenocarcinoma, melanoma, leukaemia, lymphoid
CC malignancy, squamous cell cancer, epithelial squamous cell cancer, lung
CC cancer, small-cell lung cancer, non-small cell lung cancer,
CC adenocarcinoma of the lung, squamous carcinoma of the lung, cancer of the
CC peritoneum, hepatocellular cancer, gastric or stomach cancer,
CC gastrointestinal cancer, pancreatic cancer, glioblastoma, cervical
CC cancer, ovarian cancer, liver cancer, bladder cancer, hepatoma, breast
CC cancer, colon cancer, rectal cancer, colorectal cancer, endometrial or
CC uterine carcinoma, salivary gland carcinoma, kidney or renal cancer,
CC prostate cancer, vulvar cancer, thyroid cancer, hepatic carcinoma, anal
CC carcinoma, penile carcinoma, testicular cancer, esophageal cancer, a
CC tumour of the biliary tract or head and neck cancer with anti-ErbB2
CC antibodies. The invention is also useful in gene therapy. The present
CC sequence is human variable heavy chain consensus peptide.

XX SQ Sequence 119 AA;

XX Query Match 79.8%; Score 498; DB 8; Length 119;

XX Best Local Similarity 79.8%; Pred. No. 3.3e-38; Mismatches 16; Indels 0; Gaps 0;

XX Matches 95; Conservative 8; Mismatches 16; Indels 0; Gaps 0;

Qy 1 EVQLVSGGDFVQPGSLRVSCAAGFAFSGHYAMSWVRQAPGKLEWVAIISGGSGTYY 60

Db 1 EVQLVSGGGLVPGSLRLSCAAGFTFSYAMSWVRQAPGKLEWVAIISGDSGTYY 60

Qy 61 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVLTGTYYPDSWGQGLTVTSS 119

Db 61 ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARGRVGYSLVDYWGQGLTVTSS 119

RESULT 21

ADN12055 standard; protein; 119 AA.

AC ADN12055;

DT 17-JUN-2004 (first entry)

DE Variable heavy chain consensus sequence.

DE tumor; anti-HER2 antibody; HER2/HER3; HER2/HER1; Cytostatic; cancer.

OS Homo sapiens.

PN WO2004008099-A2.

PN 22-JAN-2004.

PF 11-JUL-2003; 2003WO-US021590.

PR 15-JUL-2002; 2002US-0396290P.

PR 20-JUN-2003; 2003US-0480043P.

PA (GETH) GENENTECH INC.

PI Koll H, Bossemailer B, Mueller H, Sliwkowski MX, Kelsey SM;

DR WPI; 2004-156546/15.

PT Identifying a tumor responsive to treatment with an anti-HER2 antibody,
PT useful in treating cancer, comprises detecting the presence of a
PT HER2/HER3 and/or HER2/HER1 protein complex.

PS Disclosure; SEQ ID NO 6; 105pp; English.

CC The present invention relates to identifying a tumor responsive to
CC treatment with an anti-HER2 antibody involves detecting the presence of
CC an HER2/HER3 and/or HER2/HER1 protein complex in a sample of the tumor.

CC The method is useful in identifying a tumor as responsive to treatment
CC with an anti-HER2 antibody. The methods and antibodies are useful in
CC treating a condition or disorder including tumor or cancer, e.g. breast,
CC prostate, lung, colorectal or ovarian cancer. The present sequence
CC represents a variable heavy chain consensus sequence.

XX Sequence 119 AA;

Query Match 79.8%; Score 498; DB 8; Length 119;
Best Local Similarity 79.8%; Pred. No. 3.3e-38;
Matches 95; Conservative 8; Mismatches 16; Indels 0; Gaps 0;

QY 1 EVQLVSGDFOVPGGSLRVSCAASGPAFSPHYAMSWVRQAPGKGLEWVAIISGGSGTTY 60
DB 1 EVQLVSGGGLVPGGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVAIISGGSGTTY 60
QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVLTGTYFPDSMCGTLTVSS 119
DB 61 ADSVKGRFTISRDNKNTLYLQMRSLRAEDTAVYYCARGRVGSIVDYWGQGLTVTVSS 119

RESULT 22

ADP43329 standard; protein; 119 AA.

ADP43329;

26-AUG-2004 (first entry)

Human monoclonal variable heavy kappa chain antibody SegID 6.

human; variable heavy kappa chain; antibody;
epidermal growth factor receptor; ErbB; ErbB2;
transforming growth factor alpha; benign hyperproliferative disorder;
psoriasis; endometriosis; scleroderma; vascular disease; atherosclerosis;
resenosis; colon polyps; fibroadenoma; respiratory disease;
chronic bronchitis; cystic fibrosis; cytostatic; antipsoriatic;
gynaecological; dermatological; vasotrophic; antiarteriosclerotic;
cardiac; antineural; antidiabetic; hypotensive; antiaesthetic;
antiallergic; antiinflammatory; antitensive.

XX Homo sapiens.

XX WO2004048525-A2.

XX 10-JUN-2004.

XX 21-NOV-2003; 2003WO-US037367.

XX 21-NOV-2002; 2002US-0428027P.

XX (GENTH) GEMENTECH INC.

XX Sliwkowski MX, Brunetta PG;

XX WPI; 2004-450361/42.

XX Treating non-malignant disease or disorder such as psoriasis,
PT endometriosis, involving abnormal activation or production of epidermal
PT growth factor receptor or ErbB ligand by administering antibody that
PT binds ErbB2 to mammal.

XX Example 3; SEQ ID NO 6; 74pp; English.

XX This invention refers to a novel method for treating a non-malignant
CC disease that involves abnormal activation or production of an epidermal
CC growth factor receptor (ErbB) receptor or an ErbB ligand. Specifically,
CC it refers to the use of humanised murine anti-ErbB2 antibodies to block
CC ligand activation of the ErbB receptor, where the ErbB ligand is a
CC transforming growth factor alpha that promotes mitogen-activated protein
CC kinase (MAPK). The present invention describes conjugating the monoclonal
CC murine antibody 2C4, or more particularly the humanised antibody 574, to
CC a cytotoxic or therapeutic agent such that it can be used to treat a

CC benign hyperproliferative disorder, psoriasis, endometriosis,
CC scleroderma, vascular disease (such as atherosclerosis or resenosis),
CC colon polyps, fibroadenoma or respiratory disease (such as chronic
CC bronchitis or cystic fibrosis). Accordingly, they exhibit cytostatic,
CC antipsoriatic, gynaecological, dermatological, vasotrophic, hypotensive,
CC antiarteriosclerotic, cardiac, antineural, antidiabetic, hypotensive,
CC antiaesthetic, antiallergic, antiinflammatory and antitensive activities.
CC This polypeptide sequence is the human variable heavy kappa chain protein
CC used to humanise the murine anti-ErbB2 proteins of the invention.

XX Sequence 119 AA;

Query Match 79.8%; Score 498; DB 8; Length 119;
Best Local Similarity 79.8%; Pred. No. 3.3e-38;
Matches 95; Conservative 8; Mismatches 16; Indels 0; Gaps 0;

QY 1 EVQLVSGDFOVPGGSLRVSCAASGPAFSPHYAMSWVRQAPGKGLEWVAIISGGSGTTY 60
DB 1 EVQLVSGGGLVPGGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVAIISGGSGTTY 60
QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVLTGTYFPDSMCGTLTVSS 119
DB 61 ADSVKGRFTISRDNKNTLYLQMRSLRAEDTAVYYCARGRVGSIVDYWGQGLTVTVSS 119

RESULT 23

ABR01511 standard; protein; 224 AA.

ABR01511;

16-APR-2003 (first entry)

Human anti-TIMP-1 antibody heavy chain #9.

human; antibody; tissue inhibitor of metalloproteinase-1; TIMP-1; VLDLR3;
matrix metalloproteinase; MMP; variable heavy chain; VHCOR3; hepatotropic;
variable light chain; cytosolic; nephrotropic; cardiac; liver fibrosis;
alcoholic liver disease; cardiac fibrosis; acute coronary syndrome;
lupus nephritis; glomerulosclerotic renal disease; lung cancer;
idiopathic pulmonary fibrosis; benign prostate hypertrophy; colon cancer.

XX Homo sapiens.

XX WO200286085-A2.

XX 31-OCT-2002.

XX 24-APR-2002; 2002WO-US012801.

XX 24-APR-2001; 2001US-028563P.

XX (FARB) BAYER CORP.

XX (MORP-) MORPHOSYS AG.

XX Pan C, Knorr AM, Schauer M, Hirsch-Dietrich C, Kraft S, Krebs B;

XX WPI; 2003-129114/12.

XX N-PSDB; ABZ74762.

XX New human anti-TIMP-1 (tissue inhibitor of metalloproteinase-1) antibodies,
PT for diagnosing or ameliorating the symptoms of a disorder in which TIMP-1
PT is elevated, e.g. liver fibrosis, benign prostate hypertrophy or lung
PT cancer.

XX Claim 20; Page 153-154; 228pp; English.

XX The invention relates to a novel purified preparation of a human
CC antibody, which binds to a tissue inhibitor of metalloproteinase-1 (TIMP-1)
CC and neutralises a matrix metalloproteinase (MMP)-inhibiting activity of TIMP
CC -1. The antibody comprises a variable heavy chain (VHC)DR3 region and a
CC variable light chain (VLC)DR3 region. An antibody preparation of the
CC invention has hepatotropic, cytosolic, nephrotropic and cardiac

CC activity. The human antibody is useful for decreasing an MMP-inhibiting
 CC activity of a TIMP-1. It is especially useful for ameliorating the
 CC symptoms of a disorder in which TIMP-1 is elevated, e.g. liver fibrosis,
 CC alcoholic liver disease, cardiac fibrosis, acute coronary syndrome, lupus
 CC nephritis, glomerulonephrotic renal disease, idiopathic pulmonary
 CC fibrosis, benign prostatic hyperplasia, lung cancer or colon cancer. The
 CC antibody is also useful for detecting a TIMP-1 in a test preparation, or
 CC in diagnosing a disorder in which a TIMP-1 level is elevated. The
 CC sequences shown in ABR01502-ABR01545 represent the heavy chain regions of
 CC a human anti-TIMP-1 antibody of the invention
 XX
 SO Sequence 224 AA:
 Query Match 79.1%; Score 493.5; DB 6; Length 224;
 Best Local Similarity 79.5%; Pred. No. 1,7e-37;
 Matches 97; Conservative 7; Mismatches 13; Indels 5; Gaps 2;
 QY 1 EVQLVSSGGDFVPGGSLRVSCAASGFAFSGHYMSWVRQAPGKLEWVAISSGSGSTYY 60
 DB 1 QVQLVSSGGGLVPGGSLRLSCAASGFTFSYMSWVRQAPGKLEWVAISSGSGSTYY 60
 QY SDSVKGRTISRDNKNTLYLQNRSLRAEDSAVYFCTRVKLGTY--FDSWCGQTLTV 117
 DB 61 ADSVKGRTISRDNKNTLYLQNRSLRAEDTAVYCAR--LDITYPDLPFWGQGLVTV 118
 QY 118 SS 119
 DB 119 SS 120
 RESULT 24
 ADA89891
 ID ADA89891 standard; protein; 126 AA.
 AC ADA89891;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE MS-Roche #7 VH region amino acid sequence SEQ ID NO:6.
 XX
 KW antibody molecule; antibody; beta-A4 peptide; Abeta4; neuroprotective;
 KW neurotrophic; antiparkinsonian; gene therapy; amyloidogenesis;
 KW amyloid-plaque formation; beta-amyloid plaque; immunisation; dementia;
 KW Alzheimer's disease; motor neuropathy; Down's syndrome;
 KW Creutzfeldt Jacob disease; hereditary cerebral haemorrhage; amyloidosis;
 KW Parkinson's disease; HIV-related dementia; amyotrophic lateral sclerosis;
 KW neuronal disorder; aging.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO2003070760-A2.
 XX
 PD 28-AUG-2003.
 XX
 PF 20-FEB-2003; 2003WO-EP001759.
 XX
 PR 20-FEB-2002; 2002EP-0003844.
 XX
 XX (HOF) HOFMANN LA ROCHE & CO AG F.
 PA (MORP-) MORPHOSIS AG.
 XX
 PI Bardhoff M, Bohrmann B, Brockhaus M, Huber W, Kretzschmar T;
 PI Loehning C, Loetscher H, Nordstedt C, Rothe C;
 DR WPI; 2003-663848/62.
 XX
 PT New antibody molecule capable of specifically recognizing two regions of
 PT the beta-A4 peptide, useful for diagnosing, preventing or treating
 PT diseases associated with amyloidogenesis or amyloid-plaque formation
 PT (e.g. dementia).
 XX
 PS Claim 4; Page 39; 312pp; English.

XX The present invention describes an antibody molecule (1) capable of
 CC specifically recognising two regions of the beta-A4 peptide/Abeta4. The
 CC first region comprises the amino acid sequence Ala-Glu-Phe-Arg-His-Asp-
 CC Ser-Gly-Tyr ADA89886 or its fragment, and the second region comprises the
 CC amino acid sequence Val-His-His-Gln-Lys-Leu-Val-Phe-Phe-Ala-Glu-Asp-Val-
 CC Gly ADA89887 or its fragment. Also described: (1) a nucleic acid molecule
 CC encoding (1); (2) a vector comprising the nucleic acid of (1); (3) a host
 CC cell comprising the vector of (2); (4) preparing (1), comprising
 CC culturing the host cell of (3) under conditions that allow synthesis of
 CC (1) and recovering (1) from the culture; (5) a composition comprising (1),
 CC or an antibody molecule produced by method (4); (6) a kit comprising (1),
 CC nucleic acid of (1), vector of (2) or host cell of (3); (7) optimising
 CC (1); (8) testing the resulting Fab optimisation library by panning
 CC against Abeta4/Abeta4; (9) identifying optimised clones; (10) expressing
 CC of selected, optimised clones; (11) preparing a pharmaceutical
 CC composition, comprising optimisation of (1), and formulating the
 CC optimised antibody/antibody molecule with a carrier; and (12) a
 CC pharmaceutical composition prepared by method (8). (1) has
 CC neuroprotective, neurotrophic and antiparkinsonian activities, and can be
 CC used in gene therapy. The antibody molecule (1), nucleic acid molecule,
 CC vector or host is useful in preparing a pharmaceutical composition for
 CC the prevention and/or treatment of a disease associated with
 CC amyloidogenesis and/or amyloid-plaque formation. The antibody molecule
 CC may also be used in preparing a diagnostic composition for the detection
 CC of the disease mentioned above. The antibody is used for the
 CC differentiation of beta-amyloid plaques or for passive immunisation
 CC against beta-amyloid plaque formation. In particular, the disease is
 CC dementia, Alzheimer's disease, motor neuropathy, Down's syndrome,
 CC Creutzfeldt Jacob disease, hereditary cerebral haemorrhage with
 CC amyloidosis Dutch type, Parkinson's disease, HIV-related dementia,
 CC amyotrophic lateral sclerosis or neuronal disorders related to aging. The
 CC present sequence is used in the exemplification of the present invention.
 XX
 SO Sequence 126 AA:
 Query Match 78.9%; Score 492.5; DB 6; Length 126;
 Best Local Similarity 76.2%; Pred. No. 1.1e-37;
 Matches 96; Conservative 8; Mismatches 15; Indels 7; Gaps 1;
 QY 1 EVQLVSSGGDFVPGGSLRVSCAASGFAFSGHYMSWVRQAPGKLEWVAISSGSGSTYY 60
 DB 1 QVQLVSSGGGLVPGGSLRLSCAASGFTFSYMSWVRQAPGKLEWVAISSGSGSTYY 60
 QY SDSVKGRTISRDNKNTLYLQNRSLRAEDSAVYFCTRVKLGTY-----YFDSWCGQT 113
 DB 61 ADSVKGRTISRDNKNTLYLQNRSLRAEDTAVYCARGKGNTHKPYGYRYFDVWGQGT 120
 QY 114 LTVSS 119
 DB 121 LTVSS 126
 RESULT 25
 ADO36357
 ID ADO36357 standard; protein; 119 AA.
 AC ADO36357;
 XX
 DT 26-AUG-2004 (first entry)
 XX
 DE Intracellular interaction-related scFv protein SeqID21.
 XX
 KW immunoglobulin single domain; intracellular environment;
 KW intracellular interaction; immunoglobulin domain; scFv;
 KW single chain variable fragment.
 XX
 OS Unidentified.
 OS
 PN WO2004046185-A2.
 XX
 PD 03-JUN-2004.
 XX

PF 14-NOV-2003; 2003WO-GB004942.
XX
XX
PR 15-NOV-2002; 2002GB-00026729.
XX
XX
PA (MEDI-) MEDICAL RES COUNCIL.
XX
XX
PI Rabbits TH, Tanaka T;
XX
XX
DR WPI; 2004-431946/40.
XX
XX
PT Determining the ability of an immunoglobulin single domain to bind to a
PT target in an intracellular environment by assessing the intracellular
PT interaction between the immunoglobulin domain and the target by
PT monitoring the signal.
XX
XX
PS Disclosure; SEQ ID NO 21; 66pp; English.
XX
XX
CC This invention relates to a novel method of determining the ability of an
CC immunoglobulin single domain to bind to a target in an intracellular
CC environment comprising assessing the intracellular interaction between
CC the immunoglobulin domain and the target by monitoring the signal. The
CC method comprises providing a first molecule and a second molecule, where
CC stable interaction of the first and second molecules leads to the
CC generation of a signal; providing a single intracellular immunoglobulin
CC domain which is associated with the first molecule, where the single
CC immunoglobulin domain is free of complementary immunoglobulin domains;
CC providing an intracellular target which is associated with the second
CC molecule, such that association of the immunoglobulin domain and the
CC target leads to stable interaction of the first and second molecules and
CC generation of the signal; and assessing the intracellular interaction
CC between the immunoglobulin domain and the target by monitoring the
CC signal. The methods are useful for determining the ability of an
CC immunoglobulin single domain to bind to a target in an intracellular
CC environment. The present sequence is that of a single chain variable
CC fragment (scFv) protein which was used to illustrate the method of the
CC invention.
XX
XX
SQ Sequence 119 AA;
XX
XX
Query Match 78.8%; Score 492; DB 8; Length 119;
Best Local Similarity 78.2%; Pred. No. 1.2e-37;
Matches 93; Conservative 8; Mismatches 18; Indels 0; Gaps 0;
QY 1 EVQLVESGDDPVQPGSLRVSCAAGFARSHYAMSWVRQAPGKGLWVAIVSSGSGCTYY 60
DB 1 QVQLVSGGGLVQPGSLRLSCAASGFTFSYGMHWVRQAPGKGLWVAIFIRDSNEY 60
QY 61 SSVKGRFTISRDNKNTLYLQWRSIPAEPSAVYFCTRVKLGTYYPDSWGQGLTLTVSS 119
DB 61 VDSVKGRFTISRDNKNTLYLQWRSIPAEPSAVYFCTRVKLGTYYPDSWGQGLTLTVSS 119
XX
XX
RESULT 26
ADQ75230
ID ADQ75230 standard; protein; 119 AA.
XX
XX
AC ADQ75230;
XX
XX
DT 09-SEP-2004 (first entry)
XX
XX
DE Immunoglobulin heavy chain variable domain A28 sequence.
XX
XX
KW Immunoglobulin; variable domain.
XX
XX
OS Unidentified.
XX
XX
PN WO2004046189-A2.
XX
XX
PD 03-JUN-2004.
XX
XX
PF 14-NOV-2003; 2003WO-GB004964.
XX
XX
PR 15-NOV-2002; 2002GB-00026731.

XX
XX
PA (MEDI-) MEDICAL RES COUNCIL.
XX
XX
PI Rabbits TH, Chung G, Tanaka T, Lobato-Caballero MN, Forster A;
XX
XX
DR WPI; 2004-431950/40.
XX
XX
PT Preparing a double stranded nucleic acid comprises providing a set of
PT three or more overlapping oligonucleotides which anneal to form the + and
PT - strands of a nucleic acid that encodes at least part of an
PT immunoglobulin variable domain.
XX
XX
PS Disclosure; SEQ ID NO 21; 53pp; English.
XX
XX
CC The invention relates to a method of preparing a double stranded nucleic
CC acid, which encodes an immunoglobulin comprising providing a set of three
CC or more overlapping oligonucleotides which anneal to form the + and -
CC strands of a nucleic acid that encodes at least part of an immunoglobulin
CC variable domain. The methods are useful for preparing nucleic acids,
CC preferably immunoglobulin genes. This sequence represents one of the
CC immunoglobulin variable heavy chain produced by the method of the
CC invention.
XX
XX
SQ Sequence 119 AA;
XX
XX
Query Match 78.8%; Score 492; DB 8; Length 119;
Best Local Similarity 78.2%; Pred. No. 1.2e-37;
Matches 93; Conservative 8; Mismatches 18; Indels 0; Gaps 0;
QY 1 EVQLVESGDDPVQPGSLRVSCAAGFARSHYAMSWVRQAPGKGLWVAIVSSGSGCTYY 60
DB 1 QVQLVSGGGLVQPGSLRLSCAASGFTFSYGMHWVRQAPGKGLWVAIFIRDSNEY 60
QY 61 SSVKGRFTISRDNKNTLYLQWRSIPAEPSAVYFCTRVKLGTYYPDSWGQGLTLTVSS 119
DB 61 VDSVKGRFTISRDNKNTLYLQWRSIPAEPSAVYFCTRVKLGTYYPDSWGQGLTLTVSS 119
XX
XX
RESULT 27
ADL91330
ID ADL91330 standard; protein; 121 AA.
XX
XX
AC ADL91330;
XX
XX
DT 20-MAY-2004 (first entry)
XX
XX
DE VH chain clone A28 of an intracellularly binding immunoglobulin Seqid 21.
XX
XX
KW antibody; variable chain; cytosolic; cytoplasmic degradation;
KW intracellular relocation; specific antigen positive cancer; leukaemia;
KW lymphoma; intracellularly binding immunoglobulin; BCR-ABL.
XX
XX
OS Unidentified.
XX
XX
PN WO2003077945-A1.
XX
XX
PD 25-SEP-2003.
XX
XX
PF 14-MAR-2003; 2003WO-GB001077.
XX
XX
PR 14-MAR-2002; 2002GB-00006043.
XX
XX
PR 15-NOV-2002; 2002GB-00026723.
XX
XX
PR 15-NOV-2002; 2002GB-00026727.
XX
XX
PA (MEDI-) MEDICAL RES COUNCIL.
XX
XX
PI Lobato-Caballero MN, Rabbits TH;
XX
XX
DR WPI; 2003-779088/73.
XX
XX
PT Use of an intracellularly binding immunoglobulin comprising at least one
PT antibody variable chain, in preparing a medicament for degrading one or
PT more specific antigens, or for treating specific antigen positive cancer.

PT e.g. leukemia.
XX
PS Example 1; SEQ ID NO 21; 86pp; English.
XX
CC This invention relates to novel immunoglobulin molecules that comprise at
CC least one antibody variable chain VH or VL framework region and are
CC capable of binding to a specific antigen within an intracellular
CC environment. Specifically, it refers to antibodies that can form an
CC insoluble complex with a cognate antigen, such that it can then be target
CC for degradation via the lysosome or proteasome systems. The present
CC invention describes the specific target antigen as the oncogenic fusion
CC protein BCR-ABL or the p210 antigen, such that this method can be used to
CC prepare a cytostatic medicament for the cytoplasmic degradation or
CC intracellular relocation of such an antigen or for the treatment of the
CC specific antigen positive cancer i.e. leukaemia or lymphoma. Furthermore,
CC the immunoglobulins may also be used for therapeutic, prophylactic or
CC diagnostic applications both in vitro and in vivo, as well as for assay
CC and reagent applications or in functional genomics. This polypeptide
CC sequence is a variable heavy chain (VH) framework region of an
CC intracellularly binding anti-ABL antibody of the invention.
XX
SQ Sequence 121 AA;
Query Match 78.8%; Score 492; DB 7; Length 121;
Best Local Similarity 78.2%; Pred. No. 1.2e-37;
Matches 93; Conservative 8; Mismatches 18; Indels 0; Gaps 0;
QY 1 EVOLVSGGDFVOPGSLRVSCAASGFAFSGHYAMSWVRQAPGKGLVAVYISGGSGTYY 60
Db 3 QVOLVSGGGLVOPGSLRVSCAASGFTTSSYGMHWVRQAPGKGLVAVFIRNDGSNEY 62
QY 61 SDSVKGRFTISRDNKNTLYLQWRSLRAEDSAVYFCTRVGLGTYYPDSWGQGLTVVSS 119
Db 63 VDSVKGRFTISRDNKNTLYLQWNSLRADPTAVYYCARGRSMYTFDYGQGLTVVSS 121
RESULT 28
AAU14320
ID AAU14320 standard; protein; 313 AA.
XX
AC AAU14320;
XX
DT 24-OCT-2001 (first entry)
XX
DE Human novel protein #191.
XX
DE Human: novel protein; Antianaemic; osteopathic; antiinflammatory;
KW immunomodulatory; cyclostatic; neuroprotective; vulnerary; nocotropic;
KW anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiviral;
KW antibacterial; antiallergic; dermatological; haemostatic; antiasthmatic;
KW thrombolytic; immunogen; antibody; gene therapy; neurological disorder;
KW Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;
KW tissue regeneration; immune disorder.
XX
OS Homo sapiens.
XX
PN WO200155437-A2.
XX
PD 02-AUG-2001.
XX
PF 25-JAN-2001; 2001WO-US002623.
XX
PR 25-JAN-2000; 2000US-00491404.
XX
PA (HYSR-) HYSRQ INC.
XX
PI Tang YT, Liu C, Dymnac RT;
XX
XX WPI; 2001-451939/48.
XX
XX N-PSDB; AAS22625.
XX
PT Isolated polypeptides useful for treating anti-inflammatory diseases,
PT nervous system disorders, and for regenerating bone and cartilage.

XX
PS Example 4; Page 630-631; 894pp; English.
XX
CC The invention relates to polynucleotides encoding novel human proteins or
CC their active domains. The polypeptides, polynucleotides and antibodies
CC raised against the polypeptides are used in a method of treatment of a
CC mammal and prevention of disorders caused by the aberrant protein
CC expression or activity. The polypeptides can be used as molecular weight
CC markers, food supplements, and in antibody production. The polypeptides
CC are used to identify compounds which bind to the polypeptides.
CC Polynucleotides of the invention are used as probes and primers, for
CC sequencing, for chromosome or gene mapping, in the production of
CC recombinant proteins, and in generating anti-sense DNA or RNA and in gene
CC therapy. Polypeptides of the invention can be used to target drugs to a
CC tumour, in assays to determine biological activity, to raise
CC antibodies/elicite an immune response, to determine quantitative protein
CC levels, as tissue markers, and to isolate receptors or ligands.
CC Polypeptides of the invention may also be useful in treating platelet
CC disorders, stem cell disorders, regenerating bone, cartilage, tendon,
CC ligament and/or nerve tissue, wound healing, treating burns, promoting
CC the proliferation, differentiation and survival of stem cells, as a
CC contraceptive, treating osteoporosis and osteoarthritis, anaemia,
CC Alzheimer's, Parkinson's and Huntington's diseases, amyotrophic lateral
CC sclerosis, stroke, immune deficiencies resulting from bacterial, viral or
CC fungal infection or from autoimmunity, cancer, allergy, asthma, graft-
CC versus-host disease, eczema, haemophilia, thrombosis, anti-inflammatory
CC diseases, nervous system disorders, and infection. The present sequence
CC represents a protein of the invention
XX
SQ Sequence 313 AA;
Query Match 78.8%; Score 492; DB 4; Length 313;
Best Local Similarity 74.8%; Pred. No. 3.2e-37;
Matches 95; Conservative 9; Mismatches 15; Indels 8; Gaps 1;
QY 1 EVOLVSGGDFVOPGSLRVSCAASGFAFSGHYAMSWVRQAPGKGLVAVYISGGSGTYY 60
Db 61 EVOLVSGGGLVOPGSLRVSCAASGFTTSSYAMSWVRQAPGKGLVAVSHISGGSGTYY 120
QY 61 SDSVKGRFTISRDNKNTLYLQWRSLRAEDSAVYFCTRVGLG-----TYFFDSWGQ 112
Db 121 ADSVKGRFTISRDNKNTLYLQWNSLRADPTAVYYCARHPRGYDYSSGSGYTFDYGQ 160
QY 113 TLTVVSS 119
Db 181 TLTVVSS 187
RESULT 29
AD158099
ID AD158099 standard; protein; 251 AA.
XX
AC AD158099;
XX
DT 22-APR-2004 (first entry)
XX
DE Reg IV-specific single chain antibody fragment (scFv) #58.
XX
DE antibody; regeneration IV; Reg IV; single chain antibody fragment; scFv;
KW inflammatory bowel disorder; ulcerative colitis; Crohn's disease;
KW diabetes; non-insulin dependent diabetes; insulin dependent diabetes;
KW cancer; human.
XX
OS Homo sapiens.
XX
PN WO2004003144-A2.
XX
PD 08-JAN-2004.
XX
PF 26-JUN-2003; 2003WO-US019908.
XX
PR 01-JUL-2002; 2002US-0392382P.
XX

PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA;
 XX
 DR WPI, 2004-071976/07.
 DR N-PSDB; ADI58165.
 XX
 XX Novel antibody, useful for treating, preventing or ameliorating
 PT inflammatory bowel disorder, cancer of the gastrointestinal tract or
 PT diabetes (non-insulin dependent diabetes or insulin dependent diabetes).
 XX
 XX Claim 2; SEQ ID NO 59; 324pp; English.
 XX
 XX The invention comprises an antibody that specifically binds a
 CC regeneration IV (Reg IV) protein. The invention specifically comprises
 CC the amino acid and coding sequences of single chain antibody fragments
 CC (scFv's) that bind Reg IV protein. The antibody of the invention is
 CC useful for treating, preventing and ameliorating: inflammatory bowel
 CC disorders (e.g. ulcerative colitis or Crohn's disease), diabetes (e.g.
 CC non-insulin dependent diabetes or insulin dependent diabetes), and cancer
 CC of the gastrointestinal tract. The antibody of the invention is also
 CC useful for detecting the expression of a Reg IV protein. The present
 CC amino acid sequence represents an scFv of the invention.
 CC
 SQ Sequence 251 AA;

Query Match 78.8%; Score 491.5; DB 8; Length 251;
 Best Local Similarity 75.8%; Pred. No. 2.8e-37;
 Matches 94; Conservative 11; Mismatches 14; Indels 5; Gaps 1;

QY 1 EVQLVESGDDPVQPGSLRVSCAASGFAFSPHYAMSWVRQAPGKLEWVAIISGSGSTYY 60
 DB 1 EVQLVESGGGLVQPGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVAIISGSGSTYY 60
 QY 61 SDSVKGRFTISRDNSTKNTLYLQMRSLRAEDSAVYFCTRYKLGFT-----YFDSMGQGTLL 115
 DB 61 ADSVKGRFTISRDNSTKNTLYLQMNLSLRADTAIVYCARLGRSTWEDFYFDYWGKGTWV 120
 QY 116 TVSS 119
 DB 121 TVSS 124

RESULT 30
 ADJ95639
 ID ADJ95639 standard; protein; 118 AA.
 AC ADJ95639;
 DT 06-MAY-2004 (first entry)
 DE Insulin-like growth factor (IGF)-related protein #1.
 XX Insulin-like growth factor; IGF-I; IGF-II; diabetes;
 XX rheumatoid arthritis; cancer.
 XX
 OS Unidentified.
 XX
 PN WO2003093317-A1.
 XX
 PD 13-NOV-2003.
 PF 30-APR-2003; 2003WO-JP005505.
 PR 30-APR-2002; 2002JP-00129046.
 XX
 PA (KYOW) KYOWA HAKKO KOGYO KK.
 XX
 PI Shitara K, Nakamura K, Furuya A, Niwa R, Ohki Y, Hanai N;
 DR WPI, 2003-854482/79.
 XX
 XX Antibodies and antibody fragments recognising human insulin-like growth

PT factor for treatment and diagnosis of cancer, diabetes and rheumatoid
 PT arthritis.
 XX
 PS Example 7; SEQ ID NO 15; 115pp; Japanese.
 XX
 CC The invention comprises antibodies and antibody fragments which bind to
 CC and inhibit the function of human insulin-like growth factor (IGF-I
 CC and/or IGF-II). The antibodies and antibody fragments of the invention
 CC are useful for the treatment, prevention, and diagnosis of diabetes,
 CC rheumatoid arthritis and cancer. The present amino acid sequence
 CC represents an insulin-like growth factor-related protein of the
 CC invention.
 CC
 SQ Sequence 118 AA;

Query Match 78.6%; Score 490.5; DB 7; Length 118;
 Best Local Similarity 79.8%; Pred. No. 1.6e-37;
 Matches 95; Conservative 8; Mismatches 15; Indels 1; Gaps 1;

QY 1 EVQLVESGDDPVQPGSLRVSCAASGFAFSPHYAMSWVRQAPGKLEWVAIISGSGSTYY 60
 DB 1 EVQLVESGGGLVQPGSLRLSCAASGFTFSNRYMTWVRQAPGKLEWVAIISGSGSTYY 60
 QY 61 SDSVKGRFTISRDNSTKNTLYLQMRSLRAEDSAVYFCTRYKLGFTYYDSMGQGTLLTVSS 119
 DB 61 RDSVKGRFTISRDNSTKNTLYLQMNLSLRADTAIVYCARLDYGYWFAVWGQGTLLTVSS 118

RESULT 31
 ADA89974
 ID ADA89974 standard; protein; 126 AA.
 AC ADA89974;
 DT 20-NOV-2003 (first entry)
 DE Anti-Abeta antibody related amino acid sequence SEQ ID NO:89.
 XX

XX antibody molecule; antibody; beta-A4 peptide; Abeta4; neuroprotective;
 KW nootropic; antiparkinsonian; gene therapy; amyloidogenesis;
 KW amyloid-plaque formation; beta-amyloid plaque; immunisation; dementia;
 KW Alzheimer's disease; motor neuropathy; Down's syndrome;
 KW Creutzfeldt Jacob disease; hereditary cerebral haemorrhage; amyloidosis;
 KW Parkinson's disease; HIV-related dementia; amyotrophic lateral sclerosis;
 KW neuronal disorder; aging.
 XX
 OS Synthetic.
 OS Homo sapiens.
 PN WO2003070760-A2.
 XX
 PD 28-AUG-2003.
 PF 20-FEB-2003; 2003WO-EP001759.
 PR 20-FEB-2002; 2002EP-00003844.
 XX
 PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
 PA (MORP-) MORPHOSYS AG.
 XX
 PI Bardoff M, Bohmann B, Brockhaus M, Huber W, Kretschmar T;
 PI Loehning C, Loetscher H, Nordstedt C, Rothe C;
 XX
 DR WPI, 2003-663848/52.
 XX
 XX New antibody molecule capable of specifically recognizing two regions of
 PT the beta-A4 peptide, useful for diagnosing, preventing or treating
 PT diseases associated with amyloidogenesis or amyloid-plaque formation
 PT (e.g. dementia).
 XX
 PS Example 16; Page 53; 312pp; English.
 CC The present invention describes an antibody molecule (i) capable of

CC specifically recognising two regions of the beta-A4 peptide/Abeta4. The
 CC first region comprises the amino acid sequence Ala-Glu-Phe-Arg-His-Asp-
 CC Ser-Gly-Tyr AD89886 or its fragment, and the second region comprises the
 CC amino acid sequence Val-His-His-Gln-Lys-Leu-Val-Phe-Ala-Glu-Asp-Val-
 CC Gly AD89887 or its fragment. Also described: (1) a nucleic acid molecule
 CC encoding (1); (2) a vector comprising the nucleic acid of (1); (3) a host
 CC cell comprising the vector of (2); (4) preparing (1), comprising
 CC culturing the host cell of (3) under conditions that allow synthesis of
 CC (1) and recovering (1) from the culture; (5) a composition comprising (1)
 CC or an antibody molecule produced by method (4); (6) a kit comprising (1),
 CC nucleic acid of (1), vector of (2) or host cell of (3); (7) optimising
 CC (1); (8) testing the resulting Fab optimisation library by panning
 CC against Abeta4/Abeta4; (9) identifying optimised clones; (10) expressing
 CC composition, comprising optimisation of (1), and formulating the
 CC pharmaceutical antibody/antibody molecule with a carrier; and (12) a
 CC pharmaceutical composition prepared by method (8). (1) has
 CC neuroprotective, neurotropic and antiparkinsonian activities, and can be
 CC used in gene therapy. The antibody molecule (1), nucleic acid molecule,
 CC vector or host is useful in preparing a pharmaceutical composition for
 CC the prevention and/or treatment of a disease associated with
 CC amyloidogenesis and/or amyloid-plaque formation. The antibody molecule
 CC may also be used in preparing a diagnostic composition for the detection
 CC of the disease mentioned above. The antibody is used for the
 CC distinction of beta-amyloid plaques or for passive immunisation
 CC against beta-amyloid plaque formation. In particular, the disease is
 CC dementia, Alzheimer's disease, motor neuropathy, Down's syndrome,
 CC Creutzfeldt Jacob disease, hereditary cerebral haemorrhage with
 CC amyloidosis Dutch type, Parkinson's disease, HIV-related dementia,
 CC amyotrophic lateral sclerosis or neuronal disorders related to aging. The
 CC present sequence is used in the exemplification of the present invention.

XX Sequence 126 AA;
 SQ

Query Match 78.4%; Score 489.5; DB 6; Length 126;
 Best Local Similarity 75.4%; Pred. No.2.1e-37;
 Matches 99; Conservative 11; Mismatches 13; Indels 7; Gaps 1;

QY 1 EVOLVESGDFVPGGSLRVSCAAGFAFESHYMSWVRQAPGKLEWVAYISSGSGTYY 60
 Db 1 QVQLVSGGGLVQPGSLRISCAASGFTFSYMSWVRQAPGKLEWVSAIMNSGRTYY 60

QY 61 SDSVKGRTTISRNSKNTLYLQNRSLRAEDSAVYFCTRVKLGTY-----YFPSWQGT 113
 Db 61 ADSVKGRTTISRNSKNTLYLQNRSLRAEDTAVYVCARSGKNTHKPYGYRVYFDWQGT 120

QY 114 LRTVSS 119
 Db 121 LRTVSS 126

RESULT 32
 AAR95216
 ID AAR95216 standard; protein: 119 AA.

XX AAR95216;
 AC
 XX
 DT 16-DEC-1996 (first entry)
 XX
 DE Human foetal immunoglobulin 56p1'CL variable heavy chain.
 XX
 XX Antibody; fusion protein; single chain; inhibition; tumour; diagnosis;
 KM detection; imaging; immunotoxin; targeting; assay; immunoassay;
 KM Lewis(Y) carbohydrate antigen.
 XX
 XX Homo sapiens.
 OS
 XX
 FH Key Location/Qualifiers
 FT Domain 31..35
 FT Domain /label= CDR 1.
 FT Domain 50..66
 FT Domain /label= CDR 2.
 FT Domain 99..108

FT /label= CDR 3.
 XX
 XX MO9613594-A1.
 XX
 XX 09-MAY-1996.
 PD
 XX
 XX 26-OCT-1995; 95WO-US013811.
 XX
 XX 28-OCT-1994; 94US-00331396.
 PR 28-OCT-1994; 94US-00331397.
 PR 28-OCT-1994; 94US-00331398.
 XX
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PA
 XX Pastan I, Benhar I, Padlan EA, Jung S, Lee B, Willingham M;
 PI Fitzgerald D, Brinkmann U, Pal L;
 PI WPI; 1996-251462/25.
 DR
 XX
 XX Single chain fusion proteins and antibodies - useful to diagnose and
 PT treat cancer, specifically bind Lewis(Y) related carbohydrate antigen.
 XX
 XX Example 13; Fig 11A; 116pp; English.
 PS
 XX A novel recombinant DNA molecule which encodes a single chain fusion
 CC protein or antibody comprising the Fv region of both the light and heavy
 CC chains of an antibody (Ab) fused together, and an effector molecule,
 CC where the fusion protein or Ab has the binding specificity of monoclonal
 CC Ab (MAb) B1, B3 or B5, can be used for the production of such fusion
 CC proteins or antibodies. The fusion proteins can be used in compositions
 CC as an immunotoxin to inhibit tumour cell growth. The single chain
 CC antibody can be used to detect the presence or absence of cells bearing a
 CC Lewis(Y) carbohydrate antigen in a patient. The antibodies are also
 CC useful as multiple targeting moieties, providing at least 2 kinds of
 CC biological activity. They can also be used in diagnostic assays and for
 CC the imaging of tumours when attached to a radiolabel and for the
 CC pathological diagnosis of tumours. Humanised antibodies are less
 CC immunogenic than the mouse MAbs B1, B3 and B5, making them more suitable
 CC for long term treatment

XX Sequence 119 AA;
 SQ

Query Match 78.4%; Score 489; DB 2; Length 119;
 Best Local Similarity 79.0%; Pred. No.2.2e-37;
 Matches 94; Conservative 7; Mismatches 18; Indels 0; Gaps 0;

QY 1 EVOLVESGDFVPGGSLRVSCAAGFAFESHYMSWVRQAPGKLEWVAYISSGSGTYY 60
 Db 1 QVQLVSGGGLVQPGSLRISCAASGFTFSYMSWVRQAPGKLEWVSAIMNSGRTYY 60

QY 61 SDSVKGRTTISRNSKNTLYLQNRSLRAEDSAVYFCTRVKLGTYFDPSWQGTLLTVSS 119
 Db 61 ADSVKGRTTISRNSKNTLYLQNRSLRAEDTAVYVCARSGARTYRFDWQGTLLTVSS 119

RESULT 33
 ADA43059
 ID ADA43059 standard; protein: 143 AA.

XX ADA43059;
 AC
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Human antibody HD4 heavy chain protein.
 XX
 XX cytostatic; immunosuppressive; antiallergic; human leukocyte antigen;
 KM HLA-DR; antibody; hybridoma; diagnosis; cancer; allergy; sarcoma;
 KM myeloma; lymphoma; leukaemia.
 XX
 XX Homo sapiens.
 OS
 XX
 XX W02003033538-A1.

PD 24-APR-2003.
 XX
 XX 15-OCT-2002; 2002MO-JP010665.
 PF
 XX 15-OCT-2001; 2001JP-00317054.
 PR
 XX (KIRI) KIRIN BEER KK.
 PA
 XX Tawara T, Kataoka S;
 PI
 XX WPI: 2003-403196/38.
 DR N-PSDB; ADA43205.
 XX
 PT HLA-DR binding antibodies useful as immunosuppressant agents for
 PT treatment and prevention of cancer and allergies.
 XX
 PS Claim 57; Page 40; 147pp; Japanese.
 XX
 CC The invention relates to novel human leukocyte antigen DR (HLA-DR)
 CC binding antibodies and their functional fragments and soluble domains.
 CC The specification also includes: a) hybridomas producing the antibodies;
 CC b) nucleic acids encoding all or part of the antibodies; c) expression
 CC vectors containing the nucleic acids; d) hosts transformed by the vectors
 CC ; e) method for preparation of the antibodies by culture of the
 CC transformed hosts; and f) agents for the prevention, treatment and
 CC diagnosis of cancer and allergies, containing the antibodies. The
 CC antibodies are used in the prevention, treatment and diagnosis of
 CC allergies and of cancers including breast, colon, kidney, stomach, ovary,
 CC pancreas, uterus, oesophagus, liver, skin, bladder and vascular cancer,
 CC sarcoma, myeloma, lymphoma (including T-cell lymphoma, Hodgkin's lymphoma
 CC and non-Hodgkin's lymphoma) and leukaemia (including chronic and acute
 CC lymphocytic leukaemia). This sequence represents the heavy chain of the
 CC HD4 antibody targeted to the HLA-DR chains.
 XX
 SQ Sequence 143 AA;
 Query Match 78.4%; Score 489; DB 6; Length 143;
 Best Local Similarity 78.0%; Pred. No. 2,7e-37;
 Matches 96; Conservative 9; Mismatches 14; Indels 4; Gaps 2;
 QY 1 EVQLVSGGDFVPGGSLRVSCAAGFAFSGHYAMSWVRQAPGKGLEWVAIISGGSGTYY 60
 DB 20 EVQLVSGGGLVPGGSLRLSCAAGFTFSSYAMTWVRQAPGKGLEWVSGISGGSGTYY 79
 QY 61 SDSVKGRFTISRNKNTLYLQWRSLRAEDSAVYFCTRYK-LGTY--PDSWGQGLTLT 116
 DB 80 ADSVKGRFTISRNKNTLYLQWRSLRAEDTAVYTCARDHSGSYTPYWPDMGQGLTLT 139
 QY 117 VSS 119
 DB 140 VSS 142
 RESULT 34
 AAY15124
 ID AAY15124 standard; protein; 240 AA.
 AC AAY15124;
 DT 07-FEB-2000 (first entry)
 DE Anti-human CTLA-4 sFv.
 DE Anti-human CTLA-4 sFv.
 KW Anti-human CTLA-4 sFv; single chain antibody; phage; human CTLA-4;
 KW membrane-associated protein; ligand; activated T-cell; B7; CD28;
 KW co-stimulatory signal; T-cell proliferation; xenograft; organ transplant;
 KW xenograft-specific immunosuppression.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT 116..130
 FT Region /label= linker_region

XX
 PN WO9957266-A2.
 XX
 XX 11-NOV-1999.
 PD
 XX
 PF 30-APR-1999; 99MO-GB001350.
 XX
 XX 30-APR-1998; 98GB-00009280.
 PR
 XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
 PA
 XX Lechler IR, Dörling A;
 PI
 XX WPI: 2000-038815/03.
 DR N-PSDB; AA228996.
 XX
 PT Inhibiting T-cell mediated rejection of xenotransplanted organs.
 XX
 PS Claim 9; Fig 9; 43pp; English.
 XX
 CC The present sequence is the anti-human CTLA-4 sFv. This is a membrane -
 CC associated protein which binds to CTLA-4. The single chain antibody (sFv)
 CC from a phage displays differential binding to human CTLA-4 -Ig protein
 CC which is the recipient organism. The anti-CTLA4 sFv functions as a
 CC ligand binding to CTLA-4 on activated T-cells and antagonises the co-
 CC stimulatory signal provided by the interaction between donor B7 and
 CC recipient CD28. Cells expressing the anti-CTLA4 sFv failed to stimulate
 CC T-cell proliferation. This is used in xenograft-specific
 CC immunosuppression
 XX
 SQ Sequence 240 AA;
 Query Match 78.4%; Score 489; DB 3; Length 240;
 Best Local Similarity 79.8%; Pred. No. 4,6e-37;
 Matches 95; Conservative 6; Mismatches 16; Indels 2; Gaps 1;
 QY 1 EVQLVSGGDFVPGGSLRVSCAAGFAFSGHYAMSWVRQAPGKGLEWVAIISGGSGTYY 60
 DB 1 EVQLVSGGGLVPGGSLRLSCAAGFTFSSYAMSWVRQAPGKGLEWVAIISGGSGTYY 60
 QY 61 SDSVKGRFTISRNKNTLYLQWRSLRAEDSAVYFCTRYK-LGTY--PDSWGQGLTLT 119
 DB 61 ADSVKGRFTISRNKNTLYLQWRSLRAEDTAVYTCARA--GRILPDYWGQGLTLTVSS 117
 RESULT 35
 AAY15125
 ID AAY15125 standard; protein; 240 AA.
 AC AAY15125;
 DT 07-FEB-2000 (first entry)
 DE Anti-murine CTLA-4 M1 sFv.
 DE Anti-murine CTLA-4 M1 sFv.
 KW Anti-murine CTLA-4 sFv; M1 sFv; single chain antibody; murine CTLA4;
 KW membrane-associated protein; chimeric construct; extracellular domain;
 KW human CD8; ligand; activated T-cell; co-stimulatory signal; donor B7;
 KW recipient CD28; T-cell proliferation;
 KW xenograft-specific immunosuppression.
 XX
 OS Mus sp.
 OS Synthetic.
 PN WO9957266-A2.
 XX
 PD 11-NOV-1999.
 PF 30-APR-1999; 99MO-GB001350.
 XX
 XX 30-APR-1998; 98GB-00009280.
 PR
 XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.

XX lechler IR, Dorling A;
PI WPI; 2000-038815/03.
XX N-PSDB; AA228997.
DR
XX
PT Inhibiting T-cell mediated rejection of xenotransplanted organs.
XX
PS Claim 9; Fig 11; 43pp; English.
XX
CC The present sequence is anti-murine CTLA-4 sFv (M1 sFv). This is a
CC membrane-associated protein which binds to CTLA-4. Chimeric constructs
CC comprising DNA sequences encoding the extracellular domain of murine
CC CTLA4 and human CD8 were used for the study of anti-CTLA4-sFv protein.
CC The anti-CTLA4 sFv functions as a ligand binding to CTLA-4 on activated
CC T-cells and antagonises the co-stimulatory signal provided by the
CC interaction between donor B7 and recipient CD28. Cells expressing the
CC anti-CTLA4 sFv failed to stimulate T-cell proliferation. This is used in
CC xenograft-specific immunosuppression
XX
SQ Sequence 240 AA;
Query Match 78.4%; Score 489; DB 3; Length 240;
Best Local Similarity 79.8%; Pred. No. 4.6e-37; Mismatches 16; Indels 2; Gaps 1;
Matches 95; Conservative 6;
DB 1 EVQLVSGGDFVPGGSLRVSCAASGFAFSHYAMSWVRQAPGKLEWVAIYSSGSGSTYY 60
1 EVQLVSGGGLVPGGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVAISGSGSTYY 60
QY 61 SDSVKGRTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLGTYYPDSWGGTLLTVSS 119
61 ADSVKGRTISRDNKNTLYLQMRSLRAEDTAIVYCAASDSDSYYPDSWGGTLLTVSS 117
Db
QY
Db
RESULT 36
ADIS8058
ID ADIS8058 standard; protein; 248 AA.
XX
AC ADIS8058;
XX
XX 22-APR-2004 (first entry)
DT
XX
XX Reg IV-specific single chain antibody fragment (scFv) #17.
DE
XX
XX antibody; regeneration IV; Reg IV; single chain antibody fragment; scFv;
KM inflammatory bowel disorder; ulcerative colitis; Crohn's disease;
KM diabetes; non-insulin dependent diabetes; insulin dependent diabetes;
KM cancer; human.
XX
XX Homo sapiens.
OS
XX
XX WO2004003144-A2.
PN
XX
XX 08-JAN-2004.
PD
XX
XX 26-JUN-2003; 2003WO-US019908.
PF
XX
XX 01-JUL-2002; 2002US-0392382P.
PR
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX
XX Rosen CA;
PI
XX
XX WPI; 2004-071976/07.
DR
XX
XX N-PSDB; ADIS8124.
DR
XX
XX Novel antibody, useful for treating, preventing or ameliorating
PT inflammatory bowel disorder, cancer of the gastrointestinal tract or
PT diabetes (non-insulin dependent diabetes or insulin dependent diabetes).
XX
XX Claim 2; SEQ ID NO 18; 324pp; English.

CC The invention comprises an antibody that specifically binds a
CC regeneration IV (Reg IV) protein. The invention specifically comprises
CC the amino acid and coding sequences of single chain antibody fragments
CC (scFv/s) that bind Reg IV protein. The antibody of the invention is
CC useful for treating, preventing and ameliorating inflammatory bowel
CC disorders (e.g. ulcerative colitis or Crohn's disease), diabetes (e.g.
CC non-insulin dependent diabetes or insulin dependent diabetes), and cancer
CC of the gastrointestinal tract. The antibody of the invention is also
CC useful for detecting the expression of a Reg IV protein. The present
CC amino acid sequence represents an scFv of the invention.
XX
SQ Sequence 248 AA;
Query Match 78.4%; Score 489; DB 8; Length 248;
Best Local Similarity 77.7%; Pred. No. 4.8e-37;
Matches 94; Conservative 9; Mismatches 16; Indels 2; Gaps 1;
DB 1 EVQLVSGGDFVPGGSLRVSCAASGFAFSHYAMSWVRQAPGKLEWVAIYSSGSGSTYY 60
1 EVQLVSGGGLVPGGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVAISGSGSTYY 60
QY 61 SDSVKGRTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLGTYYPDSWGGTLLTVSS 118
61 ADSVKGRTISRDNKNTLYLQMRSLRAEDTAIVYCAASDSDSYYPDSWGGTLLTVSS 120
Db
QY 119 S 119
121 S 121
Db
RESULT 37
ABR01519
ID ABR01519 standard; protein; 220 AA.
XX
AC ABR01519;
XX
XX 16-APR-2003 (first entry)
DT
XX
XX Human anti-TIMP-1 antibody heavy chain #17.
DE
XX
XX Human; antibody; tissue inhibitor of metalloprotease-1; TIMP-1; VHCDB3;
KM matrix metalloprotease; MMP; variable heavy chain; VHCDB3; hepatotropic;
KM variable light chain; cytosolic; nephrotropic; cardiac; liver fibrosis;
KM alcoholic liver disease; cardiac fibrosis; acute coronary syndrome;
KM lupus nephritis; glomerulonephrotic renal disease; lung cancer;
KM idiopathic pulmonary fibrosis; benign prostate hypertrophy; colon cancer.
XX
XX Homo sapiens.
OS
XX
XX WO200286085-A2.
PN
XX
XX 31-OCT-2002.
PD
XX
XX 24-APR-2002; 2002WO-US012801.
PF
XX
XX 24-APR-2001; 2001US-0285683P.
PR
XX
XX (FARB) BAYER CORP.
PA (MORP-) MORPHOSYS AG.
XX
XX Pan C, Knorr AM, Schauer M, Hirth-Dietrich C, Kraft S, Krebs B;
PI
XX
XX WPI; 2003-129114/12.
DR
XX
XX N-PSDB; AB274790.
DR
XX
XX New human anti-TIMP-1 (tissue inhibitor of metalloprotease-1) antibodies,
PT for diagnosing or ameliorating the symptoms of a disorder in which TIMP-1
PT is elevated, e.g. liver fibrosis, benign prostate hypertrophy or lung
PT cancer.
XX
XX Claim 20; Page 159-160; 228pp; English.
PS
XX
XX The invention relates to a novel purified preparation of a human

	Query Match	78.1%	Score 487.5;	DB 2;	Length 443;
	Best Local Similarity	82.4%;	Pred. No. 1.2e-36;		
	Matches 98;	Conservative 6;	Mismatches 12;	Indels 3;	Gaps 2;
Qy	1 EVOLVESGCDVVOPEGSILRVSCAASGFAPSHYANSMWVAQAGKGLIEWAYISGGSGTYY	60			
Dd	1 EVOLVESGCGLVQPGSGLRLSCAASGFFPSFYANSMWVAQAQKGLEWVASISTGSS-TYY	59			
Qy	61 SDSVKGRFTTRDSNKTLLTYIQMSLRAREDSAVFCTRVKLGTYYFDSWGQCTLITVSS	119			
Dd	60 PDSVKGRTTIRDNAKNTLYIQMNSLRADPTAVVYCCARDYDG--YFDYWGGCTLTWTVSS	116			
RESULT 40					
ABB57571					
ID	ABB57571 standard; peptide; 121 AA.				
XX	ABB57571;				
AC					
XX					
DT	18-MAR-2002 (first entry)				
DE					
XX					
KM	HLA-DR-specific protein MS-GPC14 VH sequence.				
KM					
KM	Immunomodulatory human MHC class II antigen-binding protein; HLA;				
KM	human leukocyte antigen; immune system; immunosuppression; antibody;				
KM	major histocompatibility complex; antirheumatic; antiarthritic;				
KM	neuroprotective; antiinflammatory; antidiabetic; antipsoriatic;				
KM	immunosuppressive; dermatological; antithyroid; nephrotoxic; psoriasis;				
KM	thyrometric; hepatotoxic; immune response suppressor; narcolepsy;				
KM	rheumatoid arthritis; juvenile arthritis; multiple sclerosis; insulinitis;				
KM	Grave's disease; insulin-dependent diabetes; Hashimoto's disease;				
KM	systemic lupus erythematosus; ankylosing spondylitis; myasthenia gravis;				
KM	transplant rejection; graft versus host disease; pemphigus vulgaris;				
KM	glomerulonephritis; thyroiditis; pancreatitis; primary biliary cirrhosis;				
XX	irritable bowel disease; Sjogren's syndrome.				
OS	Homo sapiens.				
OS	Synthetic.				
XX					
PN	WO200187338-A1.				
PD					
PD	22-NOV-2001.				
XX					
PF	14-MAY-2001; 2001WO-US015626.				
XX					
PR	12-MAY-2000; 2000EP-00110063.				
PR	06-OCT-2000; 2000US-0238762P.				
XX					
PA	(GPCB-) GPC BIOTECH AG.				
PA	(MORP-) MORPHOSYS AG.				
XX					
PI	Nagy Z, Tesar M, Thomassen-Wolf E;				
XX					
DR	WPI, 2002-075289/10.				
XX					
PT	Composition for suppressing immune response, treating diseases of immune				
PT	system, has polypeptide comprising antibody-based antigen-binding domain				
PT	of human composition, which binds antigen expressed on a cell surface.				
XX					
XX	Example; Fig 15; 139pp; English.				
XX					
CC	The present invention describes a composition (I), comprising a				
CC	polypeptide comprising an antibody-based antigen-binding domain of human				
CC	composition with binding specificity for an antigen expressed on the				
CC	surface of a cell, where treating cells expressing the antigen with the				
CC	polypeptides leads to suppression of an immune response, and the IC50 for				
CC	the suppression of immune response is 1 microm or less. (I) has				
CC	antirheumatic, antiarthritic, neuroprotective, antiinflammatory,				
CC	antidiabetic, antiprosclerotic, immunosuppressive, dermatological,				
CC	antithyroid, nephrotoxic, thyrometric and hepatotropic activities, and				
CC	can be used as a suppressor of immune response. (I) is useful for				
CC	suppressing activation or proliferation of a cell of the immune system,				
CC	suppressing IL-2 secretion by a cell, the interaction of a cell of the				

CC immune system with another cell, immunosuppressing a patient and for
CC killing a cell expressing an antigen, human leukocyte antigen (HLA)-DR on
CC the surface of the cell, where neither cytotoxic entities nor
CC immunological mechanisms are needed to cause or lead to the killing. (1)
CC (optionally linked to cytotoxic or immunogenic agent) is useful for
CC preparing a pharmaceutical preparation for the treatment of rheumatoid
CC arthritis, juvenile arthritis, multiple sclerosis, Grave's disease,
CC insulin-dependent diabetes, narcolepsy, psoriasis, systemic lupus
CC erythematosus, ankylosing spondylitis, transplant rejection, graft versus
CC host disease, Hashimoto's disease, myasthenia gravis, pemphigus vulgaris,
CC glomerulonephritis, thyroiditis, pancreatitis, insulinitis, primary biliary
CC cirrhosis, irritable bowel disease and Sjogren's syndrome in humans.
CC ABA92469 to ABA92474 and ABB57457 to ABB57590 represent sequence used in
CC the exemplification of the present invention

Query	March	78.0%	Score 487;	DB 5;	Length 121;
Best	Local Similarity	78.5%	Pred. No. 3.4e-37;		
Matches	95; Conservative	7;	Mismatches 17;	Indels 2;	Gaps 1
OY	1	EVOLVESGDFVOPGSGSLRVSCAASGFAFSHYAMSWVRQAEKGLIEWAYISSGGSGTTY	60		
Db	1	EVOLVESGGLVPGGSGSLRLSCAASGFFSSYAMSWVRQAEKGLIEWAYSALSSGSGTTY	60		
OY	61	SDSVKGRFTTISRDNKNTLYLOMFSLRABDSAVYFCTRVKLQTY--YDSSNGQGTLLIYS	118		
Db	61	ADSVKGRFTTISRDNKNTLYLOMNSLRABEDAVYVYCARSSPMYGEGLDNGQGTLLIYS	120		
OY	119	\$ 119			
Db	121	\$ 121			

Search completed: December 17, 2004, 18:29:09
Job time : 363.68 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Comugen Ltd.

OM protein - protein search, using SW model

Run on: December 17, 2004, 18:13:27 ; Search time 72.2022 Seconds
(without alignments)
109.302 Million cell updates/sec

Title: US-10-089-500-9

Perfect score: 624
Sequence: 1 EVOLVESGDFVPGGSLRV.....KLGTYYFDWSGQGLTVSS 119Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Database: Issued Patents AA:*

- 1: /cgn2_6/prodata/1/iaa/5A_COMB.pep.*
- 2: /cgn2_6/prodata/1/iaa/5B_COMB.pep.*
- 3: /cgn2_6/prodata/1/iaa/6A_COMB.pep.*
- 4: /cgn2_6/prodata/1/iaa/6B_COMB.pep.*
- 5: /cgn2_6/prodata/1/iaa/PCTUS_COMB.pep.*
- 6: /cgn2_6/prodata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	579	92.8	130	4	US-09-225-322B-18
2	579	92.8	130	4	US-09-764-304-18
3	569	91.2	130	4	US-09-225-322B-8
4	569	91.2	130	4	US-09-764-304-8
5	498	79.8	119	4	US-09-648-067A-15
6	495.5	79.4	120	2	US-07-934-373C-4
7	495.5	79.4	120	3	US-08-437-642B-4
8	495.5	79.4	120	4	US-08-146-206C-4
9	495.5	79.4	120	4	US-09-705-686-4
10	495.5	79.4	120	4	US-09-705-392A-4
11	489	78.4	119	1	US-08-331-398A-46
12	489	78.4	119	2	US-08-331-397B-46
13	489	78.4	119	2	US-08-759-804A-46
14	489	78.4	119	3	US-09-227-693-46
15	489	78.4	125	2	US-08-428-197-1
16	489	78.4	125	5	PCT-US93-10555-1
17	487.5	78.1	135	5	US-08-579-378A-20
18	487.5	78.1	443	5	PCT-US96-11152-4
19	485.5	77.8	122	2	US-07-934-373C-21
20	485.5	77.8	122	3	US-08-437-642B-21
21	485.5	77.8	122	4	US-08-146-206C-21
22	485.5	77.8	122	4	US-09-705-686-21
23	485.5	77.8	122	5	US-09-705-392A-21
24	485.5	77.8	122	5	PCT-US93-07832-21
25	485.5	77.8	263	3	US-09-069-821-3
26	485.5	77.8	263	3	US-09-956-086-3
27	485.5	77.8	263	4	US-09-956-087-3

28	485.5	77.8	283	3	US-09-420-592A-6	Sequence 6, Appl
29	485.5	77.8	283	4	US-09-985-442-6	Sequence 6, Appl
30	485.5	77.8	283	4	US-09-983-580-6	Sequence 6, Appl
31	485	77.7	123	4	US-09-840-459-82	Sequence 82, Appl
32	485	77.7	123	4	US-09-497-625A-82	Sequence 82, Appl
33	483.5	77.5	140	3	US-08-983-607-32	Sequence 32, Appl
34	481	77.1	113	3	US-08-974-899-6	Sequence 6, Appl
35	481	77.1	113	3	US-09-795-798-6	Sequence 6, Appl
36	480.5	77.0	120	3	US-09-025-769B-38	Sequence 38, Appl
37	480.5	77.0	120	3	US-09-025-769B-63	Sequence 63, Appl
38	480.5	77.0	120	4	US-09-490-070A-38	Sequence 38, Appl
39	480.5	77.0	120	4	US-09-490-070A-63	Sequence 63, Appl
40	480.5	77.0	120	4	US-09-490-153-38	Sequence 38, Appl
41	480.5	77.0	120	4	US-09-490-153-63	Sequence 63, Appl
42	480.5	77.0	281	3	US-09-025-769B-178	Sequence 178, App
43	480.5	77.0	281	4	US-09-490-070A-178	Sequence 178, App
44	480.5	77.0	281	4	US-09-490-153-178	Sequence 178, App
45	478.5	76.7	124	4	US-09-840-459-89	Sequence 89, Appl

ALIGNMENTS

```
RESULT 1
US-09-225-322B-18
; Sequence 18, Application US/09225322B
; Patent No. 6437098
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KIMAWA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/09/225,322B
; CURRENT FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 18
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cDNA KM-641
US-09-225-322B-18

Query Match      92.8%; Score 579; DB 4; Length 130;
Best Local Similarity 91.6%; Pred. No. 1e+49;
Matches 109; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY      1 EVOLVESGDFVPGGSLRVSCAAGFAFSHYMSWROAPGKLEWVAIISGSGCTTY 60
DB      11 EVTLVESGDFVPGGSLRVSCAAGFAFSHYMSWROAPGKLEWVAIISGSGCTTY 70

QY      61 SDVSKGRFTISRDNSTLYLQNRSLRAEDSAVYFCTRYVGLGTYFDWSGQGLTVSS 119
DB      71 SDVSKGRFTISRDNSTLYLQNRSLRAEDSAVYFCTRYVGLGTYFDWSGQGLTVSS 129

RESULT 2
US-09-764-304-18
; Sequence 18, Application US/09764304
```

```
/ Patent No. 6495666
/ GENERAL INFORMATION:
/ APPLICANT: SHITTARA, KENYA
/ APPLICANT: HANAI, NOBUO
/ APPLICANT: HASEGAWA, MAMORU
/ APPLICANT: MIYAJI, HIROMASA
/ APPLICANT: KIWANA, YOSHIHISA
/ TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
/ FILE REFERENCE: 249-101
/ CURRENT APPLICATION NUMBER: US/09/764,304
/ EARLIER FILING DATE: 2001-01-19
/ EARLIER APPLICATION NUMBER: 09/225,322
/ EARLIER FILING DATE: 1999-01-05
/ EARLIER APPLICATION NUMBER: US 08/454,680
/ EARLIER FILING DATE: 1995-05-31
/ EARLIER APPLICATION NUMBER: US 08/408,133
/ EARLIER FILING DATE: 1995-03-21
/ EARLIER APPLICATION NUMBER: US 08/292,178
/ EARLIER FILING DATE: 1994-08-17
/ EARLIER APPLICATION NUMBER: US07/947,674
/ EARLIER FILING DATE: 1992-09-17
/ EARLIER APPLICATION NUMBER: JP 3-238375
/ EARLIER FILING DATE: 1991-09-18
/ NUMBER OF SEQ ID NOS: 19
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 18
/ LENGTH: 130
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: CDNA KM-641
US-09-764-304-18
```

```
Query Match          92.8%; Score 579; DB 4; Length 130;
Best Local Similarity 91.6%; Pred. No. 1e-49;
Matches 109; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
```

```
QY 1 EVOLVESGDFVPGGSLRVSCAASGFAFSHYAMSVWRQAPGKLEWVAIYSSGSGTTY 60
DB 11 EYLVESGGDFVPGGSLRVSCAASGFAFSHYAMSVWRQAPARLEWVAIYSSGSGTTY 70
QY 61 SDSVKGRFTISRDNKNTLYLQWRSLRAEDSAVYFCTRVKLGTYFPDSMGQGTLLTVSS 119
DB 71 SDSVKGRFTISRDNKNTLYLQWRSLRSEDSAMVFCITRVKLGTYFPDSMGQGTLLTVSS 129
```

```
RESULT 3
US-09-225-322B-8
/ Sequence 8, Application US/09225322B
/ Patent No. 6437098
/ GENERAL INFORMATION:
/ APPLICANT: SHITTARA, KENYA
/ APPLICANT: HANAI, NOBUO
/ APPLICANT: HASEGAWA, MAMORU
/ APPLICANT: MIYAJI, HIROMASA
/ APPLICANT: KIWANA, YOSHIHISA
/ TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
/ FILE REFERENCE: 249-101
/ CURRENT APPLICATION NUMBER: US/09/225,322B
/ EARLIER FILING DATE: 1999-01-05
/ EARLIER APPLICATION NUMBER: US 08/454,680
/ EARLIER FILING DATE: 1995-05-31
/ EARLIER APPLICATION NUMBER: US 08/408,133
/ EARLIER FILING DATE: 1995-03-21
/ EARLIER APPLICATION NUMBER: US 08/292,178
/ EARLIER FILING DATE: 1994-08-17
/ EARLIER APPLICATION NUMBER: US07/947,674
/ EARLIER FILING DATE: 1992-09-17
/ EARLIER APPLICATION NUMBER: JP 3-238375
/ EARLIER FILING DATE: 1991-09-18
/ NUMBER OF SEQ ID NOS: 19
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 8
```

```
/ LENGTH: 130
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: CDNA KM-641
US-09-225-322B-8
```

```
Query Match          91.2%; Score 569; DB 4; Length 130;
Best Local Similarity 90.8%; Pred. No. 9.6e-49;
Matches 108; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
```

```
QY 1 EVOLVESGDFVPGGSLRVSCAASGFAFSHYAMSVWRQAPGKLEWVAIYSSGSGTTY 60
DB 11 EYLVESGGDFVPGGSLRVSCAASGFAFSHYAMSVWRQAPARLEWVAIYSSGSGTTY 70
QY 61 SDSVKGRFTISRDNKNTLYLQWRSLRAEDSAVYFCTRVKLGTYFPDSMGQGTLLTVSS 119
DB 71 SDSVKGRFTISRDNKNTLYLQWRSLRSEDSAMVFCITRVKLGTYFPDSMGQGTLLTVSS 129
```

```
RESULT 4
US-09-764-304-8
/ Sequence 8, Application US/09764304
/ Patent No. 645666
```

```
/ GENERAL INFORMATION:
/ APPLICANT: SHITTARA, KENYA
/ APPLICANT: HANAI, NOBUO
/ APPLICANT: HASEGAWA, MAMORU
/ APPLICANT: MIYAJI, HIROMASA
/ APPLICANT: KIWANA, YOSHIHISA
/ TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
/ FILE REFERENCE: 249-101
/ CURRENT APPLICATION NUMBER: US/09/764,304
/ EARLIER FILING DATE: 2001-01-19
/ EARLIER APPLICATION NUMBER: 09/225,322
/ EARLIER FILING DATE: 1999-01-05
/ EARLIER APPLICATION NUMBER: US 08/454,680
/ EARLIER FILING DATE: 1995-05-31
/ EARLIER APPLICATION NUMBER: US 08/408,133
/ EARLIER FILING DATE: 1995-03-21
/ EARLIER APPLICATION NUMBER: US 08/292,178
/ EARLIER FILING DATE: 1994-08-17
/ EARLIER APPLICATION NUMBER: US07/947,674
/ EARLIER FILING DATE: 1992-09-17
/ EARLIER APPLICATION NUMBER: JP 3-238375
/ EARLIER FILING DATE: 1991-09-18
/ NUMBER OF SEQ ID NOS: 19
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 8
```

```
/ LENGTH: 130
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: CDNA KM-641
US-09-764-304-8
```

```
Query Match          91.2%; Score 569; DB 4; Length 130;
Best Local Similarity 90.8%; Pred. No. 9.6e-49;
Matches 108; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
```

```
QY 1 EVOLVESGDFVPGGSLRVSCAASGFAFSHYAMSVWRQAPGKLEWVAIYSSGSGTTY 60
DB 11 EYLVESGGDFVPGGSLRVSCAASGFAFSHYAMSVWRQAPARLEWVAIYSSGSGTTY 70
QY 61 SDSVKGRFTISRDNKNTLYLQWRSLRAEDSAVYFCTRVKLGTYFPDSMGQGTLLTVSS 119
DB 71 SDSVKGRFTISRDNKNTLYLQWRSLRSEDSAMVFCITRVKLGTYFPDSMGQGTLLTVSS 129
```

```
RESULT 5
US-09-648-067A-15
/ Sequence 15, Application US/09648067A
/ Patent No. 6627196
```

GENERAL INFORMATION:
APPLICANT: Baughman, Sharon A.
APPLICANT: Shak Steven
TITLE OF INVENTION: Dosages for Treatment with Anti-ErbB2 Antibodies
FILE REFERENCE: P1775R1
CURRENT APPLICATION NUMBER: US/09/648,067A
CURRENT FILING DATE: 2000-08-25
PRIOR APPLICATION NUMBER: US 60/151,018
PRIOR FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: US 60/213,822
PRIOR FILING DATE: 2000-06-23
NUMBER OF SEQ ID NOS: 15
SEQ ID NO 15
LENGTH: 119
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: VH consensus sequence
US-09-648-067A-15

Query Match 79.8%; Score 498; DB 4; Length 119;
Best Local Similarity 79.8%; Pred. No. 8,3e-42;
Matches 95; Conservative 8; Mismatches 16; Indels 0; Gaps 0;

QY 1 EVOLVESGDFVPGGSLRVSCAAGFAFSHYAMSWVRQAPGKGLEWVAIISGGSGTTY 60
DB 1 EVOLVESGGGLVPGGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVAIISGGSGTTY 60
QY 61 SDVKGFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLTGYYPDSWGCGTLTVSS 119
DB 61 ADSVKGFTISRDNKNTLYLQMRSLRAEDTAAYYCARDRGAVSYFDVWGCGTLTVSS 119

RESULT 6
US-07-934-373C-4
Sequence 4, Application US/07934373C
Patent No. 5821337
GENERAL INFORMATION:
APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPacIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/934,373C
FILING DATE: 21-Aug-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/952-9881
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:

LENGTH: 120 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-07-934-373C-4

Query Match 79.4%; Score 495.5; DB 2; Length 120;
Best Local Similarity 80.8%; Pred. No. 1.5e-41;
Matches 97; Conservative 7; Mismatches 15; Indels 1; Gaps 1;

QY 1 EVOLVESGDFVPGGSLRVSCAAGFAFSHYAMSWVRQAPGKGLEWVAIISGGSGTTY 60
DB 1 EVOLVESGGGLVPGGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVAIISGGSGTTY 60
QY 61 SDVKGFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLTGYYPDSWGCGTLTVSS 119
DB 61 ADSVKGFTISRDNKNTLYLQMRSLRAEDTAAYYCARDRGAVSYFDVWGCGTLTVSS 120

RESULT 7
US-08-437-642B-4
Sequence 4, Application US/08437642B
Patent No. 6054297
GENERAL INFORMATION:

APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPacIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/437,642B
FILING DATE: 09-May-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/934373
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P2C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/952-9881
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-437-642B-4

Query Match 79.4%; Score 495.5; DB 3; Length 120;
Best Local Similarity 80.8%; Pred. No. 1.5e-41;
Matches 97; Conservative 7; Mismatches 15; Indels 1; Gaps 1;

QY 1 EVOLVESGDFVOPGSLRVSCAAGFAPSHYMSWVRQAPGKLEWVAYISGGSGTTY 60
DB 1 EVOLVESGGGLVOPGSLRLSCAAGFTFSDYMSWVRQAPGKLEWVAYISNGSDTTY 60
QY 61 SDVSKRFTISRDNKNTLYLQWRSLRAEDSAVYFCTRVKLTGY-YFDSWGCGTLTVSS 119
DB 61 ADSVKRFTISRDNKNTLYLQWRSLRAEDTAVYYCARDRGAVSYFDVWGCGTLTVSS 120

RESULT 8

US-08-146-206C-4
Sequence 4, Application US/08146206C
Patent No. 6407213
GENERAL INFORMATION:
APPLICANT: Carter, Paul J.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Method for Making Humanized Antibodies
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/146,206C
FILING DATE: 17-NOV-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/952-9881
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-146-206C-4

Query Match 79.4%; Score 495.5; DB 4; Length 120;
Best Local Similarity 80.8%; Pred. No. 1.5e-41;
Matches 97; Conservative 7; Mismatches 15; Indels 1; Gaps 1;

QY 1 EVOLVESGDFVOPGSLRVSCAAGFAPSHYMSWVRQAPGKLEWVAYISGGSGTTY 60
DB 1 EVOLVESGGGLVOPGSLRLSCAAGFTFSDYMSWVRQAPGKLEWVAYISNGSDTTY 60
QY 61 SDVSKRFTISRDNKNTLYLQWRSLRAEDSAVYFCTRVKLTGY-YFDSWGCGTLTVSS 119
DB 61 ADSVKRFTISRDNKNTLYLQWRSLRAEDTAVYYCARDRGAVSYFDVWGCGTLTVSS 120

RESULT 9

US-09-705-686-4
Sequence 4, Application US/09705686
Patent No. 6639055
GENERAL INFORMATION:
APPLICANT: Carter, Paul J.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Method for Making Humanized Antibodies
NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/705,686
FILING DATE: 02-NOV-2000
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993

APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.

REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P1D3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994

TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-705-686-4

Query Match 79.4%; Score 495.5; DB 4; Length 120;
Best Local Similarity 80.8%; Pred. No. 1.5e-41;
Matches 97; Conservative 7; Mismatches 15; Indels 1; Gaps 1;

QY 1 EVOLVESGDFVOPGSLRVSCAAGFAPSHYMSWVRQAPGKLEWVAYISGGSGTTY 60
DB 1 EVOLVESGGGLVOPGSLRLSCAAGFTFSDYMSWVRQAPGKLEWVAYISNGSDTTY 60
QY 61 SDVSKRFTISRDNKNTLYLQWRSLRAEDSAVYFCTRVKLTGY-YFDSWGCGTLTVSS 119
DB 61 ADSVKRFTISRDNKNTLYLQWRSLRAEDTAVYYCARDRGAVSYFDVWGCGTLTVSS 120

RESULT 10

US-09-705-392A-4
Sequence 4, Application US/09705392A
Patent No. 6719971
GENERAL INFORMATION:
APPLICANT: Carter, Paul J.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Method for Making Humanized Antibodies
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/705,392A
FILING DATE: 02-NOV-2002

CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: 07/71572
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709PID1 REVISED
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-705-392A-4

Query Match 79.4%; Score 495.5; DB 4; Length 120;
Best Local Similarity 80.8%; Pred. No. 1.5e-41;
Matches 97; Conservative 7; Mismatches 15; Indels 1; Gaps 1;

Qy 1 EVOLVSGGDFVPGGSLRVSCAAGFAPSHYAMSWVROAPGKLEWVAIYSSGSGTTY 60
Db 1 EVOLVSGGGLVPGGSLRVSCAAGFTFSDYAMSWVROAPGKLEWVAIYSSGSGTTY 60

Qy 61 SDSVKRFTISRNSKNTLYLQMRSLRAEDSAVYFCTRVKLGTY-YFDSWGQGLTLTVSS 119
Db 61 ADSVKRFTISRDSKNTLYLQNMSLRAEDTAVYYCARDRGAVSYFDWVGQGLTLTVSS 120

RESULT 11
US-08-331-398A-46
Sequence 46, Application US/08311398A
Patent No. 5608039
GENERAL INFORMATION:
APPLICANT: Paetan, Ira
APPLICANT: Willingham, Mark
APPLICANT: Fitzgerald, David
APPLICANT: Brinkmann, Ulrich
APPLICANT: Pai, Lee
TITLE OF INVENTION: Single Chain B3 Antibody Fusion Proteins
TITLE OF INVENTION: and Their Uses (as amended)
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Stewart Street Plaza
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/331,398A
FILING DATE: 28-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/767,331
FILING DATE: 30-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/596,289
FILING DATE: 12-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 015280-126110US

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..119
OTHER INFORMATION: /note="Human fetal immunoglobulin
OTHER INFORMATION: 56P1.C1 Variable Heavy chain (V-H)"
US-08-331-398A-46

Query Match 78.4%; Score 489; DB 1; Length 119;
Best Local Similarity 79.0%; Pred. No. 6.4e-41;
Matches 94; Conservative 7; Mismatches 18; Indels 0; Gaps 0;

Qy 1 EVOLVSGGDFVPGGSLRVSCAAGFAPSHYAMSWVROAPGKLEWVAIYSSGSGTTY 60
Db 1 QVELVSGGGLVPGGSLRVSCAAGFTFSDYAMSWVROAPGKLEWVAIYSSGSGTTY 60

Qy 61 SDSVKRFTISRNSKNTLYLQMRSLRAEDSAVYFCTRVKLGTY-YFDSWGQGLTLTVSS 119
Db 61 ADSVKRFTISRDSKNTLYLQNMSLRAEDTAVYYCARDRGAVSYFDWVGQGLTLTVSS 119

RESULT 12
US-08-331-397B-46
Sequence 46, Application US/08311397B
Patent No. 5981726
GENERAL INFORMATION:
APPLICANT: Paetan, Ira
APPLICANT: Benhar, Itai
TITLE OF INVENTION: Chimeric and Mutationally Stabilized Tumor-
TITLE OF INVENTION: Specific Antibody Fragments, Fusion Proteins, and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Stewart Street Plaza
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/331,397B
FILING DATE: 28-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/767,331
FILING DATE: 30-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/596,289
FILING DATE: 12-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 015280-126120US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids

TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FEATURE:
 NAME/KEY: Protein
 LOCATION: 1..119
 OTHER INFORMATION: /note="Human fetal immunoglobulin
 OTHER INFORMATION: 56P1/CL Variable Heavy chain (V-H)"
 US-08-331-397B-46

Query Match 78.4%; Score 489; DB 2; Length 119;
 Best Local Similarity 79.0%; Pred. No. 6.4e-41;
 Matches 94; Conservative 7; Mismatches 18; Indels 0; Gaps 0;

QY 1 EVOLVESGDVPGGSLRVSCAAGFAPSHYAMSWVRQAPGKGLWVAVISSGSGTYY 60
 :|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 1 QVAVLSSGGGVVPGGSLRLSCAAGFTFSSYAMHWVRQAPGKGLWVAVISYDGSNKYY 60
 :|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 QY 61 SDSVKRFTISRDNKNTLYLQMRSLRABDSAVYFCTRVKLGTYFPDSWGQGLTLTVSS 119
 :|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 61 ADSVKRFTISRDNKNTLYLQMNSLRABDTAVYCARRSARTYFPDYGQGLTLTVSS 119
 :|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 13

US-08-759-804A-46
 Sequence 46; Application US/08759804A
 Patent No. 5990296
 GENERAL INFORMATION:
 APPLICANT: Pastan, Ira
 APPLICANT: Willingham, Mark
 APPLICANT: Fitzgerald, David J.
 APPLICANT: Brinkmann, Ulrich
 APPLICANT: Pal, Lee
 TITLE OF INVENTION: Tumor-Specific Antibody Fragments,
 TITLE OF INVENTION: Fusion Proteins, and Uses Thereof
 NUMBER OF SEQUENCES: 68
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 City: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Releasee #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/759,804A
 FILING DATE: 03-DEC-1996
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/331,398
 FILING DATE: 28-OCT-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/767,331
 FILING DATE: 30-SEP-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/596,289
 FILING DATE: 12-OCT-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: Weber, Ellen L.
 REGISTRATION NUMBER: 32,762
 REFERENCE/DOCKET NUMBER: 015280-126140US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 46:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 119 amino acids
 TYPE: amino acid

STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FEATURE:
 NAME/KEY: Protein
 LOCATION: 1..119
 OTHER INFORMATION: /note="Human fetal immunoglobulin
 OTHER INFORMATION: 56P1/CL Variable Heavy chain (V-H)"
 US-08-759-804A-46

Query Match 78.4%; Score 489; DB 2; Length 119;
 Best Local Similarity 79.0%; Pred. No. 6.4e-41;
 Matches 94; Conservative 7; Mismatches 18; Indels 0; Gaps 0;

QY 1 EVOLVESGDVPGGSLRVSCAAGFAPSHYAMSWVRQAPGKGLWVAVISSGSGTYY 60
 :|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 1 QVAVLSSGGGVVPGGSLRLSCAAGFTFSSYAMHWVRQAPGKGLWVAVISYDGSNKYY 60
 :|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 QY 61 SDSVKRFTISRDNKNTLYLQMRSLRABDSAVYFCTRVKLGTYFPDSWGQGLTLTVSS 119
 :|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 61 ADSVKRFTISRDNKNTLYLQMNSLRABDTAVYCARRSARTYFPDYGQGLTLTVSS 119
 :|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 14

US-09-227-693-46
 Sequence 46; Application US/09227693
 Patent No. 6287562
 GENERAL INFORMATION:
 APPLICANT: PASTAN, Ira
 APPLICANT: BENHAR, Itai
 APPLICANT: PADIAN, Eduardo A.
 APPLICANT: JUNG, Sun-Hee
 APPLICANT: LEE, Byungkook
 TITLE OF INVENTION: HUMANIZED TUMOR-SPECIFIC ANTIBODY
 TITLE OF INVENTION: FRAGMENTS, FUSION PROTEINS, AND USES THEREOF
 NUMBER OF SEQUENCES: 50
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend Kourie and Crew
 STREET: Stuart Street Tower, One Market Plaza
 City: San Francisco
 STATE: California
 COUNTRY: US
 ZIP: 94105-1493
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Releasee #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/227,693
 FILING DATE:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/331,396
 FILING DATE:
 APPLICATION NUMBER: US 07/767,331
 FILING DATE: 30-SEP-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/596,289
 FILING DATE: 12-OCT-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: Weber, Ellen Lauver
 REGISTRATION NUMBER: 32,762
 REFERENCE/DOCKET NUMBER: 15280-126-1-3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 543-9600
 TELEFAX: (415) 543-5043
 INFORMATION FOR SEQ ID NO: 46:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 119 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear

MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Protein
LOCATION: 1..119
OTHER INFORMATION: /note= "Human fetal immunoglobulin
OTHER INFORMATION: 56P1-CL VH region"
US-09-227-693-46

Query Match 78.4%; Score 489; DB 3; Length 119;
Best Local Similarity 79.0%; Pred. No. 6.4e-41;
Matches 94; Conservative 7; Mismatches 18; Indels 0; Gaps 0;

QY 1 EVOLVESGDFVPGGSLRVSCAAGFAPSHYMSWVRQAPGKGLVAVYISGGSGTYY 60
DB 1 EVOLVESGGGVVQPGSLRLSCAASGFTSSYMSWVRQAPGKGLVAVYISYDGSNKYY 60
QY 61 SDSVKGRFTISRNSKNTLYLQMRSLRAEDSAVYFCTRVKLTGYYPFSWGGTLLTVSS 119
DB 61 ADSVKGRFTISRNSKNTLYLQMRSLRAEDTAVYYCTKRGVLYYGGSYHMFDPWGGTLLTVSS 119

RESULT 15

US-08-428-197-1
Sequence 1, Application US/08428197
Patent No. 5891438
GENERAL INFORMATION:
APPLICANT: SILVERMAN, GREGG J.
TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH
TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONUGATES
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East - Suite 500
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/428,197
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10555
FILING DATE: 29-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Howells, Stacy L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: FD-2630
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 125 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
CLONE: 18/2
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..125
US-08-428-197-1
Query Match 78.4%; Score 489; DB 2; Length 125;

Best Local Similarity 76.0%; Pred. No. 6.7e-41;
Matches 95; Conservative 12; Mismatches 12; Indels 6; Gaps 2;

QY 1 EVOLVESGDFVPGGSLRVSCAAGFAPSHYMSWVRQAPGKGLVAVYISGGSGTYY 60
DB 1 EVOLVESGGGVVQPGGSLRLSCAASGFTSSYMSWVRQAPGKGLVAVYISGGSGTYY 60
QY 61 SDSVKGRFTISRNSKNTLYLQMRSLRAEDSAVYFCTRVKLTGYYPFSWGGTLLTVSS 114
DB 61 ADSVKGRFTISRNSKNTLYLQMRSLRAEDTAVYYCTKRGVLYYGGSYHMFDPWGGTLLTVSS 120
QY 115 LTVSS 119
DB 121 VTVSS 125

RESULT 16

PCT-US93-10555-1
Sequence 1, Application PC/TUS9310555
GENERAL INFORMATION:
APPLICANT: SILVERMAN, GREGG J.
TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH
TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONUGATES
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East - Suite 500
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10555
FILING DATE: 29-OCT-1993
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Howells, Stacy L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: FD-2630
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 125 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
CLONE: 18/2
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..125
PCT-US93-10555-1
Query Match 78.4%; Score 489; DB 5; Length 125;
Best Local Similarity 76.0%; Pred. No. 6.7e-41;
Matches 95; Conservative 12; Mismatches 12; Indels 6; Gaps 2;

Db 61 ADSVKGRFTISRDNKNTLYLQNMSLRAEDTAVYYCTKGQVLYYGGSGYHFPDMGQCTL 120
QY 115 LTVSS 119
:||||
Db 121 VTVSS 125
RESULT 17
US-08-579-378A-20
; Sequence 20, Application US/08579378A
; Patent No. 6210671
; GENERAL INFORMATION:
; APPLICANT: Co. Man Sung
; TITLE OF INVENTION: Humanized Antibodies Reactive with
; TITLE OF INVENTION: L-Selectin
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Stewart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/579,378A
; FILING DATE: 27-DEC-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/160,074
; FILING DATE: 30-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/983,946
; FILING DATE: 01-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95112895.8
; FILING DATE: 17-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95114696.8
; FILING DATE: 19-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebescheutz, Joe O.
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 11823-002220
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 135 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-579-378A-20
Query Match 78.1%; Score 487.5; DB 3; Length 135;
Best Local Similarity 82.4%; Pred. NO. 1e-40;
Matches 98; Conservative 6; Mismatches 12; Indels 3; Gaps 2;
QY 1 EVOLVESGDVFVPGGSLRVSCAAGFAPSHYAMSWVRQAPGKLEWVAYISSGSGGTTY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 20 EVQLVESGGGLVPGGSLRLSCAASGFTFTYMSWVRQAPGKLEWVAISITGGS-TYY 78
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 SDSVKGRTISRDNKNTLYLQNMSLRAEDSAVYFCTRVKLGITYYDPDSWGQGLTLTVSS 119
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 79 PDSVKGRTISRDNKNTLYLQNMSLRAEDTAVYYCARDYDQ--YFDYWGQGLTLTVSS 135
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
RESULT 18

PCT-US96-13152-4
; Sequence 4, Application PC/TUS9613152
; GENERAL INFORMATION:
; APPLICANT: Martin, Ulrich, et al.
; TITLE OF INVENTION: Anti-selectin antibodies for prevention of multiple organ fai
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felle & Lynch
; ADDRESSEE: Attn: Norman D. Hanson
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Computer Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/13152
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/578,953
; FILING DATE: 27-Dec-95
; APPLICATION NUMBER: EP 95 112 895.8
; FILING DATE: 17-Aug-95
; APPLICATION NUMBER: EP 95 114 969.9
; FILING DATE: 19-Sep-95
; ATTORNEY/AGENT INFORMATION:
; NAME: Norman D. Hanson
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: BOER 1059-PCT-PFF/NDH
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 443
; TYPE: amino acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US96-13152-4
Query Match 78.1%; Score 487.5; DB 5; Length 443;
Best Local Similarity 82.4%; Pred. No. 3.9e-40;
Matches 98; Conservative 6; Mismatches 12; Indels 3; Gaps 2;
QY 1 EVOLVESGDVFVPGGSLRVSCAAGFAPSHYAMSWVRQAPGKLEWVAYISSGSGGTTY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 EVQLVESGGGLVPGGSLRLSCAASGFTFTYMSWVRQAPGKLEWVAISITGGS-TYY 59
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 SDSVKGRTISRDNKNTLYLQNMSLRAEDSAVYFCTRVKLGITYYDPDSWGQGLTLTVSS 119
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 60 PDSVKGRTISRDNKNTLYLQNMSLRAEDTAVYYCARDYDQ--YFDYWGQGLTLTVSS 116
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
RESULT 19
US-07-934-373C-21
; Sequence 21, Application US/07934373C
; Patent No. 5821337
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California

COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/934,373C
FILING DATE: 21-Aug-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-07-934-373C-21

Query Match 77.8%; Score 485.5; DB 2; Length 122;
Best Local Similarity 77.0%; Pred. No. 1,4e-40;
Matches 94; Conservative 10; Mismatches 15; Indels 3; Gaps 1;

QY 1 EVOLVESGDFVPGGSLRVSCAASGFAFSHYAMSVWRQAPGKLEWVAYISSGSGSTYY 60
DB 1 EVOLVESGGGLVPGGSLRLSCAASGFTFSYAMSVWRQAPGKLEWVAYISSGSGSTYY 60
QY 61 SDSVKRFTISRNSKNTLYLQMRSLRAEDSAVYFCTRYKLG--TYPDSWGQGLTVTV 117
DB 61 ADSVKRFTISRNSKNTLYLQMRSLRAEDTAVYYCARGRVGYSLGLDYWGQGLTVTV 120

QY 118 SS 119
DB 121 SS 122

RESULT 20
US-08-437-642B-21
Sequence 21, Application US/08437642B
Patent No. 6054297
GENERAL INFORMATION:
APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/437,642B
FILING DATE: 09-May-1995
CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/934373
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P2C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-437-642B-21

Query Match 77.8%; Score 485.5; DB 3; Length 122;
Best Local Similarity 77.0%; Pred. No. 1,4e-40;
Matches 94; Conservative 10; Mismatches 15; Indels 3; Gaps 1;

QY 1 EVOLVESGDFVPGGSLRVSCAASGFAFSHYAMSVWRQAPGKLEWVAYISSGSGSTYY 60
DB 1 EVOLVESGGGLVPGGSLRLSCAASGFTFSYAMSVWRQAPGKLEWVAYISSGSGSTYY 60
QY 61 SDSVKRFTISRNSKNTLYLQMRSLRAEDSAVYFCTRYKLG--TYPDSWGQGLTVTV 117
DB 61 ADSVKRFTISRNSKNTLYLQMRSLRAEDTAVYYCARGRVGYSLGLDYWGQGLTVTV 120
QY 118 SS 119
DB 121 SS 122

RESULT 21
US-08-146-206C-21
Sequence 21, Application US/08146206C
Patent No. 6407213
GENERAL INFORMATION:
APPLICANT: Carter, Paul J.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Method for Making Humanized Antibodies
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/146,206C
FILING DATE: 17-No. 6407213-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.

REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-146-206C-21

Query Match 77.8%; Score 485.5; DB 4; Length 122;
Best Local Similarity 77.0%; Pred. No. 1.4e-40;
Matches 94; Conservative 10; Mismatches 15; Indels 3; Gaps 1;

QY 1 EVOLVSGGDFVPGGSLRVSCAAGPAPSHYAMSWVRQAPGKGLWVAVISSGGSGTTY 60
DB 1 EVOLVSGGGLVPGGSLRLSCAAGFTFSSYAMSWVRQAPGKGLWVSVISGDDGSTYY 60

QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLG--TYFPDSMGQGLTLTV 117
DB 61 ADSVKGRFTISRDNKNTLYLQMRSLRAEDTAIVYCARGRVGYSLGLVDYMGQGLTLTV 120

QY 118 SS 119
DB 121 SS 122

RESULT 22
US-09-705-686-21
Sequence 21, Application US/09705686
Patent No. 6639055
GENERAL INFORMATION:
APPLICANT: Carter, Paul J.
TITLE OF INVENTION: Method for Making Humanized Antibodies
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/705,686
FILING DATE: 02-Nov. 6639055-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P1D3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-09-705-686-21

Query Match 77.8%; Score 485.5; DB 4; Length 122;
Best Local Similarity 77.0%; Pred. No. 1.4e-40;
Matches 94; Conservative 10; Mismatches 15; Indels 3; Gaps 1;

QY 1 EVOLVSGGDFVPGGSLRVSCAAGPAPSHYAMSWVRQAPGKGLWVAVISSGGSGTTY 60
DB 1 EVOLVSGGGLVPGGSLRLSCAAGFTFSSYAMSWVRQAPGKGLWVSVISGDDGSTYY 60

QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLG--TYFPDSMGQGLTLTV 117
DB 61 ADSVKGRFTISRDNKNTLYLQMRSLRAEDTAIVYCARGRVGYSLGLVDYMGQGLTLTV 120

QY 118 SS 119
DB 121 SS 122

RESULT 23
US-09-705-392A-21
Sequence 21, Application US/09705392A
Patent No. 6719971
GENERAL INFORMATION:
APPLICANT: Carter, Paul J.
TITLE OF INVENTION: Method for Making Humanized Antibodies
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/705,392A
FILING DATE: 02-Nov. 6719971-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P1D1 REVISED
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-09-705-392A-21

Query Match 77.8%; Score 485.5; DB 4; Length 122;
Best Local Similarity 77.0%; Pred. No. 1.4e-40;
Matches 94; Conservative 10; Mismatches 15; Indels 3; Gaps 1;

QY 1 EVOLVSGGDFVPGGSLRVSCAAGPAPSHYAMSWVRQAPGKGLWVAVISSGGSGTTY 60
DB 1 EVOLVSGGGLVPGGSLRLSCAAGFTFSSYAMSWVRQAPGKGLWVSVISGDDGSTYY 60

QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLG--TYFPDSMGQGLTLTV 117
DB 61 ADSVKGRFTISRDNKNTLYLQMRSLRAEDTAIVYCARGRVGYSLGLVDYMGQGLTLTV 120

Db 61 ADVKGRFTSRDNRKNTLYLQMSLRADTAAYYCARGVGSLGLYDMGQTLVTY 120
QY 118 SS 119
Db 121 SS 122

RESULT 24
PCT-US93-07832-21
; Sequence 21, Application PC/TUS9307832
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07832
; FILING DATE: 19930820
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/934373
; FILING DATE: 21-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME:
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: 70922PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:
; TELEFAX: 415/952-9881
; TELEEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; PCT-US93-07832-21

Query Match 77.8%; Score 485.5; DB 5; Length 122;
Best Local Similarity 77.0%; Pred. No. 1,4e-40;
Matches 94; Conservative 10; Mismatches 15; Indels 3; Gaps 1;
QY 1 EVLVSSGGDFVPGGSLRVSCAAGPAPSHYMSWVRQAPGKLEWVAIYSSGGSTYY 60
Db 1 EVLVSSGGGLVPGGSLRLSCAAGFTFSYMSWVRQAPGKLEWVSIISGGSTYY 60
QY 61 SDVSKRFTSRDNRKNTLYLQMSLRADTAAYYCARGVGSLGLYDMGQTLVTY 117
Db 61 ADVKGRFTSRDNRKNTLYLQMSLRADTAAYYCARGVGSLGLYDMGQTLVTY 120
QY 118 SS 119
Db 121 SS 122

RESULT 25
US-09-069-821-3

; Sequence 3, Application US/09069821
; Patent No. 632332
; GENERAL INFORMATION:
; APPLICANT: FILIPULA, DAVID
; APPLICANT: MANG, MAOLIANG
; APPLICANT: SHORR, ROBERT
; APPLICANT: WHITLOW, MARC
; APPLICANT: LEE, LHSYNG S.
; TITLE OF INVENTION: SINGLE-CHAIN ANTIGEN-BINDING PROTEINS
; TITLE OF INVENTION: CAPABLE OF GLYCOSYLATION, PRODUCTION AND USES THEREOF
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVE., NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/069,821
; FILING DATE: 30-APR-1998
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/067,341
; FILING DATE: 02-DEC-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/063,074
; FILING DATE: 27-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/050,472
; FILING DATE: 23-JUN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/044,449
; FILING DATE: 30-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: KIM, JUDITH U.
; REGISTRATION NUMBER: 40,679
; REFERENCE/DOCKET NUMBER: 0977.2280003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)371-2600
; TELEFAX: (202)371-2540
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 263 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; US-09-069-821-3

Query Match 77.8%; Score 485.5; DB 3; Length 263;
Best Local Similarity 73.8%; Pred. No. 3,4e-40;
Matches 96; Conservative 9; Mismatches 14; Indels 11; Gaps 2;
QY 1 EVLVSSGGDFVPGGSLRVSCAAGPAPSHYMSWVRQAPGKLEWVAIYSSGGSTYY 58
Db 130 EVLVSSGGGLVPGGSLRLSCAAGFTFSYMSWVRQAPGKLEWVSIISGGSTYY 189
QY 59 YVSDVSKRFTSRDNRKNTLYLQMSLRADTAAYYCARGVGSLGLYDMGQTLVTY 109
Db 190 YVADSVKGRFTSRDNRKNTLYLQMSLRADTAAYYCARGVGSLGLYDMGQTLVTY 249
QY 110 GGGTLTVSS 119
Db 250 GGGTLTVSS 259

RESULT 26

```

US-09-956-086-3
: Sequence 3, Application US/09956086
: Patent No. 6743896
:
: GENERAL INFORMATION:
: APPLICANT: FILIPULA, DAVID
:             WANG, MAOLIANG
:             SHORR, ROBERT
:             WHITLOW, MARC
:             LEE, LHSYANG S
:
: TITLE OF INVENTION: SINGLE-CHAIN ANTIGEN-BINDING PROTEINS
:                     CAPABLE OF GLYCOSYLATION, PRODUCTION AND USES THEREOF
:
: NUMBER OF SEQUENCES: 33
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
: STREET: 1100 NEW YORK AVE., NW, SUITE 600
: CITY: WASHINGTON
: STATE: DC
: COUNTRY: USA
: ZIP: 20005
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.30
:
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/956,086
: FILING DATE: 20-Sep-2001
: CLASSIFICATION: <unknown>
:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 09/069,821
: FILING DATE: <unknown>
: APPLICATION NUMBER: US 60/063,074
: FILING DATE: 27-OCT-1997
: APPLICATION NUMBER: US 60/050,472
: FILING DATE: 23-JUN-1997
: APPLICATION NUMBER: US 60/044,449
: FILING DATE: 30-APR-1997
:
: ATTORNEY/AGENT INFORMATION:
: NAME: KIM, JUDITH U.
: REGISTRATION NUMBER: 40,679
: REFERENCE/DOCKET NUMBER: 0977.2280003
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202)371-2600
: TELEFAX: (202)371-2540
:
: INFORMATION FOR SEQ ID NO: 3:
:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 263 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: No. 6743896 Relevant
:
: MOLECULE TYPE: peptide
:
: SEQUENCE DESCRIPTION: SEQ ID NO: 3:
:
US-09-956-086-3

```

	Query Match	77.8%	Score 485.5	DB 4:	Length 263;
	Best Local Similarity	73.8%	Pred No. 3.4e-40;		
	Matches	96;	Conservative	9;	Mismatches 14; Indels 11; Gaps 2
Qy	1	EVOLVESGADFPVPGSGSLRVSCAASGAFPSHYSAMSWVRQAPKGLGEWVAIIS--SGGSQT	58		
Db	130	EVLIVESGGGLVQPGSGSLRLSCAAAGCFPFSYAMSWMVAQAPKGLEWVSISGKTIDGST	189		
Qy	59	YYSDSVKGRFPTISRDNKNTLYLQMRSLPAEDSAVFCTRYVKLGt-----YYFDGW	109		
Db	190	YYADSVKGRFTISRDNKNTLYLQNMSRAEPTAVAYCARGXGXSLSGXYHYHFDPW	249		
Qy	110	GQGTLITVSS	119		
Db	250	GQGTLITVSS	259		

RESULT 27
US-09-956-087-3

```

1      Sequence 3, Application US/09956087
2      Patent No. 6743908
3      GENERAL INFORMATION:
4      APPLICANT: FILPULA, DAVID
5      WANG, MAOLIANG
6      SHORR, ROBERT
7      WHITLOW, MARC
8      LEE, LIHSYNG S.
9      TITLE OF INVENTION: SINGLE-CHAIN ANTIGEN-BINDING PROTEINS
10     CAPABLE OF GLYCOSYLATION, PRODUCTION AND USES THEREOF
11     NUMBER OF SEQUENCES: 33
12     CORRESPONDENCE ADDRESS:
13     ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
14     STREET: 1100 NEW YORK AVE., NW, SUITE 600
15     CITY: WASHINGTON
16     STATE: DC
17     COUNTRY: USA
18     ZIP: 20005
19     COMPUTER READABLE FORM:
20     MEDIUM TYPE: Floppy disk
21     COMPUTER: IBM PC compatible
22     OPERATING SYSTEM: PC-DOS/MS-DOS
23     SOFTWARE: Patent in Release #1.0, Version #1.30
24     CURRENT APPLICATION DATA:
25     APPLICATION NUMBER: US/09/956,087
26     FILING DATE: 20-Sep-2001
27     CLASSIFICATION: <Unknown>
28     PRIOR APPLICATION DATA:
29     APPLICATION NUMBER: 09/069,821
30     FILING DATE: 1998-04-30
31     APPLICATION NUMBER: US 60/063,074
32     FILING DATE: 27-OCT-1997
33     APPLICATION NUMBER: US 60/050,472
34     FILING DATE: 23-JUN-1997
35     APPLICATION NUMBER: US 60/044,449
36     FILING DATE: 30-APR-1997
37     ATTORNEY/AGENT INFORMATION:
38     NAME: KIM, JUDITH U.
39     REGISTRATION NUMBER: 40,679
40     REFERENCE/DOCKET NUMBER: 0977,2280003
41     TELECOMMUNICATION INFORMATION:
42     TELEPHONE: (202)371-2600
43     TELEFAX: (202)371-2540
44     INFORMATION FOR SEQ ID NO: 3:
45     SEQUENCE CHARACTERISTICS:
46     LENGTH: 263 amino acids
47     TYPE: amino acid
48     STRANDEDNESS: single
49     TOPOLOGY: not relevant
50     MOLECULE TYPE: peptide
51     SEQUENCE DESCRIPTION: SEQ ID NO: 3:
52     US-09-956-087-3

```

Query Match	77.8%	Score 485.5	DB 4	Length 263
Best Local Similarity	73.8%	Pred. No. 3.4e-40		
Matches	96	Conservative	9	Mismatches 14; Indels 11; Gaps 2
QY	1	EVQLVESGGDGVFVDPGSGILRVSCAASGFAFHSYAMSWRQAPGKGLEWVAITIS--SGSGST	58	
Db	130	EVQLVESGGGLVQVGGSGILRVSCAASGFTFSYAMSWRQAPGKGLEWVSISGKIDGSGST	189	
QY	59	YYSNSVYGRFTISRDNSKNTLYIQMNSLRADDSAVYCTRYKLTG-----YYEPDSW	109	
Db	190	YYASVYGRFTISRDNSKNTLYIQMNSLRADDTAVYCARGRXGSLSGKYYIYHYFDYW	249	
QY	110	GQGGLITVSS	119	
Db	250	GQGGLITVSS	259	

RESULT 28
US-09-420-592A-6
; Sequence 6, Application US/09420592A

Patent No. 6333396
GENERAL INFORMATION:
APPLICANT: Filipula, David R.
APPLICANT: Wang, Maoliang
APPLICANT: Whitlow, Marc D.
TITLE OF INVENTION: No. 6333396e1 Method for Targeted Delivery of Nucleic Acids
FILE REFERENCE: 0977.2300001
CURRENT APPLICATION NUMBER: US/09/420,592A
CURRENT FILING DATE: 1999-10-19
PRIOR APPLICATION NUMBER: 60/104,949
PRIOR FILING DATE: 1998-10-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 283
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Kabat
NAME/KEY: UNSURE
LOCATION: (232)
OTHER INFORMATION: May be any amino acid.
NAME/KEY: UNSURE
LOCATION: (234)
OTHER INFORMATION: May be any amino acid.
NAME/KEY: UNSURE
LOCATION: (239)
OTHER INFORMATION: May be any amino acid.
US-09-420-592A-6

Query Match 77.8%; Score 485.5; DB 3; Length 283;
Best Local Similarity 73.8%; Pred. No. 3,7e-40;
Matches 96; Conservative 9; Mismatches 14; Indels 11; Gaps 2;

Qy 1 EVOLVESGGDVPVPGGSLRVS...SGSGGT 58
Db 130 EVOLVESGGGLVPGGSLRLSCA...SGT 189
Qy 59 YYSDSVKGRTISRDN...KTLV... 109
Db 190 YYADSVKGRFTISRDN...KTLV... 249
Qy 110 GGCTLTVSS 119
Db 250 GGCTLTVSS 259

RESULT 29
US-09-985-442-6
Sequence 6, Application US/09985442
Patent No. 6632942
GENERAL INFORMATION:
APPLICANT: Filipula, David R.
APPLICANT: Wang, Maoliang
APPLICANT: Whitlow, Marc D.
TITLE OF INVENTION: No. 6632942e1 Method for Targeted Delivery of Nucleic Acids
FILE REFERENCE: 0977.2300003
CURRENT APPLICATION NUMBER: US/09/985,442
CURRENT FILING DATE: 2001-11-02
PRIOR APPLICATION NUMBER: 09/420,592
PRIOR FILING DATE: 1999-10-19
PRIOR APPLICATION NUMBER: 60/104,949
PRIOR FILING DATE: 1998-10-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 283
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Kabat
OTHER INFORMATION: Consensus

NAME/KEY: UNSURE
LOCATION: (232)
OTHER INFORMATION: May be any amino acid.
NAME/KEY: UNSURE
LOCATION: (234)
OTHER INFORMATION: May be any amino acid.
NAME/KEY: UNSURE
LOCATION: (239)
OTHER INFORMATION: May be any amino acid.
US-09-985-442-6

Query Match 77.8%; Score 485.5; DB 4; Length 283;
Best Local Similarity 73.8%; Pred. No. 3,7e-40;
Matches 96; Conservative 9; Mismatches 14; Indels 11; Gaps 2;

Qy 1 EVOLVESGGDVPVPGGSLRVS...SGSGGT 58
Db 130 EVOLVESGGGLVPGGSLRLSCA...SGT 189
Qy 59 YYSDSVKGRTISRDN...KTLV... 109
Db 190 YYADSVKGRFTISRDN...KTLV... 249
Qy 110 GGCTLTVSS 119
Db 250 GGCTLTVSS 259

RESULT 30
US-09-983-580-6
Sequence 6, Application US/09983580
Patent No. 6764853
GENERAL INFORMATION:
APPLICANT: Filipula, David R.
APPLICANT: Wang, Maoliang
APPLICANT: Whitlow, Marc D.
TITLE OF INVENTION: No. 6764853e1 Method for Targeted Delivery of Nucleic Acids
FILE REFERENCE: 0977.2300002
CURRENT APPLICATION NUMBER: US/09/983,580
CURRENT FILING DATE: 2001-10-25
PRIOR APPLICATION NUMBER: 09/420,592
PRIOR FILING DATE: 1999-10-19
PRIOR APPLICATION NUMBER: 60/104,949
PRIOR FILING DATE: 1998-10-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 283
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Kabat
NAME/KEY: UNSURE
LOCATION: (232)
OTHER INFORMATION: May be any amino acid.
NAME/KEY: UNSURE
LOCATION: (234)
OTHER INFORMATION: May be any amino acid.
NAME/KEY: UNSURE
LOCATION: (239)
OTHER INFORMATION: May be any amino acid.
US-09-983-580-6

Query Match 77.8%; Score 485.5; DB 4; Length 283;
Best Local Similarity 73.8%; Pred. No. 3,7e-40;
Matches 96; Conservative 9; Mismatches 14; Indels 11; Gaps 2;

Qy 1 EVOLVESGGDVPVPGGSLRVS...SGSGGT 58
Db 130 EVOLVESGGGLVPGGSLRLSCA...SGT 189
Qy 59 YYSDSVKGRTISRDN...KTLV... 109


```

? MOLECULE TYPE:
? DESCRIPTION: polypeptide
?
? ORIGINAL SOURCE:
? ORGANISM: Homo sapiens (melanoma patient immu-
? ORGANISM: nized with autologous tumor cells)
? INDIVIDUAL ISOLATE: peripheral blood lymphocyte
? IMMEDIATE SOURCE:
? LIBRARY: Dm414 scFv antibodies obtained from
? LIBRARY: FUS3 fusion phage construct
? CLONE: V86
?
? FEATURE:
? NAME/KEY: heavy chain and linker
?
US-08-983-607-32

```

Query Match	77.5%;	Score	483.5;	DB	3;	length	140;
Best Local Similarity	75.0%;	Pred.	No. 2.7e-40;				
Matches	93;	Conservative	10;	Mismatches	16;	Indels	5;
						Gaps	1

QY	1	EVQLVESGGD	PFQPGGSLTVS	CAASGFAASHYMS	WVRQAPGKGL	EVAAV	ISGGSGSTYY	60
Db	1	QVQLVQSGGGLV	QPGGSLRLSCA	SGFTFSYAMS	WVRQAPGKGL	EVAAV	ISGGSGSTYY	60
QY	61	SDSYVGRFPI	SRDNSKNTLYL	QWRSLRARESA	VPCT----	RVKLTGYT	FDMSGOSTL	115
Db	61	ADSYVGRFPI	SRDNSKNTLYL	QWRSLRARESA	VPCT----	RVKLTGYT	FDMSGOSTL	120
QY	116	TVSS						
Db	121	TVSS						

```

1      RESULT 34
2      US-08-974-899-6
3      ; Sequence 6, Application US/08974899
4      ; Patent No. 6037454
5      ; GENERAL INFORMATION:
6      ; APPLICANT: Presta, Leonard G.
7      ; APPLICANT: Jardieu, Paula M.
8      ; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
9      ; NUMBER OF SEQUENCES: 24
10     ; CORRESPONDENCE ADDRESS:
11     ; ADDRESSEE: Genentech, Inc.
12     ; STREET: 1 DNA Way
13     ; CITY: South San Francisco
14     ; STATE: California
15     ; COUNTRY: USA
16     ; ZIP: 94080
17     ; COMPUTER READABLE FORM:
18     ; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
19     ; COMPUTER: IBM PC compatible
20     ; OPERATING SYSTEM: PC-DOS/MS-DOS
21     ; SOFTWARE: WinPatIn (Genentech)
22     ; CURRENT APPLICATION DATA:
23     ; APPLICATION NUMBER: US/08/974,899
24     ; FILING DATE:
25     ; CLASSIFICATION: 536
26     ; PRIOR APPLICATION DATA:
27     ; APPLICATION NUMBER: 60/031971
28     ; FILING DATE: 11/27/96
29     ; ATTORNEY/AGENT INFORMATION:
30     ; NAME: Lee, Wendy M.
31     ; REGISTRATION NUMBER: 40,378
32     ; REFERENCE/DOCKET NUMBER: P1014R1
33     ; TELECOMMUNICATION INFORMATION:
34     ; TELEPHONE: 650/425-1994
35     ; TELEFAX: 650/952-9881
36     ; INFORMATION FOR SEQ ID NO: 6:
37     ; SEQUENCE CHARACTERISTICS:
38     ; LENGTH: 113 amino acids
39     ; TYPE: Amino Acid
40     ; TOPOLOGY: Linear
41     ; US-08-974-899-6

```

Query Match	77.1%;	Score 481;	DB 3;	Length 113;
Best Local Similarity	79.0%;	Pred. No. 3,7e-40;		
Matches	94;	Conservative	6;	Mismatches 13;
				Indels 6;
				Gaps 1;

Qy 1 EVQLVESGGGLVQPGGSLRLVCAASGFAFSAHSMYVWROA PGKGLEWVATISGGSGITV 60
Db 1 EVQLVESGGGLVQPGGSLRLVCAASGFPFSSVYMWROA PGKGLMEVAVISDGGSGITY 60

Qy 61 SDSVSGFETISRNRSKNTLYLQWRSIRAPDSNYPCTRIYKLGITYYVDPDSGGCTLLTVSS 119
Db 61 ADSVSGFETISRNRSKNTLYLQWNSIRAPDITAYTCAR-----GFDYWGQGLTVVSS 113

```

RESULT 35
US-09-795-798-6
; Sequence 6, Application US/09795798
; Patent No. 6703018
; GENERAL INFORMATION:
; APPLICANT : Prestea, Leonard G.
;             Jardiou, Paula M.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/795,798
; FILING DATE: 28-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/974,899
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P1014R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 6:
;     SEQUENCE CHARACTERISTICS:
;         LENGTH: 113 amino acids
;         TYPE: Amino Acid
;         TOPOLOGY: Linear
;     SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-795-798-6

Query Match      77.1%; Score 481; DB 4; Length 113;
Best Local Similarity 79.0%; Pred. No. 3.7e+40;
Matches 94; Conservative 6; Mismatches 13; Indels 6; Gaps 1.

Cy      1 EVQLVESGGDGVDPQSGSLRVSCAASGPAFSHYAMSWRQAPGKGLIEWYAYISGGSGITYY 60
Db      1 EVQLVDSGGDGVDPQSGSLRVSCAASGPAFSHYAMSWRQAPGKGLIEWYAYISGGSGITYY 60

Cy      61 SDSVKGRFTTISRDNKSNTLYIQMNSLPAEDSAVVFCTRRVKLGITGYYPDSWGQGTLTIVSS 119
Db      61 ADSVKGRFTTISRDNKSNTLYIQMNSLPAEDTAIVTCAR-----GFDMWGQTLTVSS 113

RESULT 36
US-09-025-769B-38
; Sequence 38, Application US/09025769B
; Patent No. 6300064
```

```

Query Match          77.1%; Score 481; DB 4; Length 113;
Best Local Similarity 79.0%; Pred. No. 3.7e-40;
Matches 94; Conservative 6; Mismatches 13; Indels 6; Gaps 1.

QY 1 EVLVESGSGDFVDPGSGLRVSCAASGFAFHHYAMSWROABEGKLEWVAIYISGGSGTTY 60
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSYAMSWRQAPRGKLEWVSIISGDSSTYY 60
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

QY 61 SDSTKGRFTISRDNSKNTLYIQMSSLAEEDAVYFCRRYKLTGYTFPDSWGCGTLLTVSS 119
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 61 ADSVKGRFTISRDNSKNTLYIQMSSLAEEDAVYVYCAR-----GFDYWGCGTLLTVSS 113
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

RESULT 36
US-09-025-7698-38
; Sequence 38, Application US/09025769B
; Patent No. 6300064

```

GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckhuhn, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-769B-38

Query Match 77.0%; Score 480.5; DB 3; Length 120;
Best Local Similarity 79.2%; Pred. No. 4,4e-40;
Matches 95; Conservative 6; Mismatches 18; Indels 1; Gaps 1;

QY 1 EVOLVESGGDFVPGGSLRVSCAASGFAPSHYMSWVRQAPGKGLEWVAISSGGSGTTY 60
DB 1 EVOLVESGGGLVPGGSLRLSCAASGFTFSYMSWVRQAPGKLEWVAISSGGSGTTY 60

QY 61 SDSVKGRTISRDNKNTLYLQMRSLRAEDSAVYFCTR-VKLGTYFPDSMGOGTLLTVSS 119
DB 61 ADSVKGRTISRDNKNTLYLQMRSLRAEDTAIVYYCARWGDDGYANDYMGOGTLLTVSS 120

RESULT 37
US-09-025-769B-63
Sequence 63, Application US/09025769B
Patent No. 6300064
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckhuhn, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York

STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-769B-63

Query Match 77.0%; Score 480.5; DB 3; Length 120;
Best Local Similarity 79.2%; Pred. No. 4,4e-40;
Matches 95; Conservative 6; Mismatches 18; Indels 1; Gaps 1;

QY 1 EVOLVESGGDFVPGGSLRVSCAASGFAPSHYMSWVRQAPGKGLEWVAISSGGSGTTY 60
DB 1 EVOLVESGGGLVPGGSLRLSCAASGFTFSYMSWVRQAPGKLEWVAISSGGSGTTY 60

QY 61 SDSVKGRTISRDNKNTLYLQMRSLRAEDSAVYFCTR-VKLGTYFPDSMGOGTLLTVSS 119
DB 61 ADSVKGRTISRDNKNTLYLQMRSLRAEDTAIVYYCARWGDDGYANDYMGOGTLLTVSS 120

RESULT 38
US-09-490-070A-38
Sequence 38, Application US/09490070A
Patent No. 6696248
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckhuhn, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
White & McAuliffe
STREET: 1666 K Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Colin G. Sandercock, Esq.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37629-0005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 912-2000
TELEFAX: (202) 912-2020
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 38:
US-09-490-070A-38

Query Match 77.0%; Score 480.5; DB 4; Length 120;
Best Local Similarity 79.2%; Pred. No. 4,4e-40;
Matches 95; Conservative 6; Mismatches 18; Indels 1; Gaps 1;

Qy 1 EVOLVSSGGDFVOPGSLRVSCASGAFSHYAMSVWRQAPGKLEWVAYISGSGSTYY 60
Db 1 EVOLVSSGGDLVOPGSLRLSCASGFTPTSSYAMSVWRQAPGKLEWVAISGSGSTYY 60

Qy 61 SDSVKGRFTISRDNKNTLYLQWRSIAPDSAVYFCTR-VKLGTYFFDSMGOSTLLTVSS 119
Db 61 ADSVKGRFTISRDNKNTLYLQWRSIAPDSAVYFCTR-VKLGTYFFDSMGOSTLLTVSS 120

RESULT 39
US-09-490-070A-63
Sequence 63, Application US/09490070A
Patent No. 656248
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckhuhn, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
STREET: 1666 K Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Colin G. Sandercock, Esq.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37629-0005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 912-2000
TELEFAX: (202) 912-2020
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 63:
US-09-490-070A-63

Query Match 77.0%; Score 480.5; DB 4; Length 120;
Best Local Similarity 79.2%; Pred. No. 4,4e-40;
Matches 95; Conservative 6; Mismatches 18; Indels 1; Gaps 1;

Qy 1 EVOLVSSGGDFVOPGSLRVSCASGAFSHYAMSVWRQAPGKLEWVAYISGSGSTYY 60
Db 1 EVOLVSSGGDLVOPGSLRLSCASGFTPTSSYAMSVWRQAPGKLEWVAISGSGSTYY 60

Qy 61 SDSVKGRFTISRDNKNTLYLQWRSIAPDSAVYFCTR-VKLGTYFFDSMGOSTLLTVSS 119
Db 61 ADSVKGRFTISRDNKNTLYLQWRSIAPDSAVYFCTR-VKLGTYFFDSMGOSTLLTVSS 120

RESULT 40
US-09-490-153-38
Sequence 38, Application US/09490153
Patent No. 670648
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckhuhn, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 38:
US-09-490-153-38

Query Match 77.0%; Score 480.5; DB 4; Length 120;
Best Local Similarity 79.2%; Pred. No. 4,4e-40;
Matches 95; Conservative 6; Mismatches 18; Indels 1; Gaps 1;

Qy	1	EVQLVESGGDFVQPGGSLRVS	CAASGFAFSHYAMSWVRQAPGKLEWVA	YISSGGSGTY	60
Db	1	EVQLVESGGGLVQPGGSLRL	SCAASGFTFSYAMSWVRQAPGKLEWVA	AISSGGSGTY	60
Qy	61	SDSVKGRFTISRDN	SKNTLYLQMRSLRADSA	VYFCTR-VKLGTY	FDSWGOTLTVSS 119
Db	61	ADSVKGRFTISRDN	SKNTLYLQMNSLRAEDTA	VYCCARWGDDGFYAMDY	WGOTLTVSS 120

Search completed: December 17, 2004, 18:32:11
Job time : 73.2022 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 17, 2004, 18:20:33 ; Search time 229.978 Seconds
(without alignments)
185.159 Million cell updates/sec

Title: US-10-089-500-9

Perfect score: 624
Sequence: 1 EVQLVESGGDFVQPGGSLRV.....KLGTYYFDSWGQGTLLTVSS 119

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1589859 seqs, 357834939 residues

Total number of hits satisfying chosen parameters: 1589859

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*
1: /cgn2_6/ptodata/2/pubppa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubppa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubppa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubppa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubppa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubppa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubppa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubppa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubppa/US09_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubppa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubppa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubppa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubppa/US10_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubppa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubppa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubppa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubppa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubppa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubppa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/2/pubppa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	579	92.8	130	9	US-09-764-304-18
2	579	92.8	130	14	US-10-265-713-18
3	579	92.8	130	14	US-10-166-626-18
4	569	91.2	130	9	US-09-764-304-8
5	569	91.2	130	14	US-10-265-713-8
6	569	91.2	130	14	US-10-166-626-8
7	499	80.0	119	14	US-10-044-896-6
8	498	79.8	119	9	US-09-811-123-3
9	498	79.8	119	14	US-10-268-501-6
10	498	79.8	119	15	US-10-608-626-6
11	498	79.8	119	15	US-10-600-152-15
12	498	79.8	119	16	US-10-619-754-6
13	495.5	79.4	120	17	US-10-835-641-4

14	493.5	79.1	224	16	US-10-128-520-148	Sequence 148, App
15	492	78.8	313	14	US-10-291-265-427	Sequence 427, App
16	489	78.4	143	15	US-10-469-304-17	Sequence 17, App
17	488.5	78.3	220	16	US-10-128-520-156	Sequence 156, App
18	487.5	78.1	423	9	US-09-917-410-4	Sequence 4, App1
19	487	78.0	121	15	US-10-275-046-78	Sequence 78, App1
20	487	78.0	123	14	US-10-269-805-59	Sequence 59, App1
21	487	78.0	123	10	US-09-880-748-1953	Sequence 1953, App
22	487	78.0	247	11	US-10-293-418-1953	Sequence 1953, App
23	486.5	78.0	136	11	US-09-837-306-184	Sequence 184, App
24	486.5	78.0	136	14	US-10-045-674-487	Sequence 487, App
25	486.5	78.0	367	14	US-10-045-674-453	Sequence 453, App
26	486.5	78.0	368	11	US-09-837-306-196	Sequence 196, App
27	485.5	77.8	122	17	US-10-835-641-21	Sequence 21, App1
28	485.5	77.8	263	9	US-09-956-087-3	Sequence 3, App1
29	485.5	77.8	263	9	US-09-956-087-3	Sequence 3, App1
30	485.5	77.8	283	9	US-09-983-580-6	Sequence 6, App1
31	485.5	77.8	283	9	US-09-983-580-6	Sequence 6, App1
32	485	77.7	123	9	US-09-840-459-82	Sequence 82, App1
33	485	77.7	123	16	US-10-766-773-82	Sequence 82, App1
34	485	77.7	123	16	US-10-766-773-82	Sequence 82, App1
35	485	77.7	123	16	US-10-733-563-82	Sequence 82, App1
36	485	77.7	248	10	US-09-880-748-1421	Sequence 1421, App
37	485	77.7	248	14	US-10-293-418-1421	Sequence 1421, App
38	485	77.7	251	17	US-10-800-197-15	Sequence 15, App1
39	484.5	77.6	118	15	US-10-474-832-68	Sequence 68, App1
40	484.5	77.6	118	15	US-10-474-832-68	Sequence 68, App1
41	484.5	77.6	122	15	US-10-251-0858-93	Sequence 93, App1
42	484.5	77.6	122	16	US-10-737-252-93	Sequence 93, App1
43	484.5	77.6	124	14	US-10-040-244-16	Sequence 16, App1
44	484.5	77.6	177	16	US-10-693-629-64	Sequence 64, App1
45	484.5	77.6	447	15	US-10-474-832-4	Sequence 4, App1

ALIGNMENTS

RESULT 1
US-09-764-304-18
Sequence 18, Application US/09764304
Patent No. US20020026036A1
GENERAL INFORMATION:
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: HASEGAWA, MAMORU
APPLICANT: MIYAI, HIROMASA
TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
FILE REFERENCE: 249-101
CURRENT APPLICATION NUMBER: US/09/764,304
EARLIER APPLICATION NUMBER: 09/225,322
EARLIER FILING DATE: 1999-01-05
EARLIER APPLICATION NUMBER: US 08/454,680
EARLIER FILING DATE: 1995-05-31
EARLIER APPLICATION NUMBER: US 08/408,133
EARLIER FILING DATE: 1995-03-21
EARLIER APPLICATION NUMBER: US 08/292,178
EARLIER FILING DATE: 1994-08-17
EARLIER APPLICATION NUMBER: US07/947,674
EARLIER FILING DATE: 1992-09-17
EARLIER APPLICATION NUMBER: JP 3-238375
EARLIER FILING DATE: 1991-09-18
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 18
LENGTH: 130
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: cDNA KM-641
US-09-764-304-18

```
Query Match          92.8%; Score 579; DB 9; Length 130;
Best Local Similarity 91.6%; Pred. No. 1e-44;
Matches 109; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 1 EVOLVSGGDFVPGGSLRVSFCAAGFAFSHYAMSVWRQAPGKLEWVAIYISGGSGTYY 60
Db 11 EVTLVSGGDFVPGGSLRVSFCAAGFAFSHYAMSVWRQTPARLEWVAIYISGGSGTYY 70

Qy 61 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLGTYFPDSMGOGTLLTVSS 119
Db 71 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLGTYFPDSMGOGTLLTVSS 129

RESULT 2
US-10-265-713-18
; Sequence 18, Application US/10265713
; Publication No. US20030095964A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KIYAMA, YOSHITSA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/10/265,713
; PRIOR FILING DATE: 2002-10-08
; PRIOR APPLICATION NUMBER: US/09/225,322
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cDNA KM-641
US-10-265-713-18

Query Match          92.8%; Score 579; DB 14; Length 130;
Best Local Similarity 91.6%; Pred. No. 1e-44;
Matches 109; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 1 EVOLVSGGDFVPGGSLRVSFCAAGFAFSHYAMSVWRQAPGKLEWVAIYISGGSGTYY 60
Db 11 EVTLVSGGDFVPGGSLRVSFCAAGFAFSHYAMSVWRQTPARLEWVAIYISGGSGTYY 70

Qy 61 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLGTYFPDSMGOGTLLTVSS 119
Db 71 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLGTYFPDSMGOGTLLTVSS 129

RESULT 3
US-10-166-626-18
; Sequence 18, Application US/10166626
; Publication No. US20030166876A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KIYAMA, YOSHITSA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
US-10-166-626-18
```

```
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/10/166,626
; PRIOR FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US/09/225,322B
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cDNA KM-641
US-10-166-626-18

Query Match          92.8%; Score 579; DB 14; Length 130;
Best Local Similarity 91.6%; Pred. No. 1e-44;
Matches 109; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 1 EVOLVSGGDFVPGGSLRVSFCAAGFAFSHYAMSVWRQAPGKLEWVAIYISGGSGTYY 60
Db 11 EVTLVSGGDFVPGGSLRVSFCAAGFAFSHYAMSVWRQTPARLEWVAIYISGGSGTYY 70

Qy 61 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLGTYFPDSMGOGTLLTVSS 119
Db 71 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLGTYFPDSMGOGTLLTVSS 129

RESULT 4
US-09-764-304-8
; Sequence 8, Application US/09764304
; Patent No. US2002026036A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KIYAMA, YOSHITSA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/09/764,304
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 09/225,322
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: cDNA KM-641
US-09-764-304-8
```


Query Match 91.2%; Score 569; DB 9; Length 130;
Best Local Similarity 90.8%; Pred. No. 8.2e-44;
Matches 108; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 EVOLVESGDDPVQPGSLRVSCAASGFAFSHYAMSWVRQAPGKLEWVAIYSSGSGTTY 60
DB 11 EVTLVSGGDDPVQPGSLRVSCAASGFAFSHYAMSWVRQAPARLEWVAGISSGSGTTY 70
QY 61 SDSVKRFTISRDNKNTLYLQWRSLRAEDSAVYFCTRVKLGTYYPDSMGQGTLLTVSS 119
DB 71 SDSVKRFTISRDNKNTLYLQWRSLRSEDSAMYFCTRVKLGTYYPDSMGQGTLLTVSS 129

RESULT 5
US-10-265-713-8
Sequence 8, Application US/10265713
Publication No. US20030095964A1
GENERAL INFORMATION:
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: HASEGAWA, MAMORU
APPLICANT: MIYAJI, HIROMASA
APPLICANT: KUMANA, YOSHIHISA
TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
FILE REFERENCE: 249-101
CURRENT APPLICATION NUMBER: US/10/265,713
CURRENT FILING DATE: 2002-10-08
PRIOR APPLICATION NUMBER: US/09/225,322
PRIOR FILING DATE: 1999-01-05
PRIOR APPLICATION NUMBER: US 08/454,680
PRIOR FILING DATE: 1995-05-31
PRIOR APPLICATION NUMBER: US 08/408,133
PRIOR FILING DATE: 1995-03-21
PRIOR APPLICATION NUMBER: US 08/292,178
PRIOR FILING DATE: 1994-08-17
PRIOR APPLICATION NUMBER: US07/947,674
PRIOR FILING DATE: 1992-09-17
PRIOR APPLICATION NUMBER: JP 3-238375
PRIOR FILING DATE: 1991-09-18
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8
LENGTH: 130
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: CDNA KM-641
US-10-265-713-8

Query Match 91.2%; Score 569; DB 14; Length 130;
Best Local Similarity 90.8%; Pred. No. 8.2e-44;
Matches 108; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 EVOLVESGDDPVQPGSLRVSCAASGFAFSHYAMSWVRQAPGKLEWVAIYSSGSGTTY 60
DB 11 EVTLVSGGDDPVQPGSLRVSCAASGFAFSHYAMSWVRQAPARLEWVAGISSGSGTTY 70
QY 61 SDSVKRFTISRDNKNTLYLQWRSLRAEDSAVYFCTRVKLGTYYPDSMGQGTLLTVSS 119
DB 71 SDSVKRFTISRDNKNTLYLQWRSLRSEDSAMYFCTRVKLGTYYPDSMGQGTLLTVSS 129

RESULT 6
US-10-166-626-8
Sequence 8, Application US/10166626
Publication No. US20030166876A1
GENERAL INFORMATION:
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: HASEGAWA, MAMORU
APPLICANT: MIYAJI, HIROMASA
APPLICANT: KUMANA, YOSHIHISA

TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
FILE REFERENCE: 249-101
CURRENT APPLICATION NUMBER: US/10/166,626
CURRENT FILING DATE: 2002-06-12
PRIOR APPLICATION NUMBER: US/09/225,322B
PRIOR FILING DATE: 1999-01-05
PRIOR APPLICATION NUMBER: US 08/454,680
PRIOR FILING DATE: 1995-05-31
PRIOR APPLICATION NUMBER: US 08/408,133
PRIOR FILING DATE: 1995-03-21
PRIOR APPLICATION NUMBER: US 08/292,178
PRIOR FILING DATE: 1994-08-17
PRIOR APPLICATION NUMBER: US07/947,674
PRIOR FILING DATE: 1992-09-17
PRIOR APPLICATION NUMBER: JP 3-238375
PRIOR FILING DATE: 1991-09-18
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8
LENGTH: 130
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: CDNA KM-641
US-10-166-626-8

Query Match 91.2%; Score 569; DB 14; Length 130;
Best Local Similarity 90.8%; Pred. No. 8.2e-44;
Matches 108; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 EVOLVESGDDPVQPGSLRVSCAASGFAFSHYAMSWVRQAPGKLEWVAIYSSGSGTTY 60
DB 11 EVTLVSGGDDPVQPGSLRVSCAASGFAFSHYAMSWVRQAPARLEWVAGISSGSGTTY 70
QY 61 SDSVKRFTISRDNKNTLYLQWRSLRAEDSAVYFCTRVKLGTYYPDSMGQGTLLTVSS 119
DB 71 SDSVKRFTISRDNKNTLYLQWRSLRSEDSAMYFCTRVKLGTYYPDSMGQGTLLTVSS 129

RESULT 7
US-10-044-896-6
Sequence 6, Application US/10044896
Publication No. US20030166228A1
GENERAL INFORMATION:
APPLICANT: Chantharapai, Anan
APPLICANT: Kim, Jin K.
APPLICANT: Stewart, Timothy
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: ANTI-INTERFERON-ALPHA ANTIBODIES
FILE REFERENCE: GENENT. 074A
CURRENT APPLICATION NUMBER: US/10/044,896
CURRENT FILING DATE: 2002-01-09
PRIOR APPLICATION NUMBER: 60/270775
PRIOR FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 119
TYPE: PRT
ORGANISM: Homo sapiens
US-10-044-896-6

Query Match 80.0%; Score 499; DB 14; Length 119;
Best Local Similarity 80.7%; Pred. No. 1.6e-37;
Matches 96; Conservative 8; Mismatches 13; Indels 2; Gaps 1;

QY 1 EVOLVESGDDPVQPGSLRVSCAASGFAFSHYAMSWVRQAPGKLEWVAIYSSGSGTTY 60
DB 1 EVOLVESGDDPVQPGSLRVSCAASGFTFSSYAMSWVRQAPGKLEWVAIYSSGSGTTY 60
QY 61 SDSVKRFTISRDNKNTLYLQWRSLRAEDSAVYFCTRVKLGTYYPDSMGQGTLLTVSS 119
DB 61 ADSVKRFTISRDNKNTLYLQWRSLRAEDTAVYCARGRVG--YYDYWGQGTLLTVSS 117

RESULT 8
US-09-811-123-3
Sequence 3, Application US/09811123
Patent No. US20020001587A1
GENERAL INFORMATION:
APPLICANT: Sharon Erickson
APPLICANT: Ralph Schwall
APPLICANT: Mark Sliwkowski
TITLE OF INVENTION: METHODS OF TREATMENT USING ANTI-ERBB
TITLE OF INVENTION: ANTIBODY-MAYTANSINOID CONUGATES
FILE REFERENCE: GENENT.073A2
CURRENT APPLICATION NUMBER: US/09/811,123
CURRENT FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/238,327
PRIOR FILING DATE: 2000-10-05
PRIOR APPLICATION NUMBER: 09/602,530
PRIOR FILING DATE: 2000-06-23
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 119
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Humanized Antibody Sequence
US-09-811-123-3

Query Match 79.8%; Score 498; DB 9; Length 119;
Best Local Similarity 79.8%; Pred. No. 1.9e-37;
Matches 95; Conservative 8; Mismatches 16; Indels 0; Gaps 0;

Qy 1 EVOLVSGGDFVOPGSLRVSCAAGFASGHYAMSWVRQAPGKLEWVAIYSSGGSGTYY 60
Db 1 EVOLVSGGGLVOPGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVAIYSSGGSGTYY 60
Qy 61 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRYVLGTYYPDSWGQGLTLTVSS 119
Db 61 ADSVKGRFTISRDNKNTLYLQMRSLRAEDTAVYYCARGRVGYSLVDYWGQGLTLTVSS 119

RESULT 9
US-10-268-501-6
Sequence 6, Application US/10268501
Publication No. US20030086924A1
GENERAL INFORMATION:
APPLICANT: Sliwkowski, Mark X.
TITLE OF INVENTION: Treatment with Anti-ErbB2 Antibodies
FILE REFERENCE: P1467R2P1
CURRENT APPLICATION NUMBER: US/10/268,501
CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: US 09/602,812
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: US 60/141,316
PRIOR FILING DATE: 1999-06-25
NUMBER OF SEQ ID NOS: 13
SEQ ID NO 6
LENGTH: 119
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: heavy chain consensus sequence
US-10-268-501-6

Query Match 79.8%; Score 498; DB 14; Length 119;
Best Local Similarity 79.8%; Pred. No. 1.9e-37;
Matches 95; Conservative 8; Mismatches 16; Indels 0; Gaps 0;

Qy 1 EVOLVSGGDFVOPGSLRVSCAAGFASGHYAMSWVRQAPGKLEWVAIYSSGGSGTYY 60
Db 1 EVOLVSGGGLVOPGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVAIYSSGGSGTYY 60

Qy 61 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRYVLGTYYPDSWGQGLTLTVSS 119
Db 61 ADSVKGRFTISRDNKNTLYLQMRSLRAEDTAVYYCARGRVGYSLVDYWGQGLTLTVSS 119

RESULT 10
US-10-608-626-6
Sequence 6, Application US/10608626
Publication No. US20040013667A1
GENERAL INFORMATION:
APPLICANT: Kelsey, Stephen M.
APPLICANT: Sliwkowski, Mark X.
TITLE OF INVENTION: Treatment with Anti-ErbB2 Antibodies
FILE REFERENCE: P1467R2P2
CURRENT APPLICATION NUMBER: US/10/608,626
CURRENT FILING DATE: 2003-06-27
PRIOR APPLICATION NUMBER: US 10/268,501
PRIOR FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: US 09/602,812
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: US 60/141,316
PRIOR FILING DATE: 1999-06-25
NUMBER OF SEQ ID NOS: 13
SEQ ID NO 6
LENGTH: 119
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: heavy chain consensus sequence
US-10-608-626-6

Query Match 79.8%; Score 498; DB 15; Length 119;
Best Local Similarity 79.8%; Pred. No. 1.9e-37;
Matches 95; Conservative 8; Mismatches 16; Indels 0; Gaps 0;

Qy 1 EVOLVSGGDFVOPGSLRVSCAAGFASGHYAMSWVRQAPGKLEWVAIYSSGGSGTYY 60
Db 1 EVOLVSGGGLVOPGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVAIYSSGGSGTYY 60
Qy 61 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRYVLGTYYPDSWGQGLTLTVSS 119
Db 61 ADSVKGRFTISRDNKNTLYLQMRSLRAEDTAVYYCARGRVGYSLVDYWGQGLTLTVSS 119

RESULT 11
US-10-600-152-15
Sequence 15, Application US/10600152
Publication No. US20040037824A1
GENERAL INFORMATION:
APPLICANT: Baughman, Sharon A.
TITLE OF INVENTION: Dosages for Treatment with Anti-ErbB2 Antibodies
FILE REFERENCE: P1775R1
CURRENT APPLICATION NUMBER: US/10/600,152
CURRENT FILING DATE: 2003-06-20
PRIOR APPLICATION NUMBER: 09/648,067
PRIOR FILING DATE: 2000-08-25
PRIOR APPLICATION NUMBER: US 60/151,018
PRIOR FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: US 60/213,822
PRIOR FILING DATE: 2000-06-23
NUMBER OF SEQ ID NOS: 15
SEQ ID NO 15
LENGTH: 119
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: VH consensus sequence
US-10-600-152-15

Query Match 79.8%; Score 498; DB 15; Length 119;
Best Local Similarity 79.8%; Pred. No. 1.9e-37;
Matches 95; Conservative 8; Mismatches 16; Indels 0; Gaps 0;

```
QY 1 EVOLVESGDFVOPGSLRVSCAAGFAPSHYAMSWVRQAPGKLEWVAIISGSGSTTY 60
DB 1 EVOLVESGGGLVOPGSLRLSCAAGFTFSYAMSWVRQAPGKLEWVAIISGSGSTTY 60
QY 61 SDSVKGRFTISRDNKNTLYLQWRSRAEDSAVYFCTRVKLGITYYFDSWOGTLLTVSS 119
DB 61 ADSVKGRFTISRDNKNTLYLQWNSLRAEDTAVYCARGRGVGLVYDWGOGTLLTVSS 119

RESULT 12
US-10-619-754-6
Sequence 6, Application US/10619754
Publication No. US20040106161A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Koll, Hans
APPLICANT: Rosenmaler, Birgit
APPLICANT: Muller, Hans-Joachim
APPLICANT: Sliwkowski, Mark
APPLICANT: Kelsey, Stephen
TITLE OF INVENTION: Methods for Identifying Tumors That Are
RESPONSIVE TO TREATMENT WITH ANTI-HER2 ANTIBODIES
FILE REFERENCE: 39766-0114A
CURRENT APPLICATION NUMBER: US/10/619,754
CURRENT FILING DATE: 2003-07-14
PRIOR APPLICATION NUMBER: US 60/396,290
PRIOR FILING DATE: 2002-07-15
PRIOR APPLICATION NUMBER: US 60/480,043
PRIOR FILING DATE: 2003-06-20
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 119
TYPE: PRT
ORGANISM: Homo sapiens
US-10-619-754-6

Query Match 79.8%; Score 498; DB 16; Length 119;
Best Local Similarity 79.8%; Pred. No. 1.9e-37;
Matches 95; Conservative 8; Mismatches 16; Indels 0; Gaps 0;

QY 1 EVOLVESGDFVOPGSLRVSCAAGFAPSHYAMSWVRQAPGKLEWVAIISGSGSTTY 60
DB 1 EVOLVESGGGLVOPGSLRLSCAAGFTFSYAMSWVRQAPGKLEWVAIISGSGSTTY 60
QY 61 SDSVKGRFTISRDNKNTLYLQWRSRAEDSAVYFCTRVKLGITYYFDSWOGTLLTVSS 119
DB 61 ADSVKGRFTISRDNKNTLYLQWNSLRAEDTAVYCARGRGVGLVYDWGOGTLLTVSS 119

RESULT 13
US-10-835-641-4
Sequence 4, Application US/10835641
Publication No. US20040236078A1
GENERAL INFORMATION:
APPLICANT: Carter, Paul J.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Method for Making Humanized Antibodies
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
```

```
APPLICATION NUMBER: US/10/835,641
FILING DATE: 30-Apr-2004
CLASSIFICATION: <Unknown>
Prior APPLICATION DATA:
APPLICATION NUMBER: US/09/705,398
FILING DATE: 02-Nov-2000
APPLICATION NUMBER: 08/146206
FILING DATE: 17-Nov-1993
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P1D2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-835-641-4

Query Match 79.4%; Score 495.5; DB 17; Length 120;
Best Local Similarity 80.8%; Pred. No. 3.3e-37;
Matches 97; Conservative 7; Mismatches 15; Indels 1; Gaps 1;

QY 1 EVOLVESGDFVOPGSLRVSCAAGFAPSHYAMSWVRQAPGKLEWVAIISGSGSTTY 60
DB 1 EVOLVESGGGLVOPGSLRLSCAAGFTFSYAMSWVRQAPGKLEWVAIISGSGSTTY 60
QY 61 SDSVKGRFTISRDNKNTLYLQWRSRAEDSAVYFCTRVKLGITYYFDSWOGTLLTVSS 119
DB 61 ADSVKGRFTISRDNKNTLYLQWNSLRAEDTAVYCARGRGVGLVYDWGOGTLLTVSS 120

RESULT 14
US-10-128-520-148
Sequence 148, Application US/10128520
Publication No. US20040105862A1
GENERAL INFORMATION:
APPLICANT: PAN et al.
TITLE OF INVENTION: Human TIMP-1 Antibodies
FILE REFERENCE: 02973.00073
CURRENT APPLICATION NUMBER: US/10/128,520
CURRENT FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: US 60/285,683
PRIOR FILING DATE: 2001-04-24
NUMBER OF SEQ ID NOS: 381
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 148
LENGTH: 224
TYPE: PRT
ORGANISM: Homo sapiens
US-10-128-520-148

Query Match 79.1%; Score 493.5; DB 16; Length 224;
Best Local Similarity 79.5%; Pred. No. 9.4e-37;
Matches 97; Conservative 7; Mismatches 13; Indels 5; Gaps 2;

QY 1 EVOLVESGDFVOPGSLRVSCAAGFAPSHYAMSWVRQAPGKLEWVAIISGSGSTTY 60
DB 1 EVOLVESGGGLVOPGSLRLSCAAGFTFSYAMSWVRQAPGKLEWVAIISGSGSTTY 60
QY 61 SDSVKGRFTISRDNKNTLYLQWRSRAEDSAVYFCTRVKLGITYYFDSWOGTLLTV 117
DB 61 ADSVKGRFTISRDNKNTLYLQWNSLRAEDTAVYCAR--LDITYYDLPDYWGOGTLLTV 118
QY 118 SS 119
DB 119 SS 120
```

```
RESULT 15
US-10-291-265-427
; Sequence 427, Application US/10291265
; Publication No. US20030232054A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: Tang et al
; FILE REFERENCE: 21272-017 (785)
; CURRENT APPLICATION NUMBER: US/10/291,265
; PRIORITY FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIORITY FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIORITY FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIORITY FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIORITY FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 427
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-291-265-427

Query Match      78.8%; Score 492; DB 14; Length 313;
Best Local Similarity 74.8%; Pred. No. 1.8e-36;
Matches 95; Conservative 9; Mismatches 15; Indels 8; Gaps 1;

QY 1 EVOLVESGDFVOPGGSILRVSCAAGFAFSHYAMSWVRQAPGKGLEWVAYISSGSGSTYY 60
DB 61 EVOLVESGGLVOPGGSILRVSCAAGFTFSHYAMSWVRQAPGKGLEWVSAISSGSGSTYY 120
QY 61 SDSVKGRFTISRDNKNTLYLQNRSLRAEDSAVYFCTRVKLG-----TYFDSWGQG 112
DB 121 ADSVKGRFTISRDNKNTLYLQNRSLRAEDTAVYYCAKSHPGYYDSSGYFEDYWGQG 180
QY 113 TLTVSS 119
DB 181 TLTVSS 187

RESULT 16
US-10-469-304-17
; Sequence 17, Application US/10469304
; Publication No. US20040091974A1
; GENERAL INFORMATION:
; APPLICANT: KIRIN BEER KABUSHIKI KAISHA
; TITLE OF INVENTION: Anti HLA-DR antibody
; FILE REFERENCE: PH-1646-PCT
; CURRENT APPLICATION NUMBER: US/10/469,304
; PRIORITY FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: JP2001/317054
; PRIORITY FILING DATE: 2001-10-15
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 143
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-469-304-17

Query Match      78.4%; Score 489; DB 15; Length 143;
Best Local Similarity 78.0%; Pred. No. 1.5e-36;
Matches 96; Conservative 9; Mismatches 14; Indels 4; Gaps 2;
```

```
QY 61 SDSVKGRFTISRDNKNTLYLQNRSLRAEDSAVYFCTRVK-LGTTY---FDSWGQGTLLT 116
DB 80 ADSVKGRFTISRDNKNTLYLQNRSLRAEDTAVYYCARHDGSGSYYPWPDYWGQGTLLVT 139
QY 117 VSS 119
DB 140 VSS 142

RESULT 17
US-10-128-520-156
; Sequence 156, Application US/10128520
; Publication No. US20040105862A1
; GENERAL INFORMATION:
; APPLICANT: PAN et al.
; TITLE OF INVENTION: Human TIMP-1 Antibodies
; FILE REFERENCE: 02973.00073
; CURRENT APPLICATION NUMBER: US/10/128,520
; PRIORITY FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 60/285,683
; PRIORITY FILING DATE: 2001-04-24
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 156
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-128-520-156

Query Match      78.3%; Score 488.5; DB 16; Length 220;
Best Local Similarity 79.8%; Pred. No. 2.6e-36;
Matches 95; Conservative 9; Mismatches 12; Indels 3; Gaps 2;

QY 1 EVOLVESGDFVOPGGSILRVSCAAGFAFSHYAMSWVRQAPGKGLEWVAYISSGSGSTYY 60
DB 1 QVOLVESGGLVOPGGSILRVSCAAGFTFSHYAMSWVRQAPGKGLEWVSAISSGSGSTYY 60
QY 61 SDSVKGRFTISRDNKNTLYLQNRSLRAEDSAVYFCTRVKLGTYFDSWGQGTLLTVSS 119
DB 61 ADSVKGRFTISRDNKNTLYLQNRSLRAEDTAVYYCARL-IG--YFDLWGQGTLLTVSS 116

RESULT 18
US-09-917-410-4
; Sequence 4, Application US/09917410
; Patent No. US20020098183A1
; GENERAL INFORMATION:
; APPLICANT: MARTIN, Ulrich; HASELBECK, Anton; SCHUMACHER, Guenther;
; CO, Man S.
; TITLE OF INVENTION: ANTI-L-SELECTIN ANTIBODIES FOR PREVENTION OF
; MULTIPLE ORGAN FAILURE AFTER POLYTRAUMA AND FOR
; PREVENTION OF ACUTE ORGAN DAMAGE AFTER
; EXTRACORPOREAL BLOOD CIRCULATION
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felte & Lynch
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Computer Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII, Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/917,410
; FILING DATE: 26-Jul-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/578,953
```

FILING DATE: <Unknown>
APPLICATION NUMBER: EP 95 114 969.9
FILING DATE: 19-Sep-95
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. US20020098183A1man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: BOER 1059-PFF/NDH/SLH
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 443
TYPE: amino acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-917-410-4

Query Match 78.1%; Score 487.5; DB 9; Length 443;
Best Local Similarity 82.4%; Pred. No. 6.5e-36;
Matches 98; Conservative 6; Mismatches 12; Indels 3; Gaps 2;

Qy 1 EVOLVESGDDPVQPGGSLRVSCAAGFAFSHYAMSWVRQAPGKLEWVAIISGSGSTYY 60
Db 1 EVOLVESGGGLVQPGGSLRLSCAAGFTFTSYAMSWVRQAPGKLEWVAISITGGS-TYY 59
Qy 61 SDSVKRFTISRNSKNTLYLQWRSLRAEDSAVYFCTRVKLTYYTDSKGGTLTVSS 119
Db 60 PSDVKRFTISRNSKNTLYLQWRSLRAEDTAVYVCARDYDQ--YFDYWGQGTLLTVSS 116

RESULT 19
US-10-275-046-78
Sequence 78, Application US/10275046
Publication No. US20040019187A1
GENERAL INFORMATION:
APPLICANT: Nagy et al.
TITLE OF INVENTION: IMMUNOMODULATORY HUMAN MHC CLASS II ANTIGEN-BINDING POLYPEPTIDES
FILE REFERENCE: GPCG-P01-260
CURRENT APPLICATION NUMBER: US/10/275,046
CURRENT FILING DATE: 2002-10-31
PRIOR APPLICATION NUMBER: 00110063.5
PRIOR FILING DATE: 2000-05-12
NUMBER OF SEQ ID NOS: 97
SOFTWARE: PatentIn version 3.2
SEQ ID NO 78
LENGTH: 121
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: MS-GPC14 VH
US-10-275-046-78

Query Match 78.0%; Score 487; DB 15; Length 121;
Best Local Similarity 78.5%; Pred. No. 1.9e-36;
Matches 95; Conservative 7; Mismatches 17; Indels 2; Gaps 1;

Qy 1 EVOLVESGDDPVQPGGSLRVSCAAGFAFSHYAMSWVRQAPGKLEWVAIISGSGSTYY 60
Db 1 EVOLVESGGGLVQPGGSLRLSCAAGFTFTSYAMSWVRQAPGKLEWVAISGSGSTYY 60
Qy 61 SDSVKRFTISRNSKNTLYLQWRSLRAEDSAVYFCTRVKLTYY--YFDSWGQGTLLTVS 118
Db 61 ADSVKRFTISRNSKNTLYLQWRSLRAEDTAVYVCARSSMPYGGGFLMGQGTLLTVS 120

Qy 119 S 119
Db 121 S 121

RESULT 20

US-10-269-805-59
Sequence 59, Application US/10269805
Publication No. US20030124129A1
GENERAL INFORMATION:
APPLICANT: OLIVER, JONATHAN D.
TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS
FILE REFERENCE: A-722
CURRENT APPLICATION NUMBER: US/10/269,805
CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: US 60/328,604
PRIOR FILING DATE: 2001-10-11
NUMBER OF SEQ ID NOS: 76
SOFTWARE: PatentIn version 3.1
SEQ ID NO 59
LENGTH: 123
TYPE: PRT
ORGANISM: Homo sapiens
US-10-269-805-59

Query Match 78.0%; Score 487; DB 14; Length 123;
Best Local Similarity 76.4%; Pred. No. 2e-36;
Matches 94; Conservative 10; Mismatches 15; Indels 4; Gaps 2;

Qy 1 EVOLVESGDDPVQPGGSLRVSCAAGFAFSHYAMSWVRQAPGKLEWVAIISGSGSTYY 60
Db 1 EVOLVESGGGLVQPGGSLRLSCAAGFTFTSYAMSWVRQAPGKLEWVAISGSGSTYY 60
Qy 61 SDSVKRFTISRNSKNTLYLQWRSLRAEDSAVYFCTRVKLTYYTDSKGGTLTVSS 116
Db 61 ADSVKRFTISRNSKNTLYLQWRSLRAEDTAVYVCARSSMPYGGGFLMGQGTLLTVS 120
Qy 117 VSS 119
Db 121 VSS 123

RESULT 21
US-09-880-748-1953
Sequence 1953, Application US/09880748
Publication No. US20030059937A1
GENERAL INFORMATION:
APPLICANT: Ruden et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1953
LENGTH: 247
TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-748-1953

Query Match 78.0%; Score 487; DB 10; Length 247;
Best Local Similarity 76.5%; Pred. No. 4e-36;
Matches 91; Conservative 12; Mismatches 16; Indels 0; Gaps 0;

Qy 1 EVOLVESGDDPVQPGGSLRVSCAAGFAFSHYAMSWVRQAPGKLEWVAIISGSGSTYY 60
Db 1 EVOLVESGGGLVQPGGSLRLSCAAGFTFTSYAMSWVRQAPGKLEWVAISGSGSTYY 60
Qy 61 SDSVKRFTISRNSKNTLYLQWRSLRAEDSAVYFCTRVKLTYYTDSKGGTLTVSS 119

Db
61 ADSVGRFTISRDNSKNTLYLQMSLRADETAIYCAKGIWGYFDYWGQGLVTWSS 119

RESULT 22
US-10-293-418-1953
; Sequence 1953, Application US/10293418
; Publication No. US20030223996A1
GENERAL INFORMATION

APPLICANT: KUDEN et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blyss
FILE REFERENCE: PFS23p2
CURRENT APPLICATION NUMBER: US/10/293,418
CURRENT FILING DATE: 2003-11-02

PRIOR APPLICATION NUMBER: 60/331,465
 PRIOR FILING DATE: 2001-11-16
 PRIOR APPLICATION NUMBER: 60/340,817
 PRIOR FILING DATE: 2001-12-19
 PRIOR APPLICATION NUMBER: 09/880,748
 PRIOR FILING DATE: 2001-06-15
 PRIOR APPLICATION NUMBER: 60/293,459
 PRIOR FILING DATE: 2001-05-25
 PRIOR APPLICATION NUMBER: 60/277,379
 PRIOR FILING DATE: 2001-03-21
 PRIOR APPLICATION NUMBER: 60/276,248
 PRIOR FILING DATE: 2001-03-16
 PRIOR APPLICATION NUMBER: 60/240,816
 PRIOR FILING DATE: 2000-10-17
 PRIOR APPLICATION NUMBER: 60/212,210
 PRIOR FILING DATE: 2000-06-16
 NUMBER OF SEQ ID NOS: 3247
 SEQ ID NO 1953

ORGANISM: Homo sapiens
US-10-293-418-1953

Query Match	78.0%	Score	487	DB	14	Length	247
Best Local Similarity	76.5%	Pred. NO.	4e-36				
Matches	91	Conservative	12	Mismatches	16	Indels	0
						Gaps	0

[illegible]

```

RESULT 23
US-09-837-306-184
: Sequence 184, Application US/09837306
: Publication No. US20040029113a1
:
: GENERAL INFORMATION:
: APPLICANT: LADNER, ROBERT C.
: APPLICANT: COHEN, EDWARD H.
: APPLICANT: NASTRI, HORACIO G.
: APPLICANT: ROOKEY, KRISTIN L.
: APPLICANT: HOET, RENE
: TITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES OF GENETIC
: TITLE OF INVENTION: PACKAGES THAT COLLECTIVELY DISPLAY THE MEMBERS OF A
: TITLE OF INVENTION: DIVERSE FAMILY OF PEPTIDES, POLYPEPTIDES OR PROTEINS
: FILE REFERENCE: DTX/002
: CURRENT APPLICATION NUMBER: US/09/837,306
: CURRENT FILING DATE: 2001-09-24
: PRIOR APPLICATION NUMBER: 60/199,069
: PRIOR FILING DATE: 2000-04-17
: NUMBER OF SEQ ID NOS: 428
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 184
:
: LENGTH: 136
: TYPE: PRT

```

```

; ORGANISM: Unknown Organism
;
; FEATURE:
;
; OTHER INFORMATION: Description of Unknown Organism: V3-23
US-09-837-306-184

```

Query Match	78.0%;	Score 486.5;	DB 11;	Length 136;
Best Local Similarity	78.3%;	Pred. No. 2.4e-36;		
Matches 94;	Conservative 9;	Mismatches 16;	Indels 1;	Gaps 1;

[illegible]

RESULT 24
US-10-045-674-487
; Sequence 487, Application US/10045674
; Publication No. US2003023233A1
; GENERAL INFORMATION:

APPLICANT: LADNER, ROBERT C.
APPLICANT: COHEN, EDWARD H.
APPLICANT: NASTRI, HORATIO G.
APPLICANT: ROOKEY, KRISTIN L.

APPLICANT: HOOGENBOOM, HENDRICUS R. J. M.

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
84

CURRENT APPLICATION NUMBER: US/10/045,674

PRIOR APPLICATION NUMBER: 60/198,065

PRIOR APPLICATION NUMBER: 09/837,306

```

; NUMBER OF SEQ ID NOS: 635
;
; SOFTWARE: PatentIn Ver. 2.1

```

ORGANISM: Artificial Sequence

```

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic 3-23
; OTHER INFORMATION: VH protein sequence
UN 10 045 574 403

```

Query Match	78.0%;	Score 486.5;	DB 14;	Length 136;
Best Local Similarity	78.3%;	Pred. No. 2.4e-36;		
Matches 94; Conservative	9;	Mismatches 16;	Indels 1;	Gaps 1;

[illegible]

RESULT 25
US-10-045-674-453
: Sequence 453, Application No. US20030232333A1
: Application No. US20030232333A1
: GENERAL INFORMATION:
: APPLICANT: LADNER, ROBERT C.
: APPLICANT: COHEN, EDWARD H.
: APPLICANT: NASTRI, HORACIO G.
: APPLICANT: ROOKEY, KRISTIN L.

APPLICANT: HOET, RENE
TITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES COMPRISING
TITLE OF INVENTION: DISPLAYED AND/OR EXPRESSED MEMBERS OF A DIVERSE FAMILY
TITLE OF INVENTION: OF PEPTIDES, POLYPEPTIDES OR PROTEINS AND THE NOVEL
FILE REFERENCE: DYAX/002 CIP2
CURRENT APPLICATION NUMBER: US/10/045,674
CURRENT FILING DATE: 2001-10-25
PRIOR APPLICATION NUMBER: 60/198,069
PRIOR FILING DATE: 2000-04-17
PRIOR APPLICATION NUMBER: 09/837,306
PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 635
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 453
LENGTH: 367
TYPE: PRT
ORGANISM: Unknown Organism
FEATURE:
OTHER INFORMATION: Description of Unknown Organism: MALIA3 protein
US-10-045-674-453

Query Match 78.0%; Score 486.5; DB 14; Length 367;
Best Local Similarity 78.3%; Pred. No. 6,6e-36;
Matches 94; Conservative 9; Mismatches 16; Indels 1; Gaps 1;

1 EVOLVESGGDFVQPGGSLRVSCAAGFAPFASHYAMSWVROAPGKGLVAVIYSSGSGSTYY 60
23 EVQLVESGGGLVQPGGSLRLSCAASGFTFSYAMSWVROAPGKGLVAVIYSSGSGSTYY 82
61 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLG--YYFDSWGCGTLTVSS 119
83 ADSVKGRFTISRDNKNTLYLQMRSLRAEDTAIVYCAKDEGVAFDIMGCGTMTVSS 142

RESULT 26
US-09-837-306-196
Sequence 196, Application US/09837306
Publication No. US20040029113A1
GENERAL INFORMATION:
APPLICANT: LADNER, ROBERT C.
APPLICANT: COHEN, EDWARD H.
APPLICANT: NASTRI, HORACIO G.
APPLICANT: ROOKEY, KRISTIN L.
APPLICANT: HOET, RENE
TITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES OF GENETIC
TITLE OF INVENTION: PACKAGES THAT COLLECTIVELY DISPLAY THE MEMBERS OF A
FILE REFERENCE: DYAX/002
CURRENT APPLICATION NUMBER: US/09/837,306
CURRENT FILING DATE: 2001-09-24
PRIOR APPLICATION NUMBER: 60/198,069
PRIOR FILING DATE: 2000-04-17
NUMBER OF SEQ ID NOS: 428
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 196
LENGTH: 368
TYPE: PRT
ORGANISM: Unknown Organism
FEATURE:
OTHER INFORMATION: Description of Unknown Organism: MALIA3
US-09-837-306-196

Query Match 78.0%; Score 486.5; DB 11; Length 368;
Best Local Similarity 78.3%; Pred. No. 6,6e-36;
Matches 94; Conservative 9; Mismatches 16; Indels 1; Gaps 1;

1 EVOLVESGGDFVQPGGSLRVSCAAGFAPFASHYAMSWVROAPGKGLVAVIYSSGSGSTYY 60
23 EVQLVESGGGLVQPGGSLRLSCAASGFTFSYAMSWVROAPGKGLVAVIYSSGSGSTYY 82

61 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLG--YYFDSWGCGTLTVSS 119
83 ADSVKGRFTISRDNKNTLYLQMRSLRAEDTAIVYCAKDEGVAFDIMGCGTMTVSS 142

RESULT 27
US-10-835-641-21
Sequence 21, Application US/10835641
Publication No. US20040236078A1
GENERAL INFORMATION:
APPLICANT: Carter, Paul J.
Presta, Leonard G.
TITLE OF INVENTION: Method for Making Humanized Antibodies
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/835,641
FILING DATE: 30-Apr-2004
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/705,398
FILING DATE: 02-Nov-2000
APPLICATION NUMBER: 08/146206
FILING DATE: 17-Nov-1993
APPLICATION NUMBER: 07/715272
FILING DATE: 14-Jun-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709PID2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9681
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-10-835-641-21

Query Match 77.8%; Score 485.5; DB 17; Length 122;
Best Local Similarity 77.0%; Pred. No. 2,7e-36;
Matches 94; Conservative 10; Mismatches 15; Indels 3; Gaps 1;

1 EVOLVESGGDFVQPGGSLRVSCAAGFAPFASHYAMSWVROAPGKGLVAVIYSSGSGSTYY 60
1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSYAMSWVROAPGKGLVAVIYSSGSGSTYY 60
61 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLG--YYFDSWGCGTLTV 117
61 ADSVKGRFTISRDNKNTLYLQMRSLRAEDTAIVYCARGVGYSGLVDYWGCGTLTV 120

118 SS 119
121 SS 122

RESULT 28
US-09-956-086-3
Sequence 3, Application US/09956086
Patent No. US20020155498A1

GENERAL INFORMATION:
APPLICANT: FILIPULA, DAVID
WANG, MAOLIANG
SHORR, ROBERT
WHITLOW, MARC
LEE, LIHSYNG S.
TITLE OF INVENTION: SINGLE-CHAIN ANTIGEN-BINDING PROTEINS
CAPABLE OF GLYCOSYLATION, PRODUCTION AND USES THEREOF
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/956,086
FILING DATE: 20-Sep-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/069,821
FILING DATE: <Unknown>
APPLICATION NUMBER: US 60/063,074
FILING DATE: 27-OCT-1997
APPLICATION NUMBER: US 60/050,472
FILING DATE: 23-JUN-1997
APPLICATION NUMBER: US 60/044,449
FILING DATE: 30-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: KIM, JUDITH U.
REGISTRATION NUMBER: 40,679
REFERENCE/DOCKET NUMBER: 0977.2280003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2600
TELEFAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 263 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: No. US20020155498A1 Relevant
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-956-086-3
Query Match 77.8%; Score 485.5; DB 9; Length 263;
Best Local Similarity 73.8%; Pred. No. 5.8e-36;
Matches 96; Conservative 9; Mismatches 14; Indels 11; Gaps 2;
QY 1 EVQLVDSGGDFVQPGGSLRVSCAASGFAPSHYAMSWVRQAPGKLEWVAYIS--SGSGST 58
DB 130 EVQLVDSGGGLVQPGGSLRLSCAASGFTSSYAMSWVRQAPGKLEWVSVISGKTDGSGST 189
QY 59 YYSDSYKGRFTTISRDNKNTLYLQMSRLAEADSAVYFCRVLGT-----YYFDSM 109
DB 190 YYADSVKGRFTTISRDNKNTLYLQMSRLAEADTAIVYICARGXGKSLSGXYYYTHYFDYW 249
QY 110 GGGTLTVSS 119
DB 250 GGGTLTVSS 259
RESULT 29
US-09-956-087-3
; Sequence 3, Application US/09956087
; Patent No. US20020161201A1
; GENERAL INFORMATION:

APPLICANT: FILIPULA, DAVID
WANG, MAOLIANG
SHORR, ROBERT
WHITLOW, MARC
LEE, LIHSYNG S.
TITLE OF INVENTION: SINGLE-CHAIN ANTIGEN-BINDING PROTEINS
CAPABLE OF GLYCOSYLATION, PRODUCTION AND USES THEREOF
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/956,087
FILING DATE: 20-Sep-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/069,821
FILING DATE: 1998-04-30
APPLICATION NUMBER: US 60/063,074
FILING DATE: 27-OCT-1997
APPLICATION NUMBER: US 60/050,472
FILING DATE: 23-JUN-1997
APPLICATION NUMBER: US 60/044,449
FILING DATE: 30-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: KIM, JUDITH U.
REGISTRATION NUMBER: 40,679
REFERENCE/DOCKET NUMBER: 0977.2280003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2600
TELEFAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 263 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-956-087-3
Query Match 77.8%; Score 485.5; DB 9; Length 263;
Best Local Similarity 73.8%; Pred. No. 5.8e-36;
Matches 96; Conservative 9; Mismatches 14; Indels 11; Gaps 2;
QY 1 EVQLVDSGGDFVQPGGSLRVSCAASGFAPSHYAMSWVRQAPGKLEWVAYIS--SGSGST 58
DB 130 EVQLVDSGGGLVQPGGSLRLSCAASGFTSSYAMSWVRQAPGKLEWVSVISGKTDGSGST 189
QY 59 YYSDSYKGRFTTISRDNKNTLYLQMSRLAEADSAVYFCRVLGT-----YYFDSM 109
DB 190 YYADSVKGRFTTISRDNKNTLYLQMSRLAEADTAIVYICARGXGKSLSGXYYYTHYFDYW 249
QY 110 GGGTLTVSS 119
DB 250 GGGTLTVSS 259
RESULT 30
US-09-983-580-6
; Sequence 6, Application US/09983580
; Patent No. US20020151061A1
; GENERAL INFORMATION:
; APPLICANT: Filipula, David R.

APPLICANT: Wang, Maoliang
APPLICANT: Whitlow, Marc D.
TITLE OF INVENTION: No. US20020151061a1el Method for Targeted Delivery of Nucleic Acid
FILE REFERENCE: 0977.2300002
CURRENT APPLICATION NUMBER: US/09/983.580
CURRENT FILING DATE: 2001-10-25
PRIOR APPLICATION NUMBER: 09/420,592
PRIOR FILING DATE: 1999-10-19
PRIOR APPLICATION NUMBER: 60/104,949
PRIOR FILING DATE: 1998-10-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 6
LENGTH: 283
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Kabat
NAME/KEY: UNSURE
LOCATION: (232)
OTHER INFORMATION: May be any amino acid.
NAME/KEY: UNSURE
LOCATION: (234)
OTHER INFORMATION: May be any amino acid.
NAME/KEY: UNSURE
LOCATION: (239)
OTHER INFORMATION: May be any amino acid.
US-09-983-580-6

Query Match 77.8%; Score 485.5; DB 9; Length 283;
Best Local Similarity 73.8%; Pred. No. 6.3e-36;
Matches 96; Conservative 9; Mismatches 14; Indels 11; Gaps 2;

QY 1 EVOLVESGDFVPGGSLRVSCAASGAPFASHYMSWVRQAPGKLEWVAIYS--SGSGGT 58
DB 130 EVOLVESGGGLVPGGSLRVSCAASGFTFSYMSWVRQAPGKLEWVAIYSKTDGGST 189
QY 59 YSDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLT-----YFPDSW 109
DB 190 YADSVKGRFTISRDNKNTLYLQMRSLRAEDTAIVYCAKGRGXSLGXYYHYHFDYW 249
QY 110 GGCTLLTVSS 119
DB 250 GGCTLLTVSS 259

RESULT 31
US-09-985-442-6
Sequence 6, Application US/09985442
Patent No. US20020156248A1
GENERAL INFORMATION:
APPLICANT: Filipula, David R.
APPLICANT: Wang, Maoliang
APPLICANT: Whitlow, Marc D.
TITLE OF INVENTION: No. US20020156248A1el Method for Targeted Delivery of Nucleic Acid
FILE REFERENCE: 0977.2300003
CURRENT APPLICATION NUMBER: US/09/985.442
CURRENT FILING DATE: 2001-11-02
PRIOR APPLICATION NUMBER: 09/420,592
PRIOR FILING DATE: 1999-10-19
PRIOR APPLICATION NUMBER: 60/104,949
PRIOR FILING DATE: 1998-10-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 6
LENGTH: 283
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Kabat
NAME/KEY: UNSURE

LOCATION: (232)
OTHER INFORMATION: May be any amino acid.
NAME/KEY: UNSURE
LOCATION: (234)
OTHER INFORMATION: May be any amino acid.
NAME/KEY: UNSURE
LOCATION: (239)
OTHER INFORMATION: May be any amino acid.
US-09-985-442-6

Query Match 77.8%; Score 485.5; DB 9; Length 283;
Best Local Similarity 73.8%; Pred. No. 6.3e-36;
Matches 96; Conservative 9; Mismatches 14; Indels 11; Gaps 2;

QY 1 EVOLVESGDFVPGGSLRVSCAASGAPFASHYMSWVRQAPGKLEWVAIYS--SGSGGT 58
DB 130 EVOLVESGGGLVPGGSLRVSCAASGFTFSYMSWVRQAPGKLEWVAIYSKTDGGST 189
QY 59 YSDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLT-----YFPDSW 109
DB 190 YADSVKGRFTISRDNKNTLYLQMRSLRAEDTAIVYCAKGRGXSLGXYYHYHFDYW 249
QY 110 GGCTLLTVSS 119
DB 250 GGCTLLTVSS 259

RESULT 32
US-09-840-459-82
Sequence 82, Application US/09840459
Patent No. US20020150576A1
GENERAL INFORMATION:
APPLICANT: Larosa, Gregory J.
APPLICANT: Horvath, Christopher
APPLICANT: Newman, Walter
APPLICANT: Jones, S. Tarran
APPLICANT: O'Brien, Siobhan H.
APPLICANT: O'Keefe, Theresa
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
FILE REFERENCE: 1855.1052-012
CURRENT APPLICATION NUMBER: US/09/840.459
CURRENT FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: PCT/US01/03537
PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 09/497,625
PRIOR FILING DATE: 2000-02-03
PRIOR APPLICATION NUMBER: 09/359,193
PRIOR FILING DATE: 1999-07-22
PRIOR APPLICATION NUMBER: 09/121,781
PRIOR FILING DATE: 1998-07-23
NUMBER OF SEQ ID NOS: 107
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 82
LENGTH: 123
TYPE: PRT
ORGANISM: Homo sapiens
US-09-840-459-82

Query Match 77.7%; Score 485; DB 9; Length 123;
Best Local Similarity 76.4%; Pred. No. 3e-36;
Matches 94; Conservative 9; Mismatches 16; Indels 4; Gaps 1;

QY 1 EVOLVESGDFVPGGSLRVSCAASGAPFASHYMSWVRQAPGKLEWVAIYSSGSGT 60
DB 1 EVOLVESGGGLVPGGSLRVSCAASGFTFSYMSWVRQAPGKLEWVAIYSSGSGT 60
QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLT-----YKGTYYFDSWGCGTLT 116
DB 61 ADSVKGRFTISRDNKNTLYLQMRSLRAEDTAIVYCAKGRGXSLGXYYHYHFDYW 120
QY 117 VSS 119

```
Db          121 VSS 123

RESULT 33
US-10-766-773-82
; Sequence 82, Application US/10766773
; Publication No. US20040126851A1
; GENERAL INFORMATION:
; APPLICANT: Larosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-028
; CURRENT APPLICATION NUMBER: US/10/766,773
; PRIOR FILING DATE: 2004-01-27
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 82
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-766-773-82

Query Match          77.7%; Score 485; DB 16; Length 123;
Best Local Similarity 76.4%; Pred. No. 3e-36;
Matches 94; Conservative 9; Mismatches 16; Indels 4; Gaps 1;

QY          1 EVOLVESGDDFVOPGSLRVSCAASGAFAPSHYAMWVRQAPGKLEWVAIISGSGTYY 60
Db          1 EVOLLESGGGLVOPGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVAISGSGTYY 60
QY          61 SDSVKGRFTISRDNKNTLYLQWRSIRAPDSAVYFCTR----VKLGTYYPDSWGQGTLLT 116
Db          61 ADSVKGRFTISRDNKNTLYLQWNSIRAPEDTAVYVCARRKPDYSGSGSYLDYWGQGTLLVT 120
QY          117 VSS 119
Db          121 VSS 123

RESULT 34
US-10-766-610-82
; Sequence 82, Application US/10766610
; Publication No. US20040132980A1
; GENERAL INFORMATION:
; APPLICANT: Larosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Stobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-029
; CURRENT APPLICATION NUMBER: US/10/766,610
; PRIOR FILING DATE: 2004-01-27
; PRIOR APPLICATION NUMBER: 09/840,459
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
```

```
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 82
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-766-610-82

Query Match          77.7%; Score 485; DB 16; Length 123;
Best Local Similarity 76.4%; Pred. No. 3e-36;
Matches 94; Conservative 9; Mismatches 16; Indels 4; Gaps 1;

QY          1 EVOLVESGDDFVOPGSLRVSCAASGAFAPSHYAMWVRQAPGKLEWVAIISGSGTYY 60
Db          1 EVOLLESGGGLVOPGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVAISGSGTYY 60
QY          61 SDSVKGRFTISRDNKNTLYLQWRSIRAPDSAVYFCTR----VKLGTYYPDSWGQGTLLT 116
Db          61 ADSVKGRFTISRDNKNTLYLQWNSIRAPEDTAVYVCARRKPDYSGSGSYLDYWGQGTLLVT 120
QY          117 VSS 119
Db          121 VSS 123

RESULT 35
US-10-733-563-82
; Sequence 82, Application US/10733563
; Publication No. US20040151721A1
; GENERAL INFORMATION:
; APPLICANT: Ponath, Paul
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 10448-213001
; CURRENT APPLICATION NUMBER: US/10/733,563
; PRIOR FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: US 10/272,899
; PRIOR FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: US 60/392,364
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: US 60/350,166
; PRIOR FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 82
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-733-563-82

Query Match          77.7%; Score 485; DB 16; Length 123;
Best Local Similarity 76.4%; Pred. No. 3e-36;
Matches 94; Conservative 9; Mismatches 16; Indels 4; Gaps 1;

QY          1 EVOLVESGDDFVOPGSLRVSCAASGAFAPSHYAMWVRQAPGKLEWVAIISGSGTYY 60
Db          1 EVOLLESGGGLVOPGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVAISGSGTYY 60
QY          61 SDSVKGRFTISRDNKNTLYLQWRSIRAPDSAVYFCTR----VKLGTYYPDSWGQGTLLT 116
Db          61 ADSVKGRFTISRDNKNTLYLQWNSIRAPEDTAVYVCARRKPDYSGSGSYLDYWGQGTLLVT 120
QY          117 VSS 119
Db          121 VSS 123

RESULT 36
US-09-880-748-1421
```

```
; Sequence 1421, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF533
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1421
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1421
```

```
Query Match 77.7%; Score 485; DB 10; Length 248;
Best Local Similarity 76.8%; Pred. No. 6,1e-36;
Matches 96; Conservative 8; Mismatches 15; Indels 6; Gaps 2;
```

```
QY 1 EVOLVESGDFVQPGSLRVSCAAGFARSHYAMSVWRQAPGKLEWAVYISGGSGTTY 60
DB 1 EVOLVESGGGLVQPGGSLRLSCAASGFTFSYAMHWVRQAPGKLEWAVISYDGSNKYY 60
QY 61 SDSVKRFTISRDNKNTLYLQWRSIRAEEDSAVYFCTRVKL-----VKLG-TYYPDSWGQTL 114
DB 61 ADSVKRFTISRDNKNTLYLQWNSIRAEEDTAVYVCARAYDYDILTGYSYFDMGKGL 120
QY 115 LVVSS 119
DB 121 VTVSS 125
```

```
RESULT 37
US-10-293-418-1421
; Sequence 1421, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1421
; LENGTH: 248
; TYPE: PRT
```

```
; ORGANISM: Homo sapiens
US-10-293-418-1421
```

```
Query Match 77.7%; Score 485; DB 14; Length 248;
Best Local Similarity 76.8%; Pred. No. 6,1e-36;
Matches 96; Conservative 8; Mismatches 15; Indels 6; Gaps 2;
```

```
QY 1 EVOLVESGDFVQPGSLRVSCAAGFARSHYAMSVWRQAPGKLEWAVYISGGSGTTY 60
DB 1 EVOLVESGGGLVQPGGSLRLSCAASGFTFSYAMHWVRQAPGKLEWAVISYDGSNKYY 60
QY 61 SDSVKRFTISRDNKNTLYLQWRSIRAEEDSAVYFCTRVKL-----VKLG-TYYPDSWGQTL 114
DB 61 ADSVKRFTISRDNKNTLYLQWNSIRAEEDTAVYVCARAYDYDILTGYSYFDMGKGL 120
QY 115 LVVSS 119
DB 121 VTVSS 125
```

```
RESULT 38
US-10-800-197-15
```

```
; Sequence 15, Application US/10800197
; Publication No. US20040202655A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Morton, Philip A et al.
; TITLE OF INVENTION: ANTIBODIES TO IGF-1 RECEPTOR FOR THE TREATMENT OF CANCERS
; FILE REFERENCE: 01343/1
; CURRENT APPLICATION NUMBER: US/10/800,197
; PRIOR FILING DATE: 2004-03-12
; PRIOR APPLICATION NUMBER: 60/455,094
; PRIOR FILING DATE: 2003-03-14
; NUMBER OF SEQ ID NOS: 157
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
; LENGTH: 251
; TYPE: PRT
; ORGANISM: artificial
```

```
; FEATURE:
; OTHER INFORMATION: phage display generated antibody
US-10-800-197-15
```

```
Query Match 77.7%; Score 485; DB 17; Length 251;
Best Local Similarity 75.6%; Pred. No. 6,2e-36;
Matches 93; Conservative 10; Mismatches 16; Indels 4; Gaps 1;
```

```
QY 1 EVOLVESGDFVQPGSLRVSCAAGFARSHYAMSVWRQAPGKLEWAVYISGGSGTTY 60
DB 1 EVOLVESGGGLVQPGGSLRLSCAASGFTFSYAMHWVRQAPGKLEWVSAISGGSGTTY 60
QY 61 SDSVKRFTISRDNKNTLYLQWRSIRAEEDSAVYFCTRVKL-----GTYYFDSWGQTL 116
DB 61 ADSVKRFTISRDNKNTLYLQWNSIRAEEDTAVYVCARBPVPMWMMYIFDYVGRGTWT 120
QY 117 VSS 119
DB 121 VSS 123
```

```
RESULT 39
US-10-474-832-68
; Sequence 68, Application US/10474832
; Publication No. US20040081651A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; TITLE OF INVENTION: ANTIBODIES TO VLA-1
; FILE REFERENCE: A101 PCT
; CURRENT APPLICATION NUMBER: US/10/474,832
; PRIOR FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: 60/283,794
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/303,689
; PRIOR FILING DATE: 2001-07-06
```

```

; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 68
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: polypeptide
US-10-474-832-68

```

```

Query Match          77.6%; Score 484.5; DB 15; Length 118;
Best Local Similarity 81.5%; Pred. No. 3.2e-36;
Matches 97; Conservative 4; Mismatches 17; Indels 1; Gaps 1;

```

```

QY      1 EVOLVESGDPVOPGSLRVSCAAGFAPSHYAMSWVRQAPGKLEWVAYISSGSGTTY 60
        |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB      1 EVOLVESGGGLVOPGSLRVSCAAGFTFSRYTMSWVRQAPGKLEWVATISSGGH-TTY 59
        |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY      61 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLGTYYPDSWGQGTLLTVSS 119
        |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB      60 LDSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYCTRGFGDGGYFDVWGQGTLLTVSS 118
        |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

```

```

RESULT 40
US-10-474-832-69
; Sequence 69, Application US/10474832
; Publication No. US20040081651A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; TITLE OF INVENTION: ANTIBODIES TO VLA-1
; FILE REFERENCE: A101 PCT
; CURRENT APPLICATION NUMBER: US/10/474,832
; CURRENT FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: 60/283,794
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/303,689
; PRIOR FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 69
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: polypeptide
US-10-474-832-69

```

```

Query Match          77.6%; Score 484.5; DB 15; Length 118;
Best Local Similarity 81.5%; Pred. No. 3.2e-36;
Matches 97; Conservative 4; Mismatches 17; Indels 1; Gaps 1;

```

```

QY      1 EVOLVESGDPVOPGSLRVSCAAGFAPSHYAMSWVRQAPGKLEWVAYISSGSGTTY 60
        |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB      1 EVOLVESGGGLVOPGSLRVSCAAGFTFSRYTMSWVRQAPGKLEWVATISSGGH-TTY 59
        |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY      61 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLGTYYPDSWGQGTLLTVSS 119
        |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB      60 LDSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYCTRGFGDGGYFDVWGQGTLLTVSS 118
        |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

```

Search completed: December 17, 2004, 18:38:03
Job time : 230.978 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 17, 2004, 18:11:22 ; Search time 46.7978 Seconds
(without alignments)
244.665 Million cell updates/sec

Title: US-10-089-500-9

Perfect score: 624
Sequence: 1 EVQLVESGGDFVQPGSLRV.....KLGTYYDSMGQGTLLTVSS 119

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	501	80.3	139	2 S31107	Ig heavy chain - h
2	501	80.3	138	2 S31666	Ig heavy chain V r
3	486	77.9	119	2 D36005	Ig heavy chain V r
4	484	77.6	119	2 S31108	Ig heavy chain V r
5	483	77.4	140	2 S31686	Ig heavy chain - h
6	482.5	77.3	140	2 S70442	Ig heavy chain pre
7	480	76.9	123	2 S31114	Ig heavy chain - h
8	479	76.8	125	2 S30531	Ig heavy chain V r
9	477.5	76.5	124	2 S20782	Ig heavy chain V r
10	477.5	76.5	128	2 S26790	Ig heavy chain V r
11	474	76.0	119	2 C36005	Ig heavy chain V r
12	474	76.0	135	2 S31598	Ig heavy chain V r
13	474	76.0	140	2 S31588	Ig heavy chain V r
14	473.5	75.9	120	2 S48798	Ig heavy chain V r
15	471	75.5	160	2 S05271	Ig heavy chain pre
16	470.5	75.4	118	2 S31105	Ig heavy chain (su
17	470.5	75.4	135	2 I37778	Ig variable region
18	470	75.3	119	2 F36005	Ig heavy chain V r
19	469.5	75.2	120	2 S44111	Ig heavy chain V-D
20	469	75.2	127	2 S38489	Ig heavy chain - h
21	466.5	74.8	122	2 PC2398	anti-tetanus toxin
22	466	74.7	121	2 G36005	Ig heavy chain V r
23	466	74.7	132	2 S31603	Ig heavy chain V r
24	466	74.7	133	2 S23624	Ig heavy chain V r
25	465	74.5	134	2 S31679	Ig heavy chain V r
26	464.5	74.4	139	2 S31674	Ig heavy chain V r
27	464	74.4	121	2 S15573	Ig heavy chain - h
28	464	74.4	121	2 S19666	Ig heavy chain V r
29	464	74.4	134	2 S31699	Ig heavy chain V r

30	463.5	74.3	114	2 S31120	Ig heavy chain - h
31	463.5	74.3	147	2 I37780	Ig variable region
32	462.5	74.1	128	2 S26786	Ig heavy chain V r
33	462	74.0	139	2 I37781	Ig variable region
34	461.5	74.0	136	2 S31587	Ig heavy chain V r
35	461.5	74.0	137	2 S78054	Ig heavy chain pre
36	459.5	73.6	114	2 S46390	Ig heavy chain V r
37	459	73.6	140	2 A30532	Ig heavy chain pre
38	458.5	73.5	141	2 S31669	Ig heavy chain V r
39	457.5	73.3	122	2 E36005	Ig heavy chain V r
40	457	73.2	123	2 S26794	Ig heavy chain V r
41	455	72.9	119	2 B34353	anti-peptide Fab'
42	454.5	72.8	120	2 S31112	Ig heavy chain - h
43	453.5	72.7	118	2 S31116	Ig heavy chain - h
44	453.5	72.7	122	2 S20772	Ig heavy chain V r
45	453.5	72.7	133	2 S31510	Ig heavy chain - h

ALIGNMENTS

RESULT 1

S31107
Ig heavy chain - human
C/Species: Homo sapiens (man)
C/Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C/Accession: S31107
R/Rapporteur, F.M.; Timmer, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman, Eur. J. Immunol. 22, 247-251, 1992
A/Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comple
A/Reference number: S31104; M0ID:92111633; PMID:1730252
A/Accession: S31107
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: mRNA
A/Residues: 1-119 <RA>
A/Cross-references: EMBL:X62955
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 80.3%; Score 501; DB 2; Length 119;
Best Local Similarity 79.8%; Pred. No. 3.7e-38;
Matches 95; Conservative 8; Mismatches 16; Indels 0; Gaps 0;

QY 1 EVQLVESGGDFVQPGSLRVSCAAGFAPSHVMSVWROAPGKLEWVAIYSGSGTYY 60
DB 1 EVQLVESGGGLVQPGSLRLSCAASGFTFSVAMSVWROAPGKLEWVAIYSGSGSTYY 60
QY 61 SDSVKGRFTISRDNSKNTLYLQWRSIPRADSVAVYFCTRVYLGTYFPDSMGQGTLLTVSS 119
DB 61 ADSVKRFTISRDNSKNTLYLQWNSLRADTNVYCAKPGASVYFDYWGQGTLLTVSS 119

RESULT 2

S31666
Ig heavy chain V region - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C/Accession: S31666
R/Crispster, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelie, C.
A/Description: Mechanisms that generate human immunoglobulin diversity operate from the
A/Reference number: S31585
A/Accession: S31666
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-138 <CU>
A/Cross-references: EMBL:Z14202; NID:930963; PIDN:CAA78571.1; PID:930964
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/34-117/Domain: immunoglobulin homology <IMM>

Query Match 80.3%; Score 501; DB 2; Length 138;
Best Local Similarity 78.2%; Pred. No. 4.3e-38;
Matches 93; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

QY 1 EVOLVESGDFVPGGSLRVSCAASGFAFSHYAMSWVROAPGKLEWVAIYSSGSGSTYY 60
DB 20 EVOLVESGGGLVQPGGSLRLSCAASGFTFSYAMSWVROAPGKLEWVAIYSSGSGSTYY 79
QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLTGYYPDSMCGGTLTVSS 119
DB 80 ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAIVYCAKADRTGYFPLMGRGLTVTVSS 138

RESULT 3
Ig heavy chain V region (M43) - human
C/Species: Homo sapiens (man)
C/Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Dec-1998
C/Accession: D36005
R/Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A/Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene
A/Reference number: A36005; MUID:90349571; PMID:2117273
A/Accession: D36005
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-119 <SCH>
C/Genetics:
A/References: GB:M34024
C/Genetics:
A/Gene: GDB:IGH@; IGHDI1
A/Cross-references: GDB:118731; OMIM:146910
A/Map position: 14q32.33-14q32.33
C/Superfamily: immunoglobulin V region; immunoglobulin heavy chain variable gene
C/Keywords: heterotrimer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 77.9%; Score 486; DB 2; Length 119;
Best Local Similarity 77.3%; Pred. No. 8.2e-37;
Matches 92; Conservative 9; Mismatches 18; Indels 0; Gaps 0;

QY 1 EVOLVESGDFVPGGSLRVSCAASGFAFSHYAMSWVROAPGKLEWVAIYSSGSGSTYY 60
DB 1 EVOLVESGGGLVQPGGSLRLSCAASGFTFSYAMSWVROAPGKLEWVAIYSSGSGSTYY 60
QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLTGYYPDSMCGGTLTVSS 119
DB 61 ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAIVYCAKADRTGYFPLMGRGLTVTVSS 119

RESULT 4
Ig heavy chain - human
C/Species: Homo sapiens (man)
C/Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C/Accession: F31108
R/Raapportet, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman
Eur. J. Immunol. 22, 247-251, 1992
A/Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complement
A/Reference number: S31104; MUID:2111633; PMID:1730252
A/Accession: S31108
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: mRNA
A/Residues: 1-119 <RAA>
A/Cross-references: EMBL:X62956
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 77.6%; Score 484; DB 2; Length 119;
Best Local Similarity 78.2%; Pred. No. 1.2e-36;
Matches 93; Conservative 9; Mismatches 17; Indels 0; Gaps 0;

QY 1 EVOLVESGDFVPGGSLRVSCAASGFAFSHYAMSWVROAPGKLEWVAIYSSGSGSTYY 60
DB 1 EVOLVESGGGLVQPGGSLRLSCAASGFTFSYAMSWVROAPGKLEWVAIYSSGSGSTYY 60
QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLTGYYPDSMCGGTLTVSS 119
DB 61 ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAIVYCAKADRTGYFPLMGRGLTVTVSS 119

RESULT 5
Ig heavy chain V region - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C/Accession: S31686
R/Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A/Description: Mechanisms that generate human immunoglobulin diversity operate from the
A/Reference number: S31585
A/Accession: S31686
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-140 <CUI>
A/Cross-references: EMBL:Z14205; NID:930969; PIDN:CAA78574.1; PID:930970
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 77.4%; Score 483; DB 2; Length 140;
Best Local Similarity 77.7%; Pred. No. 1.8e-36;
Matches 94; Conservative 8; Mismatches 17; Indels 2; Gaps 1;

QY 1 EVOLVESGDFVPGGSLRVSCAASGFAFSHYAMSWVROAPGKLEWVAIYSSGSGSTYY 60
DB 20 EVOLVESGGGLVQPGGSLRLSCAASGFTFSYAMSWVROAPGKLEWVAIYSSGSGSTYY 79
QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLTGYYPDSMCGGTLTVSS 118
DB 80 SDSVKGRFTISRDNKNTLYLQMNSLRAEDTAIVYCAKADRTGYFPLMGRGLTVTVSS 139

QY 119 S 119
DB 140 S 140

RESULT 6
Ig heavy chain precursor V region (mu) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C/Accession: S70442
R/Cuisinier, A.M.; Fumoux, F.; Fougereau, M.; Tonnelle, C.
Mol. Immunol. 29, 1363-1373, 1992
A/Title: IGM kappa/lambdA EBV human B cell clone: an early step of differentiation of fet
A/Reference number: S70442; MUID:93024508; PMID:183695
A/Accession: S70442
A/Status: not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-140 <CUI>
A/Cross-references: UNIPROT:Q8WUK1
C/Superfamily: immunoglobulin V region; immunoglobulin homology
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 77.3%; Score 482.5; DB 2; Length 140;
Best Local Similarity 77.5%; Pred. No. 2e-36;
Matches 93; Conservative 9; Mismatches 17; Indels 1; Gaps 1;

QY 1 EVOLVESGDFVPGGSLRVSCAASGFAFSHYAMSWVROAPGKLEWVAIYSSGSGSTYY 60
DB 20 EVOLVESGGGLVQPGGSLRLSCAASGFTFSYAMSWVROAPGKLEWVAIYRDGSKY 79
QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLTGYYPDSMCGGTLTVSS 119
DB 61 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLTGYYPDSMCGGTLTVSS 119

Db 80 ADSVKGRFTISRDNKNTLYLQWNSLRAPDPAVYCCARHIVGATYFDYWGQGLTVTVSS 139

RESULT 7

S3114

Ig heavy chain - human

C/Species: Homo sapiens (man)

C/Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999

C/Accession: S3114

R/Martini, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Voessen, J.M.; Schuurmat

Eur. J. Immunol. 22, 247-251, 1992

A/Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comple

A/Reference number: S31104; MUID:9211633; PMID:1730252

A/Accession: S31114

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: mRNA

A/Residues: 1-123 <RA>

A/Cross-references: EMBL:X62963

A/Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 76.9%; Score 480; DB 2; Length 123;

Best Local Similarity 75.6%; Pred. No. 2.9e-36;

Matches 93; Conservative 9; Mismatches 17; Indels 4; Gaps 1;

Db 1 EVOLVESGDFVPGGSLRVSCAASGFAFSGHYAMSWVRQAPGKLEWVAYISSGSGTYY 60

1 EVOLVESGGLVPGGSLRLSCAASGFTFSYAMWVRQAPGKLEWVAYISSGSGTYY 60

QY 61 SDSVKGRFTISRDNKNTLYLQWNSLRAPDPAVYCCARHIVGATYFDYWGQGLTV 116

Db 61 ADSVKGRFTISRDNKNTLYLQWNSLRAPDPAVYCCARHIVGATYFDYWGQGLTV 120

QY 117 VSS 119

Db 121 VSS 123

RESULT 8

S30531

Ig heavy chain V region - human

C/Species: Homo sapiens (man)

C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004

C/Accession: S30531

R/Martini, F.; Newton, J.A.; Wang, J.Y.; Schroeder Jr., H.W.

submitted to the EMBL Data Library, October 1992

A/Reference number: S30520

A/Accession: S30531

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-125 <MAR>

A/Cross-references: UNIPROT:Q9UL91; EMBL:Z18317

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 76.8%; Score 479; DB 2; Length 125;

Best Local Similarity 72.8%; Pred. No. 3.7e-36;

Matches 91; Conservative 14; Mismatches 14; Indels 6; Gaps 1;

Db 1 EVOLVESGDFVPGGSLRVSCAASGFAFSGHYAMSWVRQAPGKLEWVAYISSGSGTYY 60

1 EVOLVESGGLVPGGSLRLSCAASGFTFSYAMWVRQAPGKLEWVAYISSGSGTYY 60

QY 61 SDSVKGRFTISRDNKNTLYLQWNSLRAPDPAVYCCARHIVGATYFDYWGQGLTV 114

Db 61 ADSVKGRFTISRDNKNTLYLQWNSLRAPDPAVYCCARHIVGATYFDYWGQGLTV 120

QY 115 LTVSS 119

Db 121 VTVSS 125

RESULT 9

S20782

Ig heavy chain V region - human

C/Species: Homo sapiens (man)

C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001

C/Accession: S20782

R/Martini, F.; Wang, J.; Schroeder, H.W.

submitted to the EMBL Data Library, April 1992

A/Description: Analysis of the IgH and Igg rearranged VH repertoire of human cord blood

A/Reference number: S20765

A/Accession: S20782

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-124 <MOR>

A/Cross-references: EMBL:Z11946; NID:G33897; PIDN:CAA78003.1; PID:G33898

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 76.5%; Score 477.5; DB 2; Length 124;

Best Local Similarity 72.6%; Pred. No. 5e-36;

Matches 90; Conservative 14; Mismatches 15; Indels 5; Gaps 1;

Db 1 EVOLVESGDFVPGGSLRVSCAASGFAFSGHYAMSWVRQAPGKLEWVAYISSGSGTYY 60

1 EVOLVESGGLVPGGSLRLSCAASGFTFSYAMWVRQAPGKLEWVAYISSGSGTYY 60

QY 61 SDSVKGRFTISRDNKNTLYLQWNSLRAPDPAVYCCARHIVGATYFDYWGQGLTV 115

Db 61 ADSVKGRFTISRDNKNTLYLQWNSLRAPDPAVYCCARHIVGATYFDYWGQGLTV 120

QY 116 TVSS 119

Db 121 VTVSS 124

RESULT 10

S26790

Ig heavy chain V region - human

C/Species: Homo sapiens (man)

C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000

C/Accession: S26790

R/Martini, F.; Newton, J.A.; Wang, J.Y.; Schroeder Jr., H.W.

Eur. J. Immunol. 22, 241-245, 1992

A/Title: The human cord blood antibody repertoire. Frequent usage of the V(H)7 gene faml)

A/Reference number: S26786; MUID:9211632; PMID:1730251

A/Accession: S26790

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-128 <MOR>

A/Cross-references: EMBL:X61013; NID:G32798; PIDN:CAA43347.1; PID:G1335128

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 76.5%; Score 477.5; DB 2; Length 128;

Best Local Similarity 71.1%; Pred. No. 5.1e-36;

Matches 91; Conservative 13; Mismatches 15; Indels 9; Gaps 1;

Db 1 EVOLVESGDFVPGGSLRVSCAASGFAFSGHYAMSWVRQAPGKLEWVAYISSGSGTYY 60

1 EVOLVESGGLVPGGSLRLSCAASGFTFSYAMWVRQAPGKLEWVAYISSGSGTYY 60

QY 61 SDSVKGRFTISRDNKNTLYLQWNSLRAPDPAVYCCARHIVGATYFDYWGQGLTV 111

Db 61 ADSVKGRFTISRDNKNTLYLQWNSLRAPDPAVYCCARHIVGATYFDYWGQGLTV 120

QY 112 GTLTVSS 119

Db 121 GTLTVSS 128

```

RESULT 11
C36005
Ig heavy chain V region (30pt) - human
C:/Species: Homo sapiens (man)
C:/Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Aug-1996
C:/Accession: C36005
R/Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A:/Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene
A:/Reference number: A36005; MUID: 90349571; PMID: 2117273
A:/Accession: C36005
A:/Status: preliminary
A:/Molecule type: mRNA
A:/Residues: 1-119 <SCH>
A:/Cross-references: GB:M18513
C:/Superfamily: immunoglobulin V region; immunoglobulin homology
C:/Keywords: heterodimer; immunoglobulin
C:/15-98/Domain: immunoglobulin homology <IWM>

```

Query Match	76.0%	Score 474	DB 2	Length 119
Best Local	77.3%	Pred. No. 9.8e-36		
Matches 92	Conservative	8	Mismatches 19	Indels 0
			Gaps	0

Dy

1 EVQLVESGGGFLVQPGSSLRVSCAASGFAFSHYMSWVRQAAPKGIIEWVAIYISSGSGSTYY 60
|||:|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db

1 EVQLVESGGGLVQPGSSLRITCSAASGFTFSSSYNMSWVRQAAPKGLEWVSALISGSGSTYY 60

```

QY      61 SDSVGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVLGTYYPDSMGQSTLTIVSS 119
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61 ADSVGRFTISRDNKNTLYLQMNSLRAEDTAVYCAKAGWGSGFDYWGQTLVTVSS 119

```

RESULT 12

Ig heavy chain V region - human
C/Species: Homo sapiens (man)
C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C/Accession: G31598
R/Custringer: A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A/Description: Mechanisms that generate human immunoglobulin diversity operate from the
A/Reference number: G31585
A/Accession: G31598
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-135 <CUI>
A/Cross-references: EMBL:214170; NID:G31001; PIDN:CAA78539.1; PID:G31002
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
E/31-114/Domain: immunoglobulin homology <IMM>

Query Match	75.0%	Score 474	DB 25	Length 135
Best Local Similarity	75.6%	Pred. No. 1.1e-35		
Matches 90	Conservative 9	Mismatches 20	Indels 0	Gaps 0

```
QY      1 EVQLVESGGD1YQPGGSLRVSCASGFAF2SHYANSMWRQAPGKGL3EWAYISSGSG4STYY 60
      : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
DB     17 QVQLVESGGGVQPGGSLRLSCAASGFTTSS1YGMHWVRQAPGKGL2EWAF3TRDYDSNKYY 76
```

```

Qy      61 SDSVKGKFTTISRDNSSKNTLYLQNRSLRAEDSAVYVCTRYKLGTYYPFDSWGQGLTLTVSS 115
        :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      77 ADSVKGKFTTISRDNSSKNTLYLQNRSLRAEDTAAYVYCAKISWEVSRRPDYMGQGLTVYSS 135

```

RESULT 13

Ig heavy chain V region - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 22-Nov-1993 #sequence 10-Nov-1995 #text_change 23-Jul-1995
 C/Accession: S31588
 R/Cuisinier, A.M.; Gauthier, L.; Boudli, L.; Fougereau, M.; Tonnelie, C.
 submitted to the EMBL Data Library, June 1992

A:Description:Mechanisms that generate human immunoglobulin diversity operate from the
A:Reference number: S31585
A:Accession: S31588
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-140 <CUT>
A:Cross-references: EMBL:Z14200; NID:G30957; PID:CAA78569.1; PID:G30958
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-11//Domain: immunoglobulin homology <Imm>

Query Match	76.0%;	Score 474;	DB 2;	length 140;
Best Local Similarity	76.9%;	Pred. No. 1.2e-35;		
Matches 93;	Conservative	9;	Mismatches 17;	Indels 2;
				Gaps 2;

Oy 1 EVQLVESGGDFVQPGGSLRVSACAAGFAFSHYAMSWVRQAAPGKLEWVAIISSGGSGTYY 60
|||::|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
Db 20 EVGLLESGGDLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVASAISGGSGTYY 79

```

61 SDSVKGKPTISRDNKNTLYLQMSLRADSAVYFCTR-VKLGT-YFDSWGQTLTLVS 118
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
80 ADSVKGKPTISRDNKNTLYLQMSLRADSAVYCAKDHYSNYTYFDYWGQTLTLVS 139

```

Qy	119 S	119
Db	140 S	140

RESULT 14

Ig heavy chain V region (anti-Sm, VH3/DXP4/CH4b) - human
 C/Species: Homo sapiens (man)
 C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
 C/Accession: S48798
 R/Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
 submitted to the EMBL Data Library, October 1994
 A/Description: Molecular characterization of natural human anti-Sm autoantibodies
 A/Reference number: S48797
 A/Accession: S48798
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-120 <EMBL>
 A/Cross-references: EMBL:Z46382; NID:9562324; PID:CAA6521.1; PID:g1340167
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 C/15-98/Domain: immunoglobulin homology <IMM>

Query Match	75.9%;	Score 473.5;	DB 2;	Length 120;
Best Local Similarity	76.7%;	Pred. No. 1.1e-35;		
Matches 92;	Conservative 10;	Mismatches 17;	Indels 1;	Gaps 1.

Oy 1 EVOLVESGCD FVQPGSLRVSCAASGEAFSHYAMSWWQAPGKGIEMVAIISGGSGTTY 600
||| : ||| ||||| : ||| ||||| : ||| ||||| : |||
Db 1 EVOLIESGGGLVQPGSLRLSCAASGTFTSSAYMSWWQAPGKGIEWVASISGSGSTYY 600

```
QY      61 SDSVKGRTISRDNKNTLYLQMSLRABDSAVVPCTRVK-LGTYYVPDSWGCGTLTVSS 119
        :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      61 ADSVKGRFTISRDNKNTLYLQMSLRABETAIVYCAKDREFWSGYDYMGCGTLTVSS 120
```

RESULT 15

Ig heavy chain precursor - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 30-Jun-1992 #sequence__revision 30-Jun-1992 #text_change 09-Jul-2004
 C/Accession: S05271; S04602
 R/Kishimoto, T.
 submitted to the EMBL Data Library, March 1989
 A/Reference number: S05270
 A/Accession: S05271
 A/Molecule type: mRNA
 A/Residues: 1-160 <K151>
 A/Cross-references: UniProt:Q96BB9, EMBL:X14584

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-120 <HAW>
A:Cross-references: EMBL:Z31387, NID:q472965, PIDD:CAA8362.1, PID:q940522
C:Superfamily: Immunoglobulin V region, immunoglobulin homology
C:Keywords: heterotetramer, immunoglobulin
/15-98/Domain: immunoglobulin homology <IMW>

Query Match	75.2%;	Score 469.5;	DB 2;	Length 120;
Best Local Similarity	75.0%;	Pred. No. 2.5e-35;		
Matches 90;	Conservative 10;	Mismatches 19;	Indels 1;	Gaps 1;

Oy	1	EVOLVESGADFPQPGSILRVSCAAGPAFASHYAMSVRCA	PGKLEWVYISGGSGITY	60	
		1	EVOLVESGCVVQPGSILRSCAAGFTDDYTHMHWRA	PGKLEWVLSIMDSGITY	60
Db	1	EVOLVESGCVVQPGSILRSCAAGFTDDYTHMHWRA	PGKLEWVLSIMDSGITY	60	
Oy	61	SDSVKGRFTTISDNKNTLYLMRSLRAEDSAVYFCTR	-VKLTGYFDSMGQGTLLTVSS	119	
Db	61	ADSVKGRFTTISDNKNTLYLMRSLRREDLYLYLCAKDSGSSYFDWQGTLLTVSS		120	

RESULT 20

Ig heavy chain human (fragment)
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S38489
R:Mark: J.D.: Onehand, W.H.; Bye, J.M.; Finnern, R.; Gorlick, B.D.; Yeak, D.; Thorpe, S.
submitted to the EMBL Data Library, June 1993
A:Description: Human antibody fragments specific for human blood group antigens from a p
A:Reference number: S38488
A:Accession: S38489
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-127 <MAR>
A:Cross-references: EMBL:Z23028; NID:G414025; PIDD:CAAB0563.1; PIDD:G414026
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
C:15-98/Domain: immunoglobulin homology <IMM>

Query Match	75.2%;	Score 469;	DB 2;	Length 127;
Best Local Similarity	71.7%;	Pred. No. 2.9e-35;		
Matches 91;	Conservative	9;	Mismatches 17;	Indels 10;
				Gaps 1;

[illegible]

QY	111	QGTLLTV	117
		:	
Db	121	QGTLLTV	127

RESULT 21
PC2398

anti-tetanus oxin 9F12 Fab heavy-chain - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 23-May-1997
C/Accession: PC2398
R/Esposito, G.; Scarcellì, E.; Traboni, C.
Gene 148, 167-168, 1994
A/Title: Phage display of a human antibody against Clostridium tetani toxin
A/Reference number: PC2397, WUID:95011651, PMID:7926831
A/Accession: PC2398
A/Molecule type: mRNA
A/Residues: 1-122 <ESP>
A/Cross-references: EMBL:X75388
C/Superfamily: immunoglobulin V region, immunoglobulin homology
F_15-98/Domain: immunoglobulin homology <IMM>

```
F;31-35/Region: complementarity determining region 1  
F;50-66/Region: complementarity determining region 2  
  
Query Match          74.8%   Score 466.5; DB 2; Length 123;  
Best Local Similarity 73.8%   Pred. No. 4.7e-35;  
Matches    90; Conservative 12; Mismatches 17; Indels 3; Gaps 1
```

```

Qy 1 EYLVYSGSDPFVOPGSGSLRVSCAAGGPFPSHYAMSWRQAQKGLVWVAIYSSGSGSTTY 60
      |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 1 EYLVYVSGGGLVQPGSVRLSCAAGSFSSYAMSWRQAQGLVWVAIISANGTITY 60
      |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Qy 61 SDSVKGRFPIISRDNSKNTIYLQMRSLRAEDSAVYFTRVY---LGYTFFPSWGGLTLTY 117
      ::|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 61 ADSVTGRLLTISRDNSKNTIYLHLNLRKREDVAVVYCAAGGKQMLAHYVFPSSWGGLVATV 120
      ::|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::

```

Qy	118	SS	119
Db	121	SS	122

RESULT 22

Ig heavy chain V region (M74) - human
C:Species: Homo sapiens (man)
C:Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 09-Jul-2004
C:Accession: G36005
R:Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A>Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene segments in the human IgH locus
A:Reference number: A36005; MUID:90349571; PMID:2117273
A:Accession: G36005
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-121 <SCH>
A:Cross-references: UNIPROT:Q8WUK1; GB:W34031
C:Genetics:
A:Gene: GDB: IGH@; IGHDX1
A:Cross-references: GDB:118731; OMIM:146910
A:Map position: 14q32.33-14q32.33
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match	74.7%	Score 466	DB 2	Length 121
Best Local Similarity	76.9%	Pred. No. 5.2e-35		
Matches 93	Conservative 7	Mismatches 19	Indels 2	Gaps 1

QY 1 ENVLVESGDDPFOPGSLRVSCAAGCFPSHYAAMSWRQAPGKLEAVAYISGGSGCTTY 60
Db 1 QVQLVSSGGGVQPGSLRLKSLCAASGFTFSSYAAHWRAQAGKLEAVAYISDGSNKTY 60
QY 61 SDSVKRFTTISRDNSKNTLYIQMRLSLRAEDSAVYFCTRVK--LQTYYPDSMGQGTLLTVS 118
Db 61 ADSVKRFTTISRDNSKNTLYIQMRLSLRAEDSAVYFCAADRDMQCMALFDVWGQGLTVAS 120

QY	119 S 119
Db	121 S 121

RESULT 23

S31603
Ig heavy chain V region - human
C|Species: Homo sapiens (man)
C|Date: 03-Mar-1994 #sequence revision 10-Nov-1995 #text_change 23-Jul-1999
C|Accession: S31603
R|Cuisinier, A.M.; Gauthier, L.; Boudli, L.; Fougereau, M.; Tonnelie, C.
submitted to the EMBL Data Library, June 1992
A|Description: Mechanisms that generate human immunoglobulin diversity operate from the
A|Reference number: S31585
A|Accession: S31603
A|Status: Preliminary
M|Molecule type: mRNA


```
QY 61 SDSVKGRFTISRDNASKNTLYLQWRSLRAEDSAVYFCTRV--KLGTYFPDSMGQGTLLTVSS 118
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 ADSVKGRFTISRDNASKNTLYLQWRSLRAEDTAVYYCAAPRHHAGSPDYWGQGTLLTVSS 120
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 119 S 119
      |
Db 121 S 121
      |

RESULT 28
Ig heavy chain V region (VH3DHH4) - human
C/Species: Homo sapiens (man)
C/Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000
C/Accession: S19666
R/Mark8, J.D.; Hoogenboom, H.R.; Bonner, T.P.; McCafferty, J.; Griffiths, A.D.; Winter,
J. Mol. Biol. 222, 581-597, 1991
A/Title: By-passing immunization. Human antibodies from V-gene libraries displayed on ph
A/Reference number: S19663; PMID:92085276; PMID:1748994
A/Accession: S19666
A/Molecule type: mRNA
A/Residues: 1-121 <MAR>
A/Cross-references: EMBL:X61646; NID:G37688; PIDN:CAA43827.1; PID:G135369
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 74.4%; Score 464; DB 2; Length 121;
Best Local Similarity 76.0%; Pred. No. 7.9e-35;
Matches 92; Conservative 7; Mismatches 20; Indels 2; Gaps 1;

QY 1 EVOLVESGDFVPGGSLRVSCAASGPAFSGHYAMSWVRQAPGKGLEWNAVYISGSGSTYY 60
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 QVQLVSGGGLVHPGSLRLSCAASGFTFSYGMHWVRQAPGKGLEWNAVYISYDGSNKYY 60
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 SDSVKGRFTISRDNASKNTLYLQWRSLRAEDSAVYFCTRVKLGTYFPDSMGQGTLLTVSS 118
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 ADSVKGRFTISRDNASKNTLYLQWRSLRAEDTAVYYCAKTYSGWGQGTLLTVSS 120
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 119 S 119
      |
Db 121 S 121
      |

RESULT 29
Ig heavy chain V region - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C/Accession: S31699
R/Cuisinier, A.M.; Gauthier, L.; Boublil, L.; Fougereau, M.; Tonnelie, C.
submitted to the EMBL Data Library, June 1992
A/Description: Mechanisms that generate human immunoglobulin diversity operate from the
A/Reference number: S31585
A/Accession: S31699
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-134 <CUH>
A/Cross-references: EMBL:Z14201; NID:G30961; PIDN:CAA78570.1; PID:G31062
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/34-117/Domain: immunoglobulin homology <IMM>

Query Match 74.4%; Score 464; DB 2; Length 134;
Best Local Similarity 76.5%; Pred. No. 8.8e-35;
Matches 91; Conservative 7; Mismatches 17; Indels 4; Gaps 1;

QY 1 EVOLVESGDFVPGGSLRVSCAASGPAFSGHYAMSWVRQAPGKGLEWNAVYISGSGSTYY 60
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 20 EVQLVESGGGLVHPGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWNAVYISGSGSTYY 79
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 SDSVKGRFTISRDNASKNTLYLQWRSLRAEDSAVYFCTRVKLGTYFPDSMGQGTLLTVSS 119
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

```
Db 80 SDSVKGRFTISRDNASKNTLYLQWRSLRAEDTAVYYCAARR---DDYWGQGTLLTVSS 134
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 30
Ig heavy chain - human
C/Species: Homo sapiens (man)
C/Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C/Accession: S31120
R/Raaphorst, F.M.; Timmer, E.; Kenter, M.J.H.; van Tol, M.J.D.; Voessen, J.M.; Schuurman,
Eur. J. Immunol. 22, 247-251, 1992
A/Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comple
A/Reference number: S31104; PMID:92111633; PMID:1730252
A/Accession: S31120
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: mRNA
A/Residues: 1-114 <RAA>
A/Cross-references: EMBL:X62972
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 74.3%; Score 463.5; DB 2; Length 114;
Best Local Similarity 74.8%; Pred. No. 8.2e-35;
Matches 89; Conservative 12; Mismatches 13; Indels 5; Gaps 1;

QY 1 EVOLVESGDFVPGGSLRVSCAASGPAFSGHYAMSWVRQAPGKGLEWNAVYISGSGSTYY 60
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 QVQLVSGGGLVHPGSLRLSCAASGFTFSYDMWVRQAPGKGLEWNAVYISGSGSTYY 60
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 SDSVKGRFTISRDNASKNTLYLQWRSLRAEDSAVYFCTRVKLGTYFPDSMGQGTLLTVSS 119
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 ADSVKGRFTISRDNASKNTLYLQWRSLRAEDTAVYYC-----ASGNPDYWGQGTLLTVSS 114
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 31
Ig variable region (VDU) (clone T20-11) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 23-Jul-1999
C/Accession: I37780; S25474
R/Demaison, C.; Chastagner, P.; Theze, J.; Zouali, M.
Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994
A/Title: Somatic diversification in the heavy chain variable region genes expressed by h
A/Reference number: A36876; PMID:94119917; PMID:8290556
A/Accession: I37780
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-147 <RES>
A/Cross-references: EMBL:X67943; NID:G33578; PIDN:CAA48130.1; PID:G33579
C/Superfamily: immunoglobulin V region; immunoglobulin homology
F/28-111/Domain: immunoglobulin homology <IMM>

Query Match 74.3%; Score 463.5; DB 2; Length 147;
Best Local Similarity 75.0%; Pred. No. 1.1e-34;
Matches 93; Conservative 7; Mismatches 19; Indels 5; Gaps 2;

QY 1 EVOLVESGDFVPGGSLRVSCAASGPAFSGHYAMSWVRQAPGKGLEWNAVYISGSGSTYY 60
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 14 EVQLVESGGGLVHPGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWNAVYIKDDSEKYY 73
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 SDSVKGRFTISRDNASKNTLYLQWRSLRAEDSAVYFCTRVKLGTYFPDSMGQGTLLTVSS 115
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 74 ADSVKGRFTISRDNASKNTLYLQWRSLRAEDTAVYYCAKGGEGWGLVYGGMDYWGQGTTV 133
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 116 TVSS 119
      |||||
Db 134 TVSS 137
      |||||

RESULT 32
S26786
```

Ig heavy chain V region - human

C/Species: Homo sapiens (man)

C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000

C/Accession: S26786

R/Morieri, F.; Newton, J.A.; Wang, J.Y.; Schroeder Jr., H.W.

Eur. J. Immunol. 22, 241-245, 1992

A/Title: The human cord blood antibody repertoire. Frequent usage of the V(H)7 gene family

A/Reference number: S26786; MUID:92111632; PMID:11730251

A/Accession: S26786

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-128 <MOR>

A/Cross-references: EMBL:X61014; NID:G32800; PIDN:CAA43348.1; PID:G135129

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 74.1%; Score 462.5; DB 2; Length 128;

Best Local Similarity 69.5%; Pred. No. 1.1e-34;

Matches 91; Conservative 12; Mismatches 13; Indels 15; Gaps 2;

1 EVOLVSGGDFVPGGSLRVSCAASGFAFSGHYMSWVROAPGKLEWAVAYISGSGSTTY 60

1 QVQVSGGGGLVPGGSLRVSCAASGFTSDYMSWVROAPGKLEWVSYISSSSTNY 60

1 SDSVKRFTISRDNKNTLYLQNRSLRAEDSAVYFCTRVKLGTY-----YFDS 108

61 ADSVKRFTISRDNKNTLYLQNRSLRAEDTAVYYCAR---GLYCSSTSCYMSNMWFD 117

109 WGGGTLTVSS 119

118 WGGGTLTVSS 128

RESULT 33

137781

Ig variable region (VDJ) (clone T21-9) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 23-Jul-1999

C/Accession: I37781; S25475

R/Demaision, C.; Chaetagne, P.; Theze, J.; Zouali, M.

Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994

A/Title: Somatic diversification in the heavy chain variable region genes expressed by h

A/Reference number: A36876; MUID:94119917; PMID:8290556

A/Accession: I37781

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-139 <RES>

A/Cross-references: EMBL:X67908; NID:G33580; PIDN:CAA48106.1; PID:G33581

C/Superfamily: immunoglobulin V region; immunoglobulin homology

F/35-118/Domain: immunoglobulin homology <IMM>

Query Match 74.0%; Score 462; DB 2; Length 139;

Best Local Similarity 74.8%; Pred. No. 1.4e-34;

Matches 89; Conservative 9; Mismatches 21; Indels 0; Gaps 0;

1 EVOLVSGGDFVPGGSLRVSCAASGFAFSGHYMSWVROAPGKLEWAVAYISGSGSTTY 60

21 EVOLVSGGGGLVPGGSLRVSCAASGFTSSYMSWVROAPGKLEWVAVINIKODGSEKTY 80

61 SDSVKRFTISRDNKNTLYLQNRSLRAEDSAVYFCTRVKLGTYFDSWGGTLLTVSS 119

81 VDSVKRFTISRDNKNTLYLQNRSLRAEDTAVYYCARKAKAKAFAIMWGGTMTVTVSS 139

RESULT 34

S31587

Ig heavy chain V region - human

C/Species: Homo sapiens (man)

C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

C/Accession: S31587

R/Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelie, C.

submitted to the EMBL Data Library, June 1992

Query Match 74.0%; Score 461.5; DB 2; Length 136;

Best Local Similarity 76.7%; Pred. No. 1.5e-34;

Matches 92; Conservative 7; Mismatches 20; Indels 1; Gaps 1;

1 EVOLVSGGDFVPGGSLRVSCAASGFAFSGHYMSWVROAPGKLEWAVAYISGSGSTTY 60

17 EVOLVSGGGGLVPGGSLRVSCAASGFTSSYMSWVROAPGKLEWVAVINIKODGSEKTY 76

61 SDSVKRFTISRDNKNTLYLQNRSLRAEDSAVYFCTRVKLGTYFDSWGGTLLTVSS 119

77 VDSVKRFTISRDNKNTLYLQNRSLRAEDTAVYYCARGLTGATDAFDIMWGGTMTVTVSS 136

RESULT 35

S78054

Ig heavy chain precursor V-D-J region (clone mAb 60VH) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999

C/Accession: S78054; S23719

R/Harindranath, N.

submitted to the EMBL Data Library, August 1990

A/Reference number: S78054

A/Accession: S78054

A/Molecule type: mRNA

A/Residues: 1-137 <HAR>

A/Cross-references: EMBL:X54435; NID:G37812; PIDN:CAA8304.1; PID:G37813

C/Superfamily: immunoglobulin V region; immunoglobulin homology

F/19/Domain: signal sequence #status predicted <SIG>

F/20-137/Product: Ig heavy chain (fragment) #status predicted <MAT>

F/34-116/Domain: immunoglobulin homology <IMM>

Query Match 74.0%; Score 461.5; DB 2; Length 137;

Best Local Similarity 76.5%; Pred. No. 1.5e-34;

Matches 91; Conservative 9; Mismatches 18; Indels 1; Gaps 1;

1 EVOLVSGGDFVPGGSLRVSCAASGFAFSGHYMSWVROAPGKLEWAVAYISGSGSTTY 60

20 EVOLVSGGGGLVPGGSLRVSCAASGFTSSYMSWVROAPGKLEWVAVINIKODGSEKTY 78

61 SDSVKRFTISRDNKNTLYLQNRSLRAEDSAVYFCTRVKLGTYFDSWGGTLLTVSS 119

79 ADSVKRFTISRDNKNTLYLQNRSLRAEDTAVYYCARICGGTNSPDSWGGTLLTVSS 137

RESULT 36

S46390

Ig heavy chain V region - human

C/Species: Homo sapiens (man)

C/Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000

C/Accession: S46390

R/Figini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.

J. Mol. Biol. 239, 68-78, 1994

A/Description: Mechanisms that generate human immunoglobulin diversity operate from the

A/Reference number: S31585

A/Accession: S31587

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-136 <CUI>

A/Cross-references: EMBL:Z14189; NID:G31005; PIDN:CAA78558.1; PID:G31006

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

F/31-114/Domain: immunoglobulin homology <IMM>

Query Match 74.0%; Score 461.5; DB 2; Length 136;

Best Local Similarity 76.7%; Pred. No. 1.5e-34;

Matches 92; Conservative 7; Mismatches 20; Indels 1; Gaps 1;

1 EVOLVSGGDFVPGGSLRVSCAASGFAFSGHYMSWVROAPGKLEWAVAYISGSGSTTY 60

17 EVOLVSGGGGLVPGGSLRVSCAASGFTSSYMSWVROAPGKLEWVAVINIKODGSEKTY 76

61 SDSVKRFTISRDNKNTLYLQNRSLRAEDSAVYFCTRVKLGTYFDSWGGTLLTVSS 119

77 VDSVKRFTISRDNKNTLYLQNRSLRAEDTAVYYCARGLTGATDAFDIMWGGTMTVTVSS 136

RESULT 35

S78054

Ig heavy chain precursor V-D-J region (clone mAb 60VH) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999

C/Accession: S78054; S23719

R/Harindranath, N.

submitted to the EMBL Data Library, August 1990

A/Reference number: S78054

A/Accession: S78054

A/Molecule type: mRNA

A/Residues: 1-137 <HAR>

A/Cross-references: EMBL:X54435; NID:G37812; PIDN:CAA8304.1; PID:G37813

C/Superfamily: immunoglobulin V region; immunoglobulin homology

F/19/Domain: signal sequence #status predicted <SIG>

F/20-137/Product: Ig heavy chain (fragment) #status predicted <MAT>

F/34-116/Domain: immunoglobulin homology <IMM>

Query Match 74.0%; Score 461.5; DB 2; Length 137;

Best Local Similarity 76.5%; Pred. No. 1.5e-34;

Matches 91; Conservative 9; Mismatches 18; Indels 1; Gaps 1;

1 EVOLVSGGDFVPGGSLRVSCAASGFAFSGHYMSWVROAPGKLEWAVAYISGSGSTTY 60

20 EVOLVSGGGGLVPGGSLRVSCAASGFTSSYMSWVROAPGKLEWVAVINIKODGSEKTY 78

61 SDSVKRFTISRDNKNTLYLQNRSLRAEDSAVYFCTRVKLGTYFDSWGGTLLTVSS 119

79 ADSVKRFTISRDNKNTLYLQNRSLRAEDTAVYYCARICGGTNSPDSWGGTLLTVSS 137

RESULT 36

S46390

Ig heavy chain V region - human

C/Species: Homo sapiens (man)

C/Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000

C/Accession: S46390

R/Figini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.

J. Mol. Biol. 239, 68-78, 1994

A;Title: In vitro assembly of repertoires of antibody chains on the surface of phage by
A;Reference number: S46390; MUID:94254092; PMID:8196048
A;Accession: S46390
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-114 <FIG>
A;Cross-references: EMBL:Z31686; NID:9509782; PIDs:CAA83491.1; PID:91335143
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 73.6%; Score 459.5; DB 2; Length 114;
Best Local Similarity 77.3%; Pred. No. 1.9e-34;
Matches 92; Conservative 6; Mismatches 16; Indels 5; Gaps 1;

QY 1 EVOLVESGDFVOPGSLRVSCAASGFAFSGHYAMSWVRQAPGKGLEWVAIISGSGSTYY 60
D 1 EVOLVESGGGVOPGSLRVSCAASGFTFSSYAMHWVRQAPGKGLEWVAIISDGSNKYY 60
Db 1 EVOLVESGGGVOPGSLRVSCAASGFTFSSYAMHWVRQAPGKGLEWVAIISDGSNKYY 60

QY 61 SDSVKGRFTISRDNKNTLYLQWRSLEAEDSAVYFCTRVKLGTYFPDSWQGTLLTV 119
D 61 ADSVKGRFTISRDNKNTLYLQWMSLEAEDTAVYYCAR----DWGDYWGQGTLLTV 114
Db 61 ADSVKGRFTISRDNKNTLYLQWMSLEAEDTAVYYCAR----DWGDYWGQGTLLTV 114

RESULT 37
A30532
Ig heavy chain precursor V-III region (38) - human
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 18-Oct-1996
C;Accession: A30532
R;Meeker, T.C.; Grimaldi, J.C.; O'Rourke, R.; Loeb, J.; Julinason, G.; Einhorn, S.
J. Immunol. 141, 3994-3998, 1988
A;Title: Lack of detectable somatic hypermutation in the V region of the Ig H chain gene
A;Reference number: A30532; MUID:89035542; PMID:3141510
A;Accession: A30532
A;Molecule type: DNA
A;Residues: 1-140 <ME>
A;Cross-references: GB:M23110
C;Genetics:
A;Intons: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;20-140/Product: Ig heavy chain V-III region 38 #status predicted <MAY>
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 73.6%; Score 459; DB 2; Length 140;
Best Local Similarity 73.2%; Pred. No. 2.6e-34;
Matches 90; Conservative 12; Mismatches 15; Indels 6; Gaps 2;

QY 1 EVOLVESGDFVOPGSLRVSCAASGFAFSGHYAMSWVRQAPGKGLEWVAIISGSGSTYY 60
D 20 EVOLVESGGDLVOPGSLRVSCAASGFTFSSYAMHWVRQAPGKGLEWVAIISGSGSTYY 79
QY 61 SDSVKGRFTISRDNKNTLYLQWRSLEAEDSAVYFCTRVKLGTYFPDSWQGTLLTV 116
D 80 TAAVKGKFTISRDNKNTLYLQWMSLEAEDTAVYYCAQNMGDRLTPLAY--WGQGTLLTV 137
QY 117 VSS 119
D 138 VSS 140

RESULT 38
S31669
Ig heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31669
R;Christner, A.M.; Gauthier, L.; Boublil, L.; Fougereau, M.; Tonnelie, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the
A;Reference number: S31669
A;Accession: S31669

A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-141 <CUI>
A;Cross-references: EMBL:Z14212; NID:930959; PIDs:CAA78561.1; PID:930960
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 73.5%; Score 458.5; DB 2; Length 141;
Best Local Similarity 73.8%; Pred. No. 2.9e-34;
Matches 90; Conservative 13; Mismatches 16; Indels 3; Gaps 1;

QY 1 EVOLVESGDFVOPGSLRVSCAASGFAFSGHYAMSWVRQAPGKGLEWVAIISGSGSTYY 60
D 20 EVOLVESGGGVOPGSLRVSCAASGFTFSSYAMHWVRQAPGKGLEWVAIISSSSTYY 79
QY 61 SDSVKGRFTISRDNKNTLYLQWRSLEAEDSAVYFCTRVKLGTYFPDSWQGTLLTV 117
D 80 ADSVKGRFTISRDNKNTLYLQWMSLEAEDTAVYYCARGRHLTGKGYFDLWGRGTLTV 139
QY 118 SS 119
D 140 SS 141

RESULT 39
E36005
Ig heavy chain V region (M72) - human
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Dec-1998
C;Accession: E36005
R;Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A;Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene
A;Reference number: A36005; MUID:90349571; PMID:2117273
A;Accession: E36005
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-122 <SCH>
A;Cross-references: GB:M34030
C;Genetics:
A;Gene: CDB:IGH@; IGHDI
A;Cross-references: GDB:118731; OMIM:146910
A;Map position: 14q32.33-14q32.33
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 73.3%; Score 457.5; DB 2; Length 122;
Best Local Similarity 74.6%; Pred. No. 3e-34;
Matches 91; Conservative 8; Mismatches 20; Indels 3; Gaps 1;

QY 1 EVOLVESGDFVOPGSLRVSCAASGFAFSGHYAMSWVRQAPGKGLEWVAIISGSGSTYY 60
D 1 QVOLVESGGGVOPGSLRVSCAASGFTFSSYAMHWVRQAPGKGLEWVAIISDGSNKYY 60
QY 61 SDSVKGRFTISRDNKNTLYLQWRSLEAEDSAVYFCTRVKLGTYFPDSWQGTLLTV 117
D 61 ADSVKGRFTISRDNKNTLYLQWMSLEAEDTAVYYCARDRHSSSWYTGMDVWGQGTLLTV 120
QY 118 SS 119
D 121 SS 122

RESULT 40
S26794
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 17-Mar-1999
C;Accession: S26794
R;Mortari, F.; Newton, J.A.; Wang, J.Y.; Schroeder Jr., H.W.
Eur. J. Immunol. 22, 241-245, 1992

A;Title: The human cord blood antibody repertoire. Frequent usage of the V(H)7 gene fami
A;Reference number: S26786; MUID:9211632; PMID:1730251
A;Accession: S26794
A;Status: Preliminary
A;Molecule type: mRNA
A;Residues: 1-123 <MOR>
A;Cross-references: EMBL:X61011
C;Superfamily: Immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 73.2%; Score 457; DB 2; Length 123;
Best Local Similarity 73.2%; Pred. No. 3.4e-34;
Matches 90; Conservative 11; Mismatches 18; Indels 4; Gaps 2;

QY	1	EVOLVESGDEFOVPGGSLRVSCAAGFASHYAMSWYRQAPGKGLEWVAYISSGSGTTY	60
DB	1	EVOLVESGGGLVOPGSLRLSCAASGFTFSSTYSMMWYRQAPGKGLEWVSTISSSSITTY	60
QY	61	SDSVKGRFTISRDNKNTLYIQMRSLEKADSAVYFCTR-VKL--GTYFPDSMGQSTLLT	116
DB	61	ADSVKGRFTISRDNKNTLYIQMNSLRDEDTAVYYCARSIKYDENYYGMDVWGQGTITV	120
QY	117	VSS	119
DB	121	VSS	123

Search completed: December 17, 2004, 18:30:18
Job time : 48.7978 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - proteoin search, using sw model

Run on: December 17, 2004, 18:29:23 ; Search time 355.663 Seconds
(Without alignments)
192.513 Million cell updates/sec

Title: US-10-089-500-9
Perfect score: 624
Sequence: 1 EVQLVESGDFVPGGSLRV.....KLGTYYFDSWGGTLLTVSS 119

Scoring table: BLOSUM62
Gapop 10.0 , Gapept 0.5

Searched: 1825181 seqs, 575374646 residues
Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02:.*
1: uniprot_sprot:.*
2: uniprot_trembl:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	469	75.2	121	2 Q9UL71	Q9UL71 homo sapien
2	466	74.7	128	2 BAD00406	Bad00406 camelus d
3	460	73.7	128	2 BAD00444	Bad00444 camelus d
4	459.5	73.6	471	2 AAH24289	Aah24289 homo sapi
5	459	73.6	117	2 AAL35877	Aal35877 lama glam
6	457	73.2	124	2 BAD00534	Bad00534 camelus d
7	456	73.1	464	2 Q6MZ06	Q6mz06 homo sapien
8	456	73.1	464	2 CAE45931	Caes45931 homo sapi
9	456	73.1	470	2 Q6PXA4	Q6pja4 homo sapien
10	455	73.1	470	2 AAH18747	Aah18747 homo sapi
11	455.5	73.0	125	2 BAD00491	Bad00491 camelus d
12	455.5	73.0	613	2 Q8WUK1	Q8wuk1 homo sapien
13	455	72.9	113	2 Q9UL90	Q9ul90 homo sapien
14	455	72.9	597	2 Q96BB9	Q96bb9 homo sapien
15	454	72.8	478	2 Q6P181	Q6p181 homo sapien
16	454	72.8	478	2 AAH41037	Aah41037 homo sapi
17	453	72.6	119	2 AAL35865	Aal35865 lama glam
18	451.5	72.4	118	2 Q9UL51	Q9ul51 homo sapien
19	451.5	72.4	124	2 BAD00233	Bad00233 camelus d
20	451.5	72.4	606	2 Q6GMW2	Q6gmw2 homo sapien
21	449.5	72.0	125	2 BAD00448	Bad00448 camelus d
22	449	72.0	126	2 BAD00510	Bad00510 camelus d
23	448.5	71.9	118	2 Q9UL72	Q9ul72 homo sapien
24	448.5	71.9	121	2 BAD00459	Bad00459 camelus d
25	448.5	71.9	475	2 Q6MZ06	Q6mz06 homo sapien
26	448.5	71.9	475	2 CAE45972	Caes45972 homo sapi
27	447	71.6	493	2 Q6GMX2	Q6gmx2 homo sapien
28	446.5	71.5	126	2 BAD00225	Bad00225 camelus d
29	446	71.5	119	2 Q920E7	Q920e7 mus musculu
30	446	71.5	126	2 BAD00420	Bad00420 camelus d
31	445.5	71.4	121	2 BAD00525	Bad00525 camelus d

32	444	71.2	122	2 BAD00446	Bad00446 camelus d
33	444	71.2	122	2 BAD00549	Bad00549 camelus d
34	443.5	71.1	118	2 AAL35882	Aal35882 lama glam
35	443.5	71.1	129	2 BAD00424	Bad00424 camelus d
36	443.5	71.1	473	2 Q6MZV7	Q6mzv7 homo sapien
37	443.5	71.1	473	2 CAE45920	Caes45920 homo sapi
38	443	71.0	116	2 Q9UL93	Q9ul93 homo sapien
39	443	71.0	117	2 AAL35875	Aal35875 lama glam
40	442.5	70.9	125	2 BAD00490	Bad00490 camelus d
41	442.5	70.9	131	2 BAD00494	Bad00494 camelus d
42	442.5	70.9	465	2 Q6PEC4	Q6pec4 homo sapien
43	442.5	70.8	465	2 AAH62335	Aah62335 homo sapi
44	441.5	70.8	127	2 BAD00445	Bad00445 camelus d
45	441	70.7	124	2 BAD00513	Bad00513 camelus d

ALIGNMENTS

RESULT 1	ID	Q9UL71	PRELIMINARY;	PRT;	121 AA.
AC	Q9UL71				
DT	01-MAY-2000 (TREMBlrel. 13, Created)				
DT	01-MAY-2000 (TREMBlrel. 13, Last sequence update)				
DT	01-OCT-2003 (TREMBlrel. 25, Last annotation update)				
DE	Myosin-reactive immunoglobulin heavy chain variable region (Fragment).				
DE	Homo sapiens (human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=9827139; Pubmed=9614934;				
RA	Ku X., Liu B., Van der Merwe P.L., Kalis N.N., Berny S.M.,				
RA	Young D.C.;				
RT	"Myosin-reactive autoantibodies in rheumatic carditis and normal				
RT	fetus."				
RL	Clin. Immunol. Immunopathol. 87:184-192(1998).				
DR	EMBL; AF035043; AAD56279.1; -.				
DR	HSSP; P01852; INF.				
DR	Interpro; IPR007110; Ig-like.				
DR	Interpro; IPR003596; Ig_v.				
DR	Pfam; PF00047; Ig_1.				
DR	SMART; SM00406; IgV_1.				
DR	PROSITE; PSS0835; IG_LIKE_1.				
FT	NON_TER	1			
FT	NON_TER	121			
SQ	SEQUENCE	121 AA; 13154 MW; 2F045CCFASD50736 CRC64;			
Query Match		75.2%; Score 469; DB 2; Length 121;			
Best Local Similarity		Pred. No. 2.4e-41;			
Matches	90; Conservative	11; Mismatches 18; Indels 2; Gaps 1;			
Qy	1	EVQLVDSGDFVPGGSLRVCAASGFAFSHYAMSWVRQAQPGKLEWVAISSGSGSTYY 60			
Db	1	EVQLVDSGDFVPGGSLRVCAASGFAFSHYAMSWVRQAQPGKLEWVAISSGSGSTYY 60			
Qy	61	SDSVKGRFTISRNSTKYLQMRSLRAEDSAVYFCTRVKLTYY--PDSWGCTLLTVS 118			
Db	61	ADSVKGRFTISRNSTKYLQMRSLRAEDSAVYFCTRVKLTYY--PDSWGCTLLTVS 120			
Qy	119	S 119			
Db	121	S 121			
RESULT 2					
ID	BAD00406	PRELIMINARY;	PRT;	128 AA.	
AC	BAD00406;				
DT	02-MAR-2004 (TREMBlrel. 27, Created)				

DT 02-MAR-2004 (TReMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TReMBLrel. 27, Last annotation update)
DE Immunoglobulin heavy chain VHDJ region (Fragment).
GN IGVH.
OS Camelus dromedarius (Dromedary) (Arabian camel).
OC Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
OX NCBI_TaxID=9838;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Honda T.; Akahori Y.; Kurosawa Y.;
RT "Libraries of heavy-chain antibodies reflecting camel gamma2 and
RT gamma3 in vivo repertoires."
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB092044; BAD00406.1; -.
FT NON_TER 1 1
FT NON_TER 128 128
SQ SEQUENCE 128 AA; 13856 MW; 7C23CF09C28B889A CRC64;

Query Match 74.7%; Score 466; DB 2; Length 128;
Best Local Similarity 69.6%; Pred. No. 5.4e-41;
Matches 87; Conservative 16; Mismatches 16; Indels 6; Gaps 1;

QY 1 EVOLVESGGGVDPGGSLRVSCAASGPAFESHYMSWVRQAPGKLEWVAIYSSGGSGTTY 60
DB 1 EVOLVESGGGVDPGGSLRVSCAASGFTFSSYAMNWVROAPGKLEWVAIYSSGGSGTTY 60
QY 61 SDSVKGRTISRDNKNTLYLQMSLRAPDSAVYFCTRVLT-----LGTTFPDSMGQTL 114
DB 61 ADSVKGRTISRDNKNTLYLQMSLRKTEPDTAMTYCAKDRYGGKRWLSGDYSMDYWGKTL 120

QY 115 LRVSS 119
DB 121 VTSS 125

RESULT 3
BAD00444 PRELIMINARY; PRT; 128 AA.
ID BAD00444;
AC BAD00444;
DT 02-MAR-2004 (TReMBLrel. 27, Created)
DT 02-MAR-2004 (TReMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TReMBLrel. 27, Last annotation update)
DE Immunoglobulin heavy chain VHDJ region (Fragment).
GN IGVH.
OS Camelus dromedarius (Dromedary) (Arabian camel).
OC Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
OX NCBI_TaxID=9838;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Honda T.; Akahori Y.; Kurosawa Y.;
RT "Libraries of heavy-chain antibodies reflecting camel gamma2 and
RT gamma3 in vivo repertoires."
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB092082; BAD00444.1; -.
FT NON_TER 1 1
FT NON_TER 128 128
SQ SEQUENCE 128 AA; 13775 MW; 85E9EDD39D9159F3 CRC64;

Query Match 73.7%; Score 460; DB 2; Length 128;
Best Local Similarity 71.0%; Pred. No. 2.3e-40;
Matches 88; Conservative 13; Mismatches 17; Indels 6; Gaps 1;

QY 2 VOLVESGGGVDPGGSLRVSCAASGPAFESHYMSWVRQAPGKLEWVAIYSSGGSGTTY 61
DB 2 VOLVESGGGVDPGGSLRVSCAASGFTFSSYAMNWVROAPGKLEWVAIYSSGGSGTTY 61
QY 62 DSVMGRTISRDNKNTLYLQMSLRAPDSAVYFCTRVK-----LGTTFPDSMGQTL 115
DB 62 DSVMGRTISRDNKNTLYLQMSLRKPEDTAVYCAATREYGGKRWLVGYYSMDYWGKTL 121

QY 116 TVSS 119
DB 122 TISS 125

RESULT 4
AAH24289 PRELIMINARY; PRT; 471 AA.
ID AAH24289;
AC AAH24289;
DT 02-MAR-2004 (TReMBLrel. 27, Created)
DT 02-MAR-2004 (TReMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TReMBLrel. 27, Last annotation update)
DE Homo sapiens (human).
DE Homo sapiens protein.
OC Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932;
RA Straussberg R.L.; Feingold E.A.; Grouse L.H.; Derge J.G.;
RA Klausner R.D.; Collins F.S.; Wagner L.; Shennan C.M.; Schuler G.D.;
RA Altschuler S.F.; Zeeberg B.; Buettow K.H.; Schaefer C.F.; Bhat N.K.;
RA Hopkins R.F.; Jordan H.; Moore T.; Max S.I.; Wang J.; Hsieh F.;
RA Diatchenko L.; Marusina K.; Farmer A.A.; Rubin G.M.; Hong L.;
RA Stapleton M.; Soares M.B.; Bonaldo M.F.; Casavant T.L.; Scheetz T.E.;
RA Brownstein M.J.; Udell T.B.; Tohilyuki S.; Carninci P.; Prange C.;
RA Raha S.S.; Loquellano N.A.; Peters G.J.; Abramson R.D.; Mullany S.J.;
RA Bosak S.A.; McEwan P.J.; McKernan K.J.; Malek J.A.; Gunaratne P.H.;
RA Richards S.; Worley K.C.; Hale S.; Garcia A.M.; Gay L.V.; Huiyk S.W.;
RA Villalón D.K.; Muzny D.M.; Sodergren E.J.; Lu X.; Gibbs R.A.;
RA Fahy J.; Helton E.; Kettelman M.; Madan A.; Rodriguez S.; Sanchez A.;
RA Whiting M.; Madan A.; Young A.C.; Shevchenko Y.; Bouffard G.G.;
RA Blakeley R.W.; Touchman J.W.; Green E.D.; Dickson M.C.;
RA Rodriguez A.C.; Grimwood J.; Schmutz J.; Myers R.M.; Butterfield Y.S.;
RA Krzywinski M.I.; Skalska U.; Smalins D.E.; Schnerch A.; Schein J.E.;
RA Jones S.J.; Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Straussberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC024289; AAH24289.1; -.
KW Hypothetical protein.
SQ SEQUENCE 471 AA; 51791 MW; 388F7F4CF588660E CRC64;

Query Match 73.6%; Score 459.5; DB 2; Length 471;
Best Local Similarity 73.8%; Pred. No. 1.2e-39;
Matches 90; Conservative 15; Mismatches 14; Indels 3; Gaps 2;

QY 1 EVOLVESGGGVDPGGSLRVSCAASGPAFESHYMSWVRQAPGKLEWVAIYSSGGSGTTY 60
DB 20 EVOLVESGGGVDPGGSLRVSCAASGFTFSSYAMNWVROAPGKLEWVAIYSSGGSGTTY 79
QY 61 SDSVKGRTISRDNKNTLYLQMSLRAPDSAVYFCTRVK-----VKGTY-YPDSMGQTLTY 117
DB 80 ADSVKGRTISRDNKNTLYLQMSLRAPDSAVYCARLDRLTSTYWFPLMGRTLVTV 139

QY 118 SS 119
DB 140 SS 141

RESULT 5
AAL35877 PRELIMINARY; PRT; 117 AA.
ID AAL35877;
AC AAL35877;
DT 02-MAR-2004 (TReMBLrel. 27, Created)

DT 02-MAR-2004 (TReMBLrel. 27, last sequence update)
DT 02-MAR-2004 (TReMBLrel. 27, last annotation update)
DE Immunoglobulin heavy chain variable domain (Fragment).
OS Lama glama (Llama).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Lama.
ON NCBI_TaxID=9844;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22007448; PubMed=12009207;
RA Tanha J., Dubuc G., Hirama T., Narang S.A., Mackenzie C.R.;
RT "selection by phage display of llama conventional V(H) fragments with
RT heavy chain antibody V(H) properties."
RL J. Immunol. Methods 263:97-109(2002).
DR EMBL; AF442946; AAL35877.1; -.
FT NON TER 1 1
FT SEQUENCE 117 AA; 12459 MW; 08F5E4BA02F98D1 CRC64;

Query Match 73.6%; Score 459; DB 2; Length 117;
Best Local Similarity 73.1%; Pred. No. 2.6e-40;
Matches 87; Conservative 14; Mismatches 16; Indels 2; Gaps 1;

QY 1 EVOLVESGDFVPGGSLRVSCAASGAFSHYMSWRQAPGKLEWVAIYSSGSGSTYY 60
DB 1 EVOLVSGGGLVPGGSLRVSCAASGFTFSGYAMSWRQAPGKLEWVSSINSGSGSTYY 60
QY 61 SDSVKGFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLTGYTYPDSWGQGLTLTVSS 119
DB 61 ADSVKGFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLTGYTYPDSWGQGLTLTVSS 117

RESULT 6
BAD00534 PRELIMINARY; PRT; 124 AA.

AC BAD00534;
DT 02-MAR-2004 (TReMBLrel. 27, Created)
DT 02-MAR-2004 (TReMBLrel. 27, last sequence update)
DT 02-MAR-2004 (TReMBLrel. 27, last annotation update)
DE Immunoglobulin heavy chain VHDJ region (Fragment).
GN IGTV.
OS Camelus dromedarius (Dromedary) (Arabian camel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
ON NCBI_TaxID=9838;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Spine;
RA Honda T., Akahori Y., Kurosawa Y.;
RT "libraries of heavy-chain antibodies reflecting camel gamma2 and
RT gamma3 in vivo repertoires."
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB092172; BAD00534.1; -.
FT NON TER 1 1
FT SEQUENCE 124 AA; 13421 MW; B31996777375A27E CRC64;

Query Match 73.2%; Score 457; DB 2; Length 124;
Best Local Similarity 70.2%; Pred. No. 4.6e-40;
Matches 85; Conservative 16; Mismatches 18; Indels 2; Gaps 1;

QY 1 EVOLVESGDFVPGGSLRVSCAASGAFSHYMSWRQAPGKLEWVAIYSSGSGSTYY 60
DB 1 QVOLVESGGLVPGGSLRVSCAASGFTFSGYAMSWRQAPGKLEWVSSINSGSGSTYY 60
QY 61 SDSVKGFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLTGYTYPDS--WGQGLTLTVS 118
DB 61 ADSVKGFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLTGYTYPDS--WGQGLTLTVS 120
QY 119 S 119
DB 121 S 121

RESULT 7

Q6MZU6 PRELIMINARY; PRT; 464 AA.
AC Q6MZU6;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, last sequence update)
DE Hypothetical protein DKFP686C15213.
GN Name=DKFP686C15213;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
ON NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Human rectum tumor;
RA THE GERMAN HUMAN CDNA CONSORTIUM;
RA Bloecher H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640874; CAE45931.1; -.
DR InterPro; IPR003599; Ig-like.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003066; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; Ig; 2.
DR SMART; SM00407; IGL1; 3.
DR SMART; SM00406; IG; 1.
DR PROSITE; PSS0835; IG_LIKE; 4.
DR PROSITE; PSS0290; IG_MHC; UNKNOWN_2.
KM Hypothetical protein.

QY SEQUENCE 464 AA; 51099 MW; 2FCA72C66B8A0ABC CRC64;

Query Match 73.1%; Score 456; DB 2; Length 464;
Best Local Similarity 75.0%; Pred. No. 2.7e-39;
Matches 90; Conservative 13; Mismatches 15; Indels 2; Gaps 2;

QY 1 EVOLVESGDFVPGGSLRVSCAASGAFSHYMSWRQAPGKLEWVAIYSSGSGSTY 59
DB 20 EVOLVSGGGLVPGGSLRVSCAASGFTFSGYAMSWRQAPGKLEWVSSINSGSGSTY 79
QY 60 YSDSVKGFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLTGYTYPDSWGQGLTLTVSS 119
DB 80 YADVKGFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLTGYTYPDSWGQGLTLTVSS 138

RESULT 8

CAE45931 PRELIMINARY; PRT; 464 AA.

AC CAE45931;
DT 02-MAR-2004 (TReMBLrel. 27, Created)
DT 02-MAR-2004 (TReMBLrel. 27, last sequence update)
DT 02-MAR-2004 (TReMBLrel. 27, last annotation update)
DE Hypothetical protein DKFP686C15213.
GN DKFP686C15213.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
ON NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Human rectum tumor;
RA Bloecher H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640874; CAE45931.1; -.
KM Hypothetical protein.
QY SEQUENCE 464 AA; 51099 MW; 2FCA72C66B8A0ABC CRC64;

```

Query Match      73.1%; Score 456; DB 2; Length 464;
Best Local Similarity 75.0%; Pred. No. 2.7e-39;
Matches 90; Conservative 13; Mismatches 15; Indels 2; Gaps 2;

QY 1 EVOLVESGDFVOPGSLRVSCAASGFAFSGHYMSWVRQAPGKLEWVAYISSGSGCTY 59
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 20 EVOLVESGGGLVPGGSLRLSCAASGFTFSISYMNWVRQAPGKLEWVSSFSFGSSEY 79
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 60 YDSVKRFTISRDNKNTLYLQNRSLRAEDSAVYFCTRVKLGTYFPDSWGQTLTVSS 119
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 80 YDSVKRFTISRDNKNTLYLQNRSLRAEDTAVYCAR-DLGMFGLDYWGQGLTVTVSS 138
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

RESULT 9
Q6PJ4 06PJ4 PRELIMINARY; PRT; 470 AA.
ID 06PJ4;
AC 06PJ4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pabey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butcherfield Y.S.,
RA Krzywniński M.I., Skalska U., Smallus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DB EMBL, BC018747, AA018747.1; -.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003597; Ig cl.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig v.
DR Pfam: PF07654; Cl-sec; 3.
DR Pfam: PF00047; Ig; 4.
DR SMART: SM00409; Ig; 2.
DR SMART: SM00407; IGL1; 3.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PSS0835; IG_LIKE; 4.
DR PROSITE: PSS00290; IG_MHC; UNKNOWN_2.
KM Hypothetical protein.
SQ SEQUENCE 470 AA; 51715 MW; 7B49556A11FD7D99 CRC64;

Query Match      73.1%; Score 456; DB 2; Length 470;
Best Local Similarity 74.4%; Pred. No. 2.7e-39;
Matches 90; Conservative 7; Mismatches 22; Indels 2; Gaps 1;

```

```

QY 1 EVOLVESGDFVOPGSLRVSCAASGFAFSGHYMSWVRQAPGKLEWVAYISSGSGCTY 60
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 20 EVOLVESGGGLVPGGSLRLSCVSGFTFSYMNWVRQAPGKLEWVANI KDDGSEKYY 79
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 61 SDSVKRFTISRDNKNTLYLQNRSLRAEDSAVYFCTRVKLGTY--YFDSWGQTLTVSS 118
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 80 VDSVKRFTISRDNKNTLYLQNRSLRAEDTAVYCARDDSSWYRDWFDPMGGQTLTVSS 139
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

RESULT 10
AA018747 06PJ4 PRELIMINARY; PRT; 470 AA.
ID AA018747;
AC AA018747;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pabey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butcherfield Y.S.,
RA Krzywniński M.I., Skalska U., Smallus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DB EMBL, BC018747, AA018747.1; -.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003597; Ig cl.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig v.
DR Pfam: PF07654; Cl-sec; 3.
DR Pfam: PF00047; Ig; 4.
DR SMART: SM00409; Ig; 2.
DR SMART: SM00407; IGL1; 3.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PSS0835; IG_LIKE; 4.
DR PROSITE: PSS00290; IG_MHC; UNKNOWN_2.
KM Hypothetical protein.
SQ SEQUENCE 470 AA; 51715 MW; 7B49556A11FD7D99 CRC64;

Query Match      73.1%; Score 456; DB 2; Length 470;
Best Local Similarity 74.4%; Pred. No. 2.7e-39;
Matches 90; Conservative 7; Mismatches 22; Indels 2; Gaps 1;

```

```

Db          140 S 140

RESULT 11
BAD00491    PRELIMINARY;      PRT;      125 AA.
AC          BAD00491;
DT          02-MAR-2004 (TReMBLrel. 27, Created)
DT          02-MAR-2004 (TReMBLrel. 27, Last sequence update)
DT          02-MAR-2004 (TReMBLrel. 27, Last annotation update)
DE          Immunoglobulin heavy chain VHDJ region (Fragment).
GN          IGHV.
OS          Camelus dromedarius (Dromedary) (Arabian camel).
OC          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC          Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
OX          NCBI_TaxID=9838;
RN          [1]
RP          SEQUENCE FROM N.A.
RC          TISSUE=Spleen;
RA          Honda T., Akahori Y., Kurosawa Y.;
RT          "Libraries of heavy-chain antibodies reflecting camel gamma2 and
RT          gamma3 in vivo repertoires."
RL          Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR          EMBL; AF092129; BAD00491.1; -.
FT          NON_TER      1
FT          NON_TER      125
SQ          SEQUENCE      125 AA; 13593 MW; F1637892B028E48C CRC64;

Query Match      73.0%; Score 455.5; DB 2; Length 125;
Best Local Similarity 70.5%; Pred. No. 6,7e-40;
Matches      86; Conservative 17; Mismatches 16; Indels 3; Gaps 1;

QY          1 EVOLVESGGDFVPGGSLRVSCAASGFAFSHVMSWVRQAPGKLEWVAIYSSGGSGTYY 60
DB          1 EVOLVESGGGVVPGGSLRLSCAASGFTFSYGMHWVRQAPGKLEWVAIINSGGSGTYY 60
QY          61 SDSVKGRFTISRNSKNTLYLQWNSLRADSDAVYFCTRYVLTGYT--FDSWGGTLLTV 117
DB          61 TEEVKGRFTISRDNKNTLYVGFNSLKTEDTAVYCAKGYNSDIDRTFAMWGQGTIVTV 120
QY          118 SS 119
DB          121 SS 122

RESULT 12
Q8WUK1      PRELIMINARY;      PRT;      613 AA.
AC          Q8WUK1;
DT          01-MAR-2002 (TReMBLrel. 20, Created)
DT          01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT          01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE          IGHM protein.
OS          Homo sapiens (human).
OC          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC          Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX          NCBI_TaxID=9606;
RN          [1]
RP          SEQUENCE FROM N.A.
RC          TISSUE=Primary B-Cells;
RA          MEDLINE=23388257; PubMed=12477932;
RA          Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA          Altschul S.F., Zeeberg B., Bietow K.H., Schaefer C.F., Bhat N.K.,
RA          Hopkins R.F., Jordan H., Moore T., Max S.T., Wang J., Heien F.,
RA          Dlatchevo L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA          Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Schaefer T.E.,
RA          Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA          Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA          Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA          Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA          Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA          Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,

```

```

RA          Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA          Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA          Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA          Krzywinski M.I., Skalek U., Smalhus D.E., Scherch A., Schein J.E.,
RA          Jones S.J., Marra M.A.;
RT          "Generation and initial analysis of more than 15,000 full-length human
RT          and mouse cDNA sequences."
RL          Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN          [2]
RP          SEQUENCE FROM N.A.
RC          TISSUE=Primary B-Cells;
RA          Strausberg R.;
RL          Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR          EMBL; BC020240; AAH02040.1; -.
DR          PIR; F36005; F36005.
DR          PIR; G36005; G36005.
DR          PIR; PH1642; PH1642.
DR          PIR; PH1643; PH1643.
DR          PIR; PH1645; PH1645.
DR          PIR; PH1646; PH1646.
DR          PIR; PL0098; PL0098.
DR          PIR; PL0120; PL0120.
DR          PIR; S15590; S15590.
DR          PIR; S31116; S31116.
DR          PIR; S31119; S31119.
DR          PIR; S70442; S70442.
DR          HSSP; P01861; IADQ.
DR          InterPro; IPR007110; Ig-like.
DR          InterPro; IPR003597; Ig_C1.
DR          InterPro; IPR003006; Ig_MHC.
DR          InterPro; IPR003596; Ig_V.
DR          Pfam; PF07654; C1-set; 4.
DR          Pfam; PF00047; Ig_1.
DR          SMART; SM00406; IGV; 1.
DR          PROSITE; PSS0835; IG_LIKE; 5.
DR          PROSITE; PSS0290; IGMHC; UNKNOWN_3.
SQ          SEQUENCE      613 AA; 67295 MW; 60C7F5950671B315 CRC64;

Query Match      73.0%; Score 455.5; DB 2; Length 613;
Best Local Similarity 75.0%; Pred. No. 4,2e-39;
Matches      90; Conservative 8; Mismatches 21; Indels 1; Gaps 1;

QY          1 EVOLVESGGDFVPGGSLRVSCAASGFAFSHVMSWVRQAPGKLEWVAIYSSGGSGTYY 60
DB          20 QVQLVSGGQVVPGRSLRLSCAASGFTFSYGMHWVRQAPGKLEWVAIYSDGSNKYY 79
QY          61 SDSVKGRFTISRNSKNTLYLQWNSLRADSDAVYFCTRYVLTGYT--FDSWGGTLLTVSS 119
DB          80 ADSVKGRFTISRNSKNTLYLQWNSLRADSDAVYCAKOWSEGEVETFDIWGGGTWTVSS 139

RESULT 13
Q9UL90      PRELIMINARY;      PRT;      113 AA.
AC          Q9UL90;
DT          01-MAY-2000 (TReMBLrel. 13, Created)
DT          01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT          01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE          Myosin-reactive immunoglobulin heavy chain variable region
DE          (fragment).
OS          Homo sapiens (human).
OC          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC          Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX          NCBI_TaxID=9606;
RN          [1]
RP          SEQUENCE FROM N.A.
RC          MEDLINE=9827139; PubMed=9614934;
RA          Wu X., Liu B., Van der Werwe P.L., Kalie N.N., Berny S.M.,
RA          Young D.C.;
RT          "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT          fetus."
RL          Clin. Immunol. Immunopathol. 87:184-192 (1998).
DR          EMBL; AF035024; AAD56260.1; -.

```


DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGI; 3.
DR SMART; SM00406; IGI; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 478 AA; 52666 MW; 17BED38D917970D6 CRC64;

Query Match 72.8%; Score 454; DB 2; Length 478;
Best Local Similarity 71.3%; Pred. No. 4,5e-39;
Matches 92; Conservative 7; Mismatches 20; Indels 10; Gaps 2;

QY 1 EVOLVESGDFVQPGGSLRVSCAASGPAFESHYMSVWROAPGKLEWAVYISSGSGCTTY 60
DB 20 EVOLVESGGGLVQPGGSLRLSCAASGFTFSYMSVWROAPGKLEWAVANIKODGSEKTY 79
QY 61 SDVSKRFTISRNSKNTLYLQWRSLRAEDSAVYFCTR-----VKGTTF--DSWG 110
DB 80 VDSVKRFTISRNSKNTLYLQWRSLRAEDTAVYCARPEFESTMTTNADYYFYNDVWG 139
QY 111 OGTLTVSS 119
DB 140 KGTITVSS 148

RESULT 16
AAH41037 PRELIMINARY; PRT; 478 AA.

AC AAH41037
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22386257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,
RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares W.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Heiton E., Kettelman M., Nahan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywiński M.I., Szalka U., Smallin D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC041037; AAH41037.1; -.
KW Hypothetical protein.
SQ SEQUENCE 478 AA; 52666 MW; 17BED38D917970D6 CRC64;

Query Match 72.8%; Score 454; DB 2; Length 478;
Best Local Similarity 71.3%; Pred. No. 4,5e-39;
Matches 92; Conservative 7; Mismatches 20; Indels 10; Gaps 2;

QY 1 EVOLVESGDFVQPGGSLRVSCAASGPAFESHYMSVWROAPGKLEWAVYISSGSGCTTY 60
DB 20 EVOLVESGGGLVQPGGSLRLSCAASGFTFSYMSVWROAPGKLEWAVANIKODGSEKTY 79
QY 61 SDVSKRFTISRNSKNTLYLQWRSLRAEDSAVYFCTR-----VKGTTF--DSWG 110
DB 80 VDSVKRFTISRNSKNTLYLQWRSLRAEDTAVYCARPEFESTMTTNADYYFYNDVWG 139
QY 111 OGTLTVSS 119
DB 140 KGTITVSS 148

RESULT 17
AAL35865 PRELIMINARY; PRT; 119 AA.

AC AAL35865
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Immunoglobulin heavy chain variable domain (fragment).
OS Lama glama (llama).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Lama.
OX NCBI_TaxID=9844;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22007448; PubMed=12009207;
RA Tanha J., Dubuc G., Hirama T., Naring S.A., Mackenzie C.R.;
RT "Selection by phage display of llama conventional V(H) fragments with
heavy chain antibody V(H)H properties.";
RL J. Immunol. Methods 263:97-109(2002).
DR EMBL; AF442934; AAL35865.1; -.
FT NON_TER 1 119
FT NON_TER 1 119
SQ SEQUENCE 119 AA; 12650 MW; E4CDD04BF367A2D7 CRC64;

Query Match 72.6%; Score 453; DB 2; Length 119;
Best Local Similarity 73.1%; Pred. No. 1,2e-39;
Matches 87; Conservative 9; Mismatches 23; Indels 0; Gaps 0;

QY 1 EVOLVESGDFVQPGGSLRVSCAASGPAFESHYMSVWROAPGKLEWAVYISSGSGCTTY 60
DB 1 EVOLVESGGGLVQPGGSLRLSCAASGFTFSYMSVWROAPGKLEWAVANIKODGSEKTY 79
QY 61 SDVSKRFTISRNSKNTLYLQWRSLRAEDSAVYFCTRVLTGYYPDSWGCGTLTVSS 119
DB 61 ADSVKRFTISRNSKNTLYLQWRSLRAEDTAVYCARAHGTYGARGSGWGQGTIVSS 119

RESULT 18

Q9UL91 PRELIMINARY; PRT; 118 AA.

AC Q9UL91
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 26, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (fragment).
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9827139; PubMed=9614934;
RA Wu X., Liu B., Van der Werwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus.";
RT Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035023; AAD56259.1; -.

```
DR PIR; PH0875; PH0875.
DR PIR; S21205; S21205.
DR PIR; S30531; S30531.
DR HSP; P01783; IIGC.
DR InterPro; IPR007110; Ig_Like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Ig; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON TER 1
FT NON TER 118
SQ SEQUENCE 118 AA; 12843 MW; D0633949F2AC149D CRC64;

Query Match 72.4%; Score 451.5; DB 2; Length 118;
Best Local Similarity 74.6%; Pred. No. 1.6e-39;
Matches 88; Conservative 12; Mismatches 17; Indels 1; Gaps 1;

QY 1 EVOLVSGGDFVOPGSGSLRVSCAAGFAFSHYAMSVWRQAPGKGLMWAVYISSGGSGTTY 60
DB 1 EVOLVSGGGLVOPGSGSLRLSCAAGFTFSYSMMVWRQAPGKGLMWVSYISSSTITITY 60
QY SDSVKRFTISRNSKNTLYLQKRSIARAEDSAVYFCFTR-----VKGTTFPDSMGQTLT 118
DB 61 SDSVKRFTISRNSKNTLYLQKRSIARAEDSAVYFCFTR-----VKGTTFPDSMGQTLT 115
DB 61 ADSVKRFTISRNSKNTLYLQKRSIARAEDSAVYFCFTR-----VKGTTFPDSMGQTLT 120
QY 116 TVSS 119
DB 121 TVSS 124

RESULT 20
Q6GMV2 PRELIMINARY; PRT; 606 AA.
AC 06GMV2;
DT 05-JUL-2004 (TREMblrel. 27, Created)
```

```
DT 05-JUL-2004 (TREMblrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMblrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
ON NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932;
RA Klausner R.D., Collins F.S., Wagner L., Shemmen G.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marcusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Shapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toehlyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073758; AAH73758.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig_Like.
DR InterPro; IPR003597; Ig_C1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-setc 4.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; Ig; 2.
DR SMART; SM00407; IGL1; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 5.
DR PROSITE; PS00250; IG_MHC; UNKNOWN_3.
KW Hypothetical protein.
SQ SEQUENCE 606 AA; 66184 MW; B6B38B5114E4C55 CRC64;

Query Match 72.4%; Score 451.5; DB 2; Length 606;
Best Local Similarity 67.2%; Pred. No. 1.1e-38;
Matches 90; Conservative 12; Mismatches 17; Indels 15; Gaps 2;

QY 1 EVOLVSGGDFVOPGSGSLRVSCAAGFAFSHYAMSVWRQAPGKGLMWAVYISSGGSGTTY 60
DB 20 EVOLVSGGGLVOPGSGSLRLSCAAGFTFSYSMMVWRQAPGKGLMWVSYISSSTITITY 79
QY SDSVKRFTISRNSKNTLYLQKRSIARAEDSAVYFCFTR-----VKGTTFPDSMGQTLT 106
DB 61 SDSVKRFTISRNSKNTLYLQKRSIARAEDSAVYFCFTR-----VKGTTFPDSMGQTLT 106
DB 80 ADSVKRFTISRNSKNTLYLQKRSIARAEDSAVYFCFTR-----VKGTTFPDSMGQTLT 139
QY 107 TVSS 119
DB 140 MDVWGQGITVTVSS 153

RESULT 21
BAD00448 PRELIMINARY; PRT; 125 AA.
AC BAD00448;
DT 05-JUL-2004 (TREMblrel. 27, Created)
```


DT 02-MAR-2004 (TREMBlrel. 27, Created)
DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)
DE Immunoglobulin heavy chain VHJ region (Fragment).
GN IGVH.
OS Camelus dromedarius (Dromedary) (Arabian camel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
OX NCBI_TaxID=9838;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Honda T., Akahori Y., Kurosawa Y.;
RT "Libraries of heavy-chain antibodies reflecting camel gamma2 and
RT gamma3 in vivo repertoires."
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB092086; BAD00448.1; -.
FT NON_TER 1
FT NON_TER 125
SQ SEQUENCE 125 AA; 13671 MW; C04D1D2DA57PDCDB CRC64;

Query Match 72.0%; Score 449.5; DB 2; Length 125;
Best Local Similarity 71.3%; Pred. No. 2.8e-39;
Matches 87; Conservative 16; Mismatches 16; Indels 3; Gaps 2;

QY 1 EVOLVESGDFVPGGSLRVSACAAGFAFSHYAMSWROAPGKLEWAVYISSGSGSTYY 60
1 EVOLVESGGLVPGGSLRLSCAASGFTFNMDMSWRQAPGKGLDVSIVNSGSGSTYY 60
DB 1 EVOLVESGGLVPGGSLRLSCAASGFTFNMDMSWRQAPGKGLDVSIVNSGSGSTYY 60
QY 61 SDSVKGRFTISRDNKNTLYLQNRSLRAEDSAVYFC-TRYVLTGYTF--DSWGQTLTIV 117
61 ADSVKGRFTISRDNKNTLYLQNMNVKPEDTAVYVCTRRGDGWDYSDMYWKGKTLVTI 120
DB 118 SS 119
QY 121 SS 122
DB 121 SS 122

RESULT 22

BAD00510 PRELIMINARY; PRT; 126 AA.

AC BAD00510;
DT 02-MAR-2004 (TREMBlrel. 27, Created)
DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)
DE Immunoglobulin heavy chain VHJ region (Fragment).
GN IGVH.
OS Camelus dromedarius (Dromedary) (Arabian camel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
OX NCBI_TaxID=9838;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Honda T., Akahori Y., Kurosawa Y.;
RT "Libraries of heavy-chain antibodies reflecting camel gamma2 and
RT gamma3 in vivo repertoires."
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB092148; BAD00510.1; -.
FT NON_TER 1
FT NON_TER 126
SQ SEQUENCE 126 AA; 13665 MW; A0358DPDFBFB6E CRC64;

Query Match 72.0%; Score 449; DB 2; Length 126;
Best Local Similarity 69.1%; Pred. No. 3.2e-39;
Matches 85; Conservative 15; Mismatches 19; Indels 4; Gaps 1;

QY 1 EVOLVESGDFVPGGSLRVSACAAGFAFSHYAMSWROAPGKLEWAVYISSGSGSTYY 60
1 EVOLVESGGLVPGGSLRLSCAASGFTFNMDMSWRQAPGKGLDVSIVNSGSGSTYY 60
DB 1 EVOLVESGGLVPGGSLRLSCAASGFTFNMDMSWRQAPGKGLDVSIVNSGSGSTYY 60
QY 61 SDSVKGRFTISRDNKNTLYLQNRSLRAEDSAVYFC-TRYVLTGYTF--YFDSWGQTLTIV 116
61 ADSVKGRFTISRDNKNTLYLQNMNVKPEDTAVYVCTRRGDGWDYSDMYWKGKTLVTI 120

DB 61 ADSVKGRFTISRDNKNTLYLQNRSLRAEDSAVYFC-TRYVLTGYTF--YFDSWGQTLTIV 120
QY 117 VSS 119
DB 121 ISS 123

RESULT 23

Q9UL72 PRELIMINARY; PRT; 118 AA.

AC Q9UL72;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berny S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus."
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
DR EMBL: AF035042; AAD56278.1; -.
DR FPI; S21205; S21205.
DR HSSP; P01783; 11GC.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGV_1.
DR PROSITE; PS50835; IG_Like; 1.
FT NON_TER 1
FT NON_TER 118
SQ SEQUENCE 118 AA; 12872 MW; B4D1A5944B2D5CCA CRC64;

Query Match 71.9%; Score 448.5; DB 2; Length 118;
Best Local Similarity 74.8%; Pred. No. 3.4e-39;
Matches 89; Conservative 10; Mismatches 19; Indels 1; Gaps 1;

QY 1 EVOLVESGDFVPGGSLRVSACAAGFAFSHYAMSWROAPGKLEWAVYISSGSGSTYY 60
1 EVOLVESGGLVPGGSLRLSCAASGFTVSNMNVWRQAPGKGLSVSYTSGGS-SY 59
DB 1 EVOLVESGGLVPGGSLRLSCAASGFTVSNMNVWRQAPGKGLSVSYTSGGS-SY 59
QY 61 SDSVKGRFTISRDNKNTLYLQNRSLRAEDSAVYFC-TRYVLTGYTF--YFDSWGQTLTIV 119
61 ADSVKGRFTISRDNKNTLYLQNMNVKPEDTAVYVCTRRGDGWDYSDMYWKGKTLVTI 120
DB 60 ADSVKGRFTISRDNKNTLYLQNMNVKPEDTAVYVCTRRGDGWDYSDMYWKGKTLVTI 120

RESULT 24

BAD00459 PRELIMINARY; PRT; 121 AA.

AC BAD00459;
DT 02-MAR-2004 (TREMBlrel. 27, Created)
DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)
DE Immunoglobulin heavy chain VHJ region (Fragment).
GN IGVH.
OS Camelus dromedarius (Dromedary) (Arabian camel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
OX NCBI_TaxID=9838;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Honda T., Akahori Y., Kurosawa Y.;
RT "Libraries of heavy-chain antibodies reflecting camel gamma2 and
RT gamma3 in vivo repertoires."
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.

QY 1 EVOLVESGDFVPGGSLRVSACAAGFAFSHYAMSWROAPGKLEWAVYISSGSGSTYY 60
1 EVOLVESGGLVPGGSLRLSCAASGFTVSNMNVWRQAPGKGLSVSYTSGGS-SY 59
DB 1 EVOLVESGGLVPGGSLRLSCAASGFTVSNMNVWRQAPGKGLSVSYTSGGS-SY 59
QY 61 SDSVKGRFTISRDNKNTLYLQNRSLRAEDSAVYFC-TRYVLTGYTF--YFDSWGQTLTIV 119
61 ADSVKGRFTISRDNKNTLYLQNMNVKPEDTAVYVCTRRGDGWDYSDMYWKGKTLVTI 120

```
DR EMBL; AB092097; BAD00459.1; -.
FT NON TER 1
FT NON TER 121 121
SQ SEQUENCE 121 AA; 12957 MW; A55F627A3F977A6D CRC64;

Query Match
Best Local Similarity 71.9%; Score 448.5; DB 2; Length 121;
Matches 85; Conservative 18; Mismatches 15; Indels 1; Gaps 1;

QY 1 EVOLVSGGDFVPGGSLRVSCAASGPAFSPHYAMSWROAPGKGLWVAVYISSGSGCTTY 60
Db 1 EVOLVSGGGLVPGGSLRLSCAASGFTFRNVMNWRQAPGKGLWVAVYISSGSGSNWY 60

QY 61 SDSVKGRFTISRDNSKNTLYLQMRSLRAEDSAVYFCTRYVLGTYPDSSWGCGT 113
Db 61 ADSVKGRFTISRDNAKNTLYLQNLSTKTEDTAVYYCVK-NPSTWYFELMGQTLVTVSS 118

RESULT 25
Q6M2Q6 PRELIMINARY; PRT; 475 AA.
ID Q6M2Q6;
AC Q6M2Q6;
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DE Hypothetical protein DKFZp686G1190.
GN Name=DKFZp686G1190;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human esophagus tumor;
RG THE GERMAN HUMAN CDNA CONSORTIUM;
RA Lauber J., Bahr A., Mewes H.W., Well B., Amid C., Oanger A., Fobo G.,
RA Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640947; CAE45972.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-1ike.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003066; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 3.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 475 AA; 52043 MW; B7EAE255A26F4B8E CRC64;

Query Match
Best Local Similarity 71.9%; Score 448.5; DB 2; Length 475;
Matches 87; Conservative 13; Mismatches 19; Indels 7; Gaps 1;

QY 1 EVOLVSGGDFVPGGSLRVSCAASGPAFSPHYAMSWROAPGKGLWVAVYISSGSGCTTY 60
Db 20 EVOLVSGGGLVPGGSLRLSCAASGFTFRNVMNWRQAPGKGLWVAVYISSGSGVNTTY 79

QY 61 SDSVKGRFTISRDNSKNTLYLQMRSLRAEDSAVYFCTRYVLGTYPDSSWGCGT 113
Db 80 ADSVKGRFTISRDNSKNTLYLQMRSLRAEDTAVYYCARADYRYQVSPAYWYFDVWGRT 139

QY 114 LITVSS 119
Db 140 LVSUSA 145

RESULT 26
CAE45972
```

```
ID CAE45972 PRELIMINARY; PRT; 475 AA.
AC CAE45972;
DT 02-MAR-2004 (T-EMBLrel. 27, Created)
DT 02-MAR-2004 (T-EMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (T-EMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686G1190.
GN DKFZp686G1190.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primata; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human esophagus tumor;
RA Lauber J., Bahr A., Mewes H.W., Well B., Amid C., Oanger A., Fobo G.,
RA Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640947; CAE45972.1; -.
KW Hypothetical protein.
SQ SEQUENCE 475 AA; 52043 MW; B7EAE255A26F4B8E CRC64;

Query Match
Best Local Similarity 69.0%; Pred. No. 1.7e-38;
Matches 87; Conservative 13; Mismatches 19; Indels 7; Gaps 1;

QY 1 EVOLVSGGDFVPGGSLRVSCAASGPAFSPHYAMSWROAPGKGLWVAVYISSGSGCTTY 60
Db 20 EVOLVSGGGLVPGGSLRLSCAASGFTFRNVMNWRQAPGKGLWVAVYISSGSGVNTTY 79

QY 61 SDSVKGRFTISRDNSKNTLYLQMRSLRAEDSAVYFCTRYVLGTYPDSSWGCGT 113
Db 80 ADSVKGRFTISRDNSKNTLYLQMRSLRAEDTAVYYCARADYRYQVSPAYWYFDVWGRT 139

QY 114 LITVSS 119
Db 140 LVSUSA 145

RESULT 27
Q6GMX2 PRELIMINARY; PRT; 493 AA.
ID Q6GMX2;
AC Q6GMX2;
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,
RA Diatchenko L., Marisina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulhany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.W., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Munzy D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.B.,
RA Jones S.J., Marra M.A.;
RT "generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
```

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN (2)
RC SEQUENCE FROM N.A.
RA Tissue-Spleen;
RA Straussberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
EMBL: BC073771; AAH73771.1; -
DR InterPro: IPR003599; IG.
DR InterPro: IPR007110; IG-1ike.
DR InterPro: IPR003597; IG-1.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF07654; C1-set; 2.
DR Pfam: PF00447; IG; 3.
DR SMART: SM00409; IG; 4.
DR SMART: SM00407; IG1; 2.
DR SMART: SM00406; IG; 1.
DR PROSITE: PS50835; IG_Like; 4.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 493 AA; 52865 MW; 55B999305B286203 CRC64;

Query Match 71.6%; Score 447; DB 2; Length 493;
Best Local Similarity 73.6%; Pred. No. 2.6e-38;
Matches 89; Conservative 9; Mismatches 21; Indels 2; Gaps 1;

QY 1 EVOLVESGDFVPGGSLRVSCAASGAFPSHYMSVWRQAPGKLEWVAYISSGSGTYY 60
DB 20 EVOLVSGGGLVPGGSLRVSCAASGTFPSYMSVWRQAPGKLVWVSHINDSGSTY 79
QY 61 SDSVKGRFTISRDNKNLTLYLQMSLRAPDSAVYFCFTR--VKLTGYYPDSWGQTLTVS 118
DB 80 ADSVKGRFTISRDNKNLTLYLQMSLRGSDAAVYCARGVSLPRSTLDIWGGTWTVS 139
QY 119 S 119
DB 140 S 140

RESULT 28

BAD00225 PRELIMINARY; PRT; 126 AA.
ID BAD00225;
AC BAD00225;
DT 02-MAR-2004 (T-EMBLrel. 27, Created)
DT 02-MAR-2004 (T-EMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (T-EMBLrel. 27, Last annotation update)
DE Immunoglobulin heavy chain VHDJ region (Fragment).
GN IGVH.
OS Camelus dromedarius (Dromedary) (Arabian camel).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
OX NCBI_TaxID=9838;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral blood;
RA Honda T., Akahori Y., Kurosawa Y.;
RT "Libraries of heavy-chain antibodies reflecting camel gamma2 and
RT gamma3 in vivo repertoires";
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
EMBL: A0091863; BAD00225.1; -
FT NON_TER 1
FT NON_TER 126
SQ SEQUENCE 126 AA; 13717 MW; 486B1D741474BF26 CRC64;

Query Match 71.6%; Score 446.5; DB 2; Length 126;
Best Local Similarity 68.3%; Pred. No. 5.9e-39;
Matches 86; Conservative 17; Mismatches 16; Indels 7; Gaps 2;

QY 1 EVOLVESGDFVPGGSLRVSCAASGAFPSHYMSVWRQAPGKLEWVAYISSGSGTYY 60
DB 1 QVQLVDSGGGLVPGGSLRVSCAASGTFPSGYMSVWRQAPGKLEWVSHINDSGSTYY 60
QY 61 SDSVKGRFTISRDNKNLTLYLQMSLRAPDSAVYFCFTRVL--GTYT-----PDSWGQGT 113

DB 61 ADSVKGRFTISRDNKNLTLYLQMSLRKTEDTAVYCAKOLFQGGSNYKOLHGFNMGQT 120
QY 114 LRTVSS 119
DB 121 QVTVSS 126

RESULT 29

Q920E7 PRELIMINARY; PRT; 119 AA.
ID Q920E7;
AC Q920E7;
DT 01-DEC-2001 (T-EMBLrel. 19, Created)
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Pterin-mimicking anti-idiotypic heavy chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Atkin J.D., Tabe A., Jennings I.G., Horatis O., Cotton R.G.H.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
EMBL: AF307937; AAL09421.1; -
DR PIR; C25913; C25913.
DR HSP; P01783; IIGC.
DR InterPro: IPR007110; IG-1like.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF00447; IG; 1.
DR SMART: SM00406; IG; 1.
DR PROSITE: PS50835; IG_Like; 1.
FT NON_TER 1
FT NON_TER 119
SQ SEQUENCE 119 AA; 13025 MW; F6B904044381CA7C CRC64;

Query Match 71.5%; Score 446; DB 2; Length 119;
Best Local Similarity 73.6%; Pred. No. 6.3e-39;
Matches 89; Conservative 11; Mismatches 17; Indels 4; Gaps 2;

QY 1 EVOLVESGDFVPGGSLRVSCAASGAFPSHYMSVWRQAPGKLEWVAYISSGSGTYY 60
DB 1 EVOLVSGGGLVPGGSLRVSCAASGTFPSYMSVWRQPPDRLEWVAYISSGSGTYY 60
QY 61 SDSVKGRFTISRDNKNLTLYLQMSLRAPDSAVYFCFTRVLTGY--YFDSWGQTLTVS 118
DB 61 PDSVKGRFTISRDNKNLTLYLQMSLRKSEDTAVYCAR--HGDDYDVFAYWGQTLTVS 118
QY 119 S 119
DB 119 A 119

RESULT 30

BAD00420 PRELIMINARY; PRT; 126 AA.
ID BAD00420;
AC BAD00420;
DT 02-MAR-2004 (T-EMBLrel. 27, Created)
DT 02-MAR-2004 (T-EMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (T-EMBLrel. 27, Last annotation update)
DE Immunoglobulin heavy chain VHDJ region (Fragment).
GN IGVH.
OS Camelus dromedarius (Dromedary) (Arabian camel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
OX NCBI_TaxID=9838;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Honda T., Akahori Y., Kurosawa Y.;
RT "Libraries of heavy-chain antibodies reflecting camel gamma2 and
RT gamma3 in vivo repertoires";

QY 1 EVOLVESGDFVPGGSLRVSCAASGAFPSHYMSVWRQAPGKLEWVAYISSGSGTYY 60
DB 1 QVQLVDSGGGLVPGGSLRVSCAASGTFPSGYMSVWRQAPGKLEWVSHINDSGSTYY 60
QY 61 SDSVKGRFTISRDNKNLTLYLQMSLRAPDSAVYFCFTRVL--GTYT-----PDSWGQGT 113

RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB092058; BAD00420.1; -.
FT NON TER 1
FT NON TER 126
SQ SEQUENCE 126 AA; 13569 MW; A8F3B29E6C9BE29D CRC64;
Query Match
Best Local Similarity 71.5%; Score 446; DB 2; Length 126;
Matches 86; Conservative 15; Mismatches 16; Indels 8; Gaps 2;
QY 1 EVOLVESGGDFVQPGGSLRVSCAASGPAFSGHYAMSWVROAPGKGLEWVAYISGSGGTTY 60
DB 1 QVQLVSSGGLVQPGGSLRLSCAASGFTSTYMSWVROAPGKGLEWVSAINSGGSTYY 60
QY 61 SDSVKGRFTISRDNKNTLYLQWRSIARSDSAVYFCTRVKLGTYFPDS-----WGQGTLL 114
DB 61 ADSVKGRFTISRDNMAKNTLYLQNLSTKTEDTANYC--ANMDSLVDGNMLGYVMWGGQAQ 118
QY 115 LTVSS 119
DB 119 VTVSS 123
RESULT 31
BAD00525 PRELIMINARY; PRT; 121 AA.
AC BAD00525;
DT 02-MAR-2004 (TEMBLrel. 27, Created)
DT 02-MAR-2004 (TEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TEMBLrel. 27, Last annotation update)
DE Immunoglobulin heavy chain VHDJ region (Fragment).
GN IGVH.
OS Camelus dromedarius (Dromedary) (Arabian camel).
OC Eukaryota; Metazoa; Chordata; Cranialta; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
OX NCBI_TaxID=9838;
RN [1]_TaxID=9838;
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Honda T., Akahori Y., Kurosawa Y.;
RT "Libraries of heavy-chain antibodies reflecting camel gamma2 and
RT gamma3 in vivo repertoires.";
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB092163; BAD00525.1; -.
FT NON TER 1
FT NON TER 121
SQ SEQUENCE 121 AA; 12951 MW; A6D50E79D505ESB4 CRC64;
Query Match
Best Local Similarity 71.4%; Score 445.5; DB 2; Length 121;
Matches 85; Conservative 16; Mismatches 17; Indels 1; Gaps 1;
QY 1 EVOLVESGGDFVQPGGSLRVSCAASGPAFSGHYAMSWVROAPGKGLEWVAYISGSGGTTY 60
DB 1 DVQLVSSGGGLVQPGGSLRLSCAASGFTSTYMSWVROAPGKGLEWVSAINDGS--TYY 59
QY 61 SDSVKGRFTISRDNKNTLYLQWRSIARSDSAVYFCTRVKLGTYFPDSWGQGTLLTVSS 119
DB 60 ADSVKGRFTISRDNMAKNTLYLQNLSTKTEDTANYCYMDGSWASNALDAMWGQGTLLTVSS 118
RESULT 32
BAD00446 PRELIMINARY; PRT; 122 AA.
AC BAD00446;
DT 02-MAR-2004 (TEMBLrel. 27, Created)
DT 02-MAR-2004 (TEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TEMBLrel. 27, Last annotation update)
DE Immunoglobulin heavy chain VHDJ region (Fragment).
GN IGVH.
OS Camelus dromedarius (Dromedary) (Arabian camel).
OC Eukaryota; Metazoa; Chordata; Cranialta; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.

OX NCBI_TaxID=9838;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Honda T., Akahori Y., Kurosawa Y.;
RT "Libraries of heavy-chain antibodies reflecting camel gamma2 and
RT gamma3 in vivo repertoires.";
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB092084; BAD00446.1; -.
FT NON TER 1
FT NON TER 122
SQ SEQUENCE 122 AA; 13395 MW; 27043A8FC3A4771D CRC64;
Query Match
Best Local Similarity 71.2%; Score 444; DB 2; Length 122;
Matches 84; Conservative 14; Mismatches 21; Indels 0; Gaps 0;
QY 1 EVOLVESGGDFVQPGGSLRVSCAASGPAFSGHYAMSWVROAPGKGLEWVAYISGSGGTTY 60
DB 1 DVQLVSSGGGLVQPGGSLRLSCAASGFTSTYMTWVROAPGKGLEWVSGINDGSNTYY 60
QY 61 SDSVKGRFTISRDNKNTLYLQWRSIARSDSAVYFCTRVKLGTYFPDSWGQGTLLTVSS 119
DB 61 LDSVKGRFTISRDNMAKNTLYLQNLSTKSDTLALYCAWPEVYAGWVGWGGGTQVTVSS 119
RESULT 33
BAD00549 PRELIMINARY; PRT; 122 AA.
AC BAD00549;
DT 02-MAR-2004 (TEMBLrel. 27, Created)
DT 02-MAR-2004 (TEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TEMBLrel. 27, Last annotation update)
DE Immunoglobulin heavy chain VHDJ region (Fragment).
GN IGVH.
OS Camelus dromedarius (Dromedary) (Arabian camel).
OC Eukaryota; Metazoa; Chordata; Cranialta; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
OX NCBI_TaxID=9838;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Honda T., Akahori Y., Kurosawa Y.;
RT "Libraries of heavy-chain antibodies reflecting camel gamma2 and
RT gamma3 in vivo repertoires.";
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB092187; BAD00549.1; -.
FT NON TER 1
FT NON TER 122
SQ SEQUENCE 122 AA; 13354 MW; 1DC6AF409EB3A526 CRC64;
Query Match
Best Local Similarity 71.2%; Score 444; DB 2; Length 122;
Matches 83; Conservative 14; Mismatches 22; Indels 0; Gaps 0;
QY 1 EVOLVESGGDFVQPGGSLRVSCAASGPAFSGHYAMSWVROAPGKGLEWVAYISGSGGTTY 60
DB 1 QVQLVSSGGGLVQPGGSLRLSCAASGFTSTYMTWVROAPGKGLEWVSAINGGSDATYY 60
QY 61 SDSVKGRFTISRDNKNTLYLQWRSIARSDSAVYFCTRVKLGTYFPDSWGQGTLLTVSS 119
DB 61 PDSVKGRFTISRDNMAKNTLYLQNLSTKIDTATYCAKEIGEDYCFDYGQGTQVTVSS 119
RESULT 34
AAL35882 PRELIMINARY; PRT; 118 AA.
AC AAL35882;
DT 02-MAR-2004 (TEMBLrel. 27, Created)
DT 02-MAR-2004 (TEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TEMBLrel. 27, Last annotation update)
DE Immunoglobulin heavy chain variable domain (Fragment).
GN Lama glama (Llama).
OS

```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Lama.
OX NCBI_TaxID=9844;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22007448; PubMed=12009207;
RA Tanha J., Dubuc G., Hiram T., Narang S.A., Mackenzie C.R.;
RT "Selection by phage display of llama conventional V(H) fragments with
RT heavy chain antibody V(H)H properties."
RL J. Immunol. Methods 263:97-109(2002).
DR EMBL: AF442951; AAL35882.1; -.
FT NON-TER
FT NON-TER
SQ SEQUENCE 118 AA; 12916 MW; B1127A094C16B57 CRC64;

Query Match 71.1%; Score 443.5; DB 2; Length 118;
Best Local Similarity 73.1%; Pred. No. 1.1e-38;
Matches 87; Conservative 11; Mismatches 20; Indels 1; Gaps 1;

QY 1 EVOLVESGDPVPGGSLRVSCAAGFAPSHYAMSWROAPGKLEWVAYISSGSGCTYY 60
DB 1 DVLQASGGGLVPGGSLRVSCAAGFTFSNHYHVMWROAPGKLEWVSTINIDGCTYY 60
QY 61 SDVKGKFTISRDNKNTLYLQNRSLRAEDSAVYFCTRVKLGTY----YFDSWGCTLL 119
DB 61 ADSVKGKFTISRDNKNTLYLQNRSLRAEDTALYYCVRDGCTRY-DYWGCGTQVTVSS 118

RESULT 35
BAD00424 PRELIMINARY; PRT; 129 AA.
ID BAD00424;
AC BAD00424;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Immunoglobulin heavy chain VHJ region (Fragment).
GN IGVH.
OS Camelus dromedarius (Dromedary) (Arabian camel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
OX NCBI_TaxID=9838;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Honda T., Akahori Y., Kurosawa Y.;
RT "Libraries of heavy-chain antibodies reflecting camel gamma2 and
RT gamma3 in vivo repertoires."
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB092062; BAD00424.1; -.
FT NON-TER
FT NON-TER
SQ SEQUENCE 129 AA; 13971 MW; 243F7C8B1A436C50 CRC64;

Query Match 71.1%; Score 443.5; DB 2; Length 129;
Best Local Similarity 68.5%; Pred. No. 1.3e-38;
Matches 87; Conservative 12; Mismatches 19; Indels 9; Gaps 2;

QY 1 EVOLVESGDPVPGGSLRVSCAAGFAPSHYAMSWROAPGKLEWVAYISSGSGCTYY 60
DB 1 DVLQASGGGLVPGGSLRVSCAAGFTFSNHYHVMWROAPGKLEWVSTISRAAGATYY 60
QY 61 SDVKGKFTISRDNKNTLYLQNRSLRAEDSAVYFCTRVKLGTY-----YFDSWGCG 112
DB 61 ADSVKGKFTISRDNKNTLYLQNRSLRAEDTGMWYCTQ-DPGDYSDATWTSQNGYWGCG 119
QY 113 TLLTVSS 119
DB 120 TVTVSS 126

RESULT 36
Q6MZV7 PRELIMINARY; PRT; 473 AA.
ID Q6MZV7

```

```

AC Q6MZV7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686C11235.
GN Name=DKFZp686C11235;
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human small intestine;
RA BLOECKER H., BOECKER M., MEWES H.W., WEIL B., AMID C., OSANGER A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: BX640853; CAB45920.1; -.
QY 1 EVOLVESGDPVPGGSLRVSCAAGFAPSHYAMSWROAPGKLEWVAYISSGSGCTYY 60
DB 20 EILVLSGGGLVPGGSLRVSCAAGFTFSFEMNVMWROAPGKLEWVSTISGNTVY 79
QY 61 SDVKGKFTISRDNKNTLYLQNRSLRAEDSAVYFCTRVKLGTY----YFDSWGCTLL 115
DB 80 ADSLQKFTISRDNKNTLYLQNRSLRAEDTAVYCARQNEHTSPWYPSFFDYWGCGILV 139
QY 116 TVSS 119
DB 140 TVSS 143

RESULT 37
CAB45920 PRELIMINARY; PRT; 473 AA.
ID CAB45920;
AC CAB45920;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686C11235.
GN DKFZp686C11235.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primata; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human small intestine;
RA BLOECKER H., BOECKER M., MEWES H.W., WEIL B., AMID C., OSANGER A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: BX640853; CAB45920.1; -.
QY 1 EVOLVESGDPVPGGSLRVSCAAGFAPSHYAMSWROAPGKLEWVAYISSGSGCTYY 60
DB 20 EILVLSGGGLVPGGSLRVSCAAGFTFSFEMNVMWROAPGKLEWVSTISGNTVY 79
QY 61 SDVKGKFTISRDNKNTLYLQNRSLRAEDSAVYFCTRVKLGTY----YFDSWGCTLL 115
DB 80 ADSLQKFTISRDNKNTLYLQNRSLRAEDTAVYCARQNEHTSPWYPSFFDYWGCGILV 139
QY 116 TVSS 119
DB 140 TVSS 143

Query Match 71.1%; Score 443.5; DB 2; Length 473;
Best Local Similarity 66.9%; Pred. No. 5.7e-38;
Matches 83; Conservative 18; Mismatches 18; Indels 5; Gaps 1;

```

```

Query Match      71.1%; Score 443.5; DB 2; Length 473;
Best Local Similarity 66.9%; Pred. No. 5,7e-36;
Matches 83; Conservative 18; Mismatches 18; Indels 5; Gaps 1;

QY 1 EVOLVESGDFVPGGSLRVSCAASGFAFESHYMSWVRQAPGKLEWVAIYSSGGSGTTY 60
DB 20 EIQLVESGGGLVPGGSLRVSCAASGFTFSSFYHMAWVRQAPGKLEWVAIYSSGNTVY 79
QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLTG-----YFDSWGQGTLL 115
DB 80 ADSLQGRFTISRDNKNTLYLQMRSLRAEDTAIVYCARQMRHNSPMWPSFPDVGQGLIV 139
QY 116 TVSS 119
DB 140 TVSS 143

RESULT 38
QY 09UL93 PRELIMINARY; PRT; 116 AA.
AC Q9UL93;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE 01-MAR-2004 (TREMBlrel. 25, Last annotation update)
DE Myosin-reactive Immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9827139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035021; AAD56257.1; -.
DR PIR; P1644; P1644.
DR PIR; P10120; P10120.
DR HSP; P01772; 2F84.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IgV_1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 116
SQ SEQUENCE 116 AA; 12434 MW; 0DA0348154DD6061 CRC64;

Query Match      71.0%; Score 443; DB 2; Length 116;
Best Local Similarity 76.5%; Pred. No. 1,3e-38;
Matches 91; Conservative 6; Mismatches 18; Indels 4; Gaps 2;

QY 2 VOLVESGDFVPGGSLRVSCAASGFAFESHYMSWVRQAPGKLEWVAIYSSGGSGTTY 61
DB 1 VOLVESGGGLVPGGSLRVSCAASGFTFSSFYHMAWVRQAPGKLEWVAIYSSGNTVY 60
QY 62 DSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLTGTYFDSWGQGTLLTVSS 119
DB 61 DSVKGRFTISRDNKNTLYLQMRSLRAEDTAIVYCARQMRHNSPMWPSFPDVGQGLIV 116

RESULT 39
QY AAL35875 PRELIMINARY; PRT; 117 AA.
AC AAL35875;
DT 02-MAR-2004 (TREMBlrel. 27, Created)
DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)
DE Immunoglobulin heavy chain variable domain (Fragment).
DE Lama glama (Llama).

```

```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Lama.
OX NCBI_TaxID=9844;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22007448; PubMed=12009207;
RA Tanha J., Dubuc G., Hirama T., Narang S.A., Mackenzie C.R.;
RT "Selection by phage display of llama conventional VH fragments with
RT heavy chain antibody V(H)H properties.";
RL J. Immunol. Methods 263:97-109(2002).
DR EMBL; AF442944; AAL35875.1; -.
FT NON_TER 1
FT NON_TER 117
SQ SEQUENCE 117 AA; 12416 MW; CA010A137CB01461 CRC64;

Query Match      71.0%; Score 443; DB 2; Length 117;
Best Local Similarity 71.4%; Pred. No. 1,3e-38;
Matches 85; Conservative 12; Mismatches 20; Indels 2; Gaps 1;

QY 1 EVOLVESGDFVPGGSLRVSCAASGFAFESHYMSWVRQAPGKLEWVAIYSSGGSGTTY 60
DB 1 EVOLVSGGGLVPGGSLRVSCAASGFTFSSFYHMAWVRQAPGKLEWVAIYSSGNTVY 60
QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLTGTYFDSWGQGTLLTVSS 119
DB 61 ADSVKGRFTISRDNKNTLYLQMRSLRAEDTAIVYCARQMRHNSPMWPSFPDVGQGLIV 117

RESULT 40
QY BAD00490 PRELIMINARY; PRT; 125 AA.
AC BAD00490;
DT 02-MAR-2004 (TREMBlrel. 27, Created)
DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)
DE Immunoglobulin heavy chain VHDJ region (Fragment).
DE IGvH.
OS Camelus dromedarius (Dromedary) (Arabian camel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
OX NCBI_TaxID=9838;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Spleen;
RA Honda T., Akahori Y., Kurosawa Y.;
RT "Libraries of heavy-chain antibodies reflecting camel gamma2 and
RT gamma3 in vivo repertoires.";
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB092128; BAD00490.1; -.
FT NON_TER 1
FT NON_TER 125
SQ SEQUENCE 125 AA; 13518 MW; F11D6CBE62BD171 CRC64;

Query Match      70.9%; Score 442.5; DB 2; Length 125;
Best Local Similarity 70.5%; Pred. No. 1,5e-38;
Matches 86; Conservative 12; Mismatches 21; Indels 3; Gaps 1;

QY 1 EVOLVESGDFVPGGSLRVSCAASGFAFESHYMSWVRQAPGKLEWVAIYSSGGSG 57
DB 1 QVOLVESGGGLVPGGSLRVSCAASGFTFSSFYHMAWVRQAPGKLEWVAIYSSGNTVY 60
QY 58 TYVSDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLTGTYFDSWGQGTLLTV 117
DB 61 TYVSDSVKGRFTISRDNKNTLYLQMRSLRAEDTAIVYCARQMRHNSPMWPSFPDVGQGLIV 120

QY 118 SS 119
DB 121 SS 122

Search completed: December 17, 2004, 19:14:45
Job time : 356.663 secs

```